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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 05:18:47 ; Search time 908.004 Seconds

(without alignments)  
17413.610 Million cell updates/sec

Title: US-10-688-676A-1

Perfect score: 2671

Sequence: 1 aagatgggtctctaccgcat.....aaataaaattggcaaaa 2671

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

- 1: Geneseqn1980s.\*
- 2: Geneseqn1990s.\*
- 3: Geneseqn2000s.\*
- 4: Geneseqn2001as.\*
- 5: Geneseqn2001bs.\*
- 6: Geneseqn2002as.\*
- 7: Geneseqn2002bs.\*
- 8: Geneseqn2003as.\*
- 9: Geneseqn2003bs.\*
- 10: Geneseqn2003cs.\*
- 11: Geneseqn2003ds.\*
- 12: Geneseqn2004as.\*
- 13: Geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2671	100.0	2671	6	ABK83964 Human cDN
2	2671	100.0	2671	12	Adj74847 Marker ge
3	2671	100.0	2707	12	Adq37893 DNA encod
4	2660	99.6	3103	9	Aad57515 Human enz
5	2644.2	99.0	2844	6	Ab160541 Human lip
6	1306	48.9	2048	10	Abt42155 Toxicity
7	1272	47.6	1992	12	Adj75763 Marker ge
8	1055.6	39.5	2311	13	Adso9997 Human the
9	1030.4	38.6	2302	13	Adso9995 Human the
10	1016.4	38.3	2368	13	Adq39008 Human SNP
11	1016.4	38.1	2867	13	Adq39009 Human SNP
12	1013.6	37.9	2343	3	Aac58018 Arachidon
13	918.6	34.4	2218	13	Adso9996 Human the
14	901.6	33.8	2227	13	Adsl1347 Human the
15	901.6	33.8	2227	13	Adsl1348 Human the
16	901.6	33.8	2227	13	Adsl1349 Human the
17	515.6	19.3	584	12	Adm99845 Human ALO
18	514	19.2	584	12	Adm99844 Human ALO
19	382.6	14.3	2420	3	Aad24665 Human 5-1
20	382.6	14.3	2484	3	AAA35131 Human ade

21	382.6	14.3	2484	3	AAF21253	Aaf21253 Human low
22	382.6	14.3	2484	10	ADe85077	Ad85077 Farnesy1
23	382.6	14.3	2484	10	ABz96947	Abz96947 Human nuc
24	382.6	14.3	2484	10	ACf63369	Acf63369 Human lip
25	382.6	14.3	2484	11	ABD20796	Abd20796 Human pul
26	382.6	14.3	2497	3	AAA35132	Aaa35132 Human ade
27	382.6	14.3	2497	3	AAF21254	Aaf21254 Human low
28	382.6	14.3	2497	6	ABL65632	Ab165632 Lung canc
29	382.6	14.3	2497	6	ABL67646	Ab167646 Oesophagu
30	382.6	14.3	2497	6	ABL67509	Ab167509 Thyroid c
31	382.6	14.3	2497	6	ABT11115	Abt11115 Human 5-1
32	382.6	14.3	2497	6	ABK83762	Abk83762 Human cDN
33	382.6	14.3	2497	6	AA24664	Aad24664 Human 5-1
34	382.6	14.3	2497	8	ACA89905	Aca89905 Gene diff
35	382.6	14.3	2497	8	ACC57722	Acc57722 Human 5-1
36	382.6	14.3	2497	10	ABz96948	Abz96948 Human nuc
37	382.6	14.3	2497	11	ADI31829	Adi31829 Human cDN
38	382.6	14.3	2497	11	ABD20797	Abd20797 Human pul
39	382.6	14.3	2497	13	ADP54501	Adp54501 Human PRO
40	382.6	14.3	2500	3	AAA35130	Aaa35130 Human ade
41	382.6	14.3	2500	3	AAF21252	Aaf21252 Human low
42	382.6	14.3	2500	10	ABz96946	Abz96946 Human nuc
43	382.6	14.3	2500	11	ABD20795	Abd20795 Human pul
44	382.6	14.3	11151	3	AAA35133	Aaa35133 Human ade
45	382.6	14.3	11181	3	AAF21255	Aaf21255 Human low

#### ALIGNMENTS

#### RESULT 1

ABK83964

ID ABK83964 standard; cDNA; 2671 BP.

XX AC ABK83964;

XX DT 14-AUG-2002 (first entry)

XX DE Human cDNA differentially expressed in granulocytic cells #535.

XX KW Human; ss; granulocytic cell; DNA chip; bacterial infection;  
 KW viral infection; parasitic infection; protozoal infection;  
 KW fungal infection; sterile inflammatory disease; psoriasis;  
 KW rheumatoid arthritis; glomerulonephritis; asthma; thrombosis;  
 KW cardiac reperfusion injury; renal reperfusion injury; ARDS;  
 KW adult respiratory distress syndrome; inflammatory bowel disease;  
 KW Crohn's disease; ulcerative colitis; periodontal disease;  
 KW granulocyte activation; chronic inflammation; allergy.

XX OS Homo sapiens.

XX PN WO200228999-A2.

XX PD 11-APR-2002.

XX PF 03-OCT-2001; 2001WO-US030821.

XX PR 03-OCT-2000; 2000US-0237189P.

XX (GENE-) GENE LOGIC INC.

XX Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;

XX WPI; 2002-435328/46.

XX PT Detecting granulocyte activation by detecting differential expression of  
 PT genes associated with granulocyte activation, which serves as diagnostic  
 PT markers that is useful for monitoring disease states and drug toxicity.

XX PS Claim 1; SEQ ID NO 535; 114pp; English.

XX CC The invention relates to detecting (M1) granulocyte (GC) activation  
 CC (GCA), by detecting the level of expression of gene(s) (Gs) identified by

DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GCA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g., psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above conditions. The present sequence represents a gene differentially expressed in granulocytes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences)

Sequence 2671 BP; 580 A; 743 C; 718 G; 630 T; 0 U; 0 Other;

Query Match 100.0%; Score 2671; DB 6; Length 2671;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGATGGGTCTTACCGCATCCGGGTGTCCACTGGGGCCCTCGCTCTATGCGGTTCGAAC 60  
Db 1 AAGATGGGTCTTACCGCATCCGGGTGTCCACTGGGGCCCTCGCTCTATGCGGTTCGAAC 60

Qy 61 AACAGGTGAGCTGTGGTGTGGCGAGCAGCGGGAGCGCGCTCGGGAAGCACTG 120  
Db 61 AACAGGTGAGCTGTGGTGTGGCGAGCAGCGGGAGCGCGCTCGGGAAGCACTG 120

Qy 121 TGGCCCGCACGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCAGATATCTGGGCGG 180  
Db 121 TGGCCCGCACGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCAGATATCTGGGCGG 180

Qy 181 CTGCTGTTTGTGAACCTGCGAAACGGCACCTCTTAAAGACAGACGGCTGTTCGAAC 240  
Db 181 CTGCTGTTTGTGAACCTGCGAAACGGCACCTCTTAAAGACAGACGGCTGTTCGAAC 240

Qy 241 TGGATCTCTGTGAGGCGCCCGAGCGGGAGCGAGGTTCCTCTGTACCGCTGG 300  
Db 241 TGGATCTCTGTGAGGCGCCCGAGCGGGAGCGAGGTTCCTCTGTACCGCTGG 300

Qy 301 GTGAGGGCAACGGCGCTCTGAGCCTTGCCTGAAGGCAACCGGCGCACTGTGGGCGAGGAC 360  
Db 301 GTGAGGGCAACGGCGCTCTGAGCCTTGCCTGAAGGCAACCGGCGCACTGTGGGCGAGGAC 360

Qy 361 CCTCAGGCGCTGTTCGAAGAACACCGGGAAGAGAGCTGGAAGAGAGAGAGTTGTAC 420  
Db 361 CCTCAGGCGCTGTTCGAAGAACACCGGGAAGAGAGCTGGAAGAGAGAGAGTTGTAC 420

Qy 421 CGGTGGGGAACCTGGAAGAGCGGTAAATCTGAATATGCTGGGGCAAACTATATGAC 480  
Db 421 CGGTGGGGAACCTGGAAGAGCGGTAAATCTGAATATGCTGGGGCAAACTATATGAC 480

Qy 481 CTCCCTGTGGATGAGCGATTCTGGGAAGACAGAGAGTTGACTTTGAGGTTTCGCTGGCC 540

Db 481 CTCCCTGTGGATGAGCGATTCTGGGAAGACAGAGAGTTGACTTTGAGGTTTCGCTGGCC 540  
Qy 541 AAGGGGCTGGCGGCACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGAGAT 600  
Db 541 AAGGGGCTGGCGGCACTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGAGAT 600  
Qy 601 CTAGATGACTTCAACCGGATTTTCTGGTGTGTGTCAGAGCAAGCTGGCTGAGCGGTGCGG 660  
Db 601 CTAGATGACTTCAACCGGATTTTCTGGTGTGTGTCAGAGCAAGCTGGCTGAGCGGTGCGG 660  
Qy 661 GACTCTGGAAGAGATGCTTATTTGGTACCAAGTTTCTTAATGGGCGCAACCCCGTG 720  
Db 661 GACTCTGGAAGAGATGCTTATTTGGTACCAAGTTTCTTAATGGGCGCAACCCCGTG 720  
Qy 721 GTGCTGAGCGCTCTGCTCACCTCTCTGCTCCCTAGTGTCTCCCTCCAGGCATGAGGAA 780  
Db 721 GTGCTGAGCGCTCTGCTCACCTCTCTGCTCCCTAGTGTCTCCCTCCAGGCATGAGGAA 780  
Qy 781 CTGAGGGCCAGCTGGAGAAGGAGCTGGAGGAGGCACACTGTTGAAAGCTGACTTCTCC 840  
Db 781 CTGAGGGCCAGCTGGAGAAGGAGCTGGAGGAGGCACACTGTTGAAAGCTGACTTCTCC 840  
Qy 841 CTGCTGGATGGATCAAGGCCAAAGTCATTCTGTAGCCAGCAGCACCTGGCTGCCCT 900  
Db 841 CTGCTGGATGGATCAAGGCCAAAGTCATTCTGTAGCCAGCAGCACCTGGCTGCCCT 900  
Qy 901 CTAGTCATCTGAAATTTGAGGCTGATGGAAATCTTCTGCCATGGTCATCAGCTCCAG 960  
Db 901 CTAGTCATCTGAAATTTGAGGCTGATGGAAATCTTCTGCCATGGTCATCAGCTCCAG 960  
Qy 961 CTGCCCCGCAAGGATCCCCACCACTCTCCCTTTTCTGCTACGGATCCCCCAATGGCC 1020  
Db 961 CTGCCCCGCAAGGATCCCCACCACTCTCCCTTTTCTGCTACGGATCCCCCAATGGCC 1020  
Qy 1021 TGGCTTCTGGCAAAATGCTGGGTGGCAGCTCTGACTTCAGCTTCAGCTCCAGCTGCACTCT 1080  
Db 1021 TGGCTTCTGGCAAAATGCTGGGTGGCAGCTCTGACTTCAGCTTCAGCTCCAGCTGCACTCT 1080  
Qy 1081 CATCTTCTCAGGGGACACTTGTATGGCTGAGGTCAATTTGTGGCCACCAATGAGGTGCCCTG 1140  
Db 1081 CATCTTCTCAGGGGACACTTGTATGGCTGAGGTCAATTTGTGGCCACCAATGAGGTGCCCTG 1140  
Qy 1141 CGGTGATACATCTTAATTTCAAGCTTAATTTCCCACTGCGATACACCTCGGAAAT 1200  
Db 1141 CGGTGATACATCTTAATTTCAAGCTTAATTTCCCACTGCGATACACCTCGGAAAT 1200  
Qy 1201 AAGCTCGGGCCAGGACCTGGCTGTCTGACNTGGGAATTTTCAGCCAGATAATGAGC 1260  
Db 1201 AAGCTCGGGCCAGGACCTGGCTGTCTGACNTGGGAATTTTCAGCCAGATAATGAGC 1260  
Qy 1261 ACTGGTGGGGGAGGCCACGTGACGTGCTCAAGCAAGCTGGAGCCTTCTTAACTACAGC 1320  
Db 1261 ACTGGTGGGGGAGGCCACGTGACGTGCTCAAGCAAGCTGGAGCCTTCTTAACTACAGC 1320  
Qy 1321 TCCCTCTGTCCTGATCACTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCTCTTC 1380  
Db 1321 TCCCTCTGTCCTGATCACTTGGCCGACCGGGGCTCTCTGGAGTGAAGTCTTCTCTTC 1380  
Qy 1381 TATGCCCAAGATGCGCTGCGGCTCTGGGAATCATCTATCGGTATCTGGAAGGAATCGTG 1440  
Db 1381 TATGCCCAAGATGCGCTGCGGCTCTGGGAATCATCTATCGGTATCTGGAAGGAATCGTG 1440  
Qy 1441 AGTCTCACTATAAGACAGACGTGGCTGTGAAGAGAGCCAGAGCTGCAGACCTGGTGT 1500  
Db 1441 AGTCTCACTATAAGACAGACGTGGCTGTGAAGAGAGCCAGAGCTGCAGACCTGGTGT 1500  
Qy 1501 CGAGAGATCACTGAAATCGGGCTGCAAGGGGCCCGAGACCGAGGGTTTCTCTCTTTA 1560  
Db 1501 CGAGAGATCACTGAAATCGGGCTGCAAGGGGCCCGAGACCGAGGGTTTCTCTCTTTA 1560  
Qy 1561 CAGGCTCGGACAGGTTTGCCACTTTGTTCACCATGTTATCTTACCTGACCGGCCAA 1620



Db 1561 CAGGCTCGGACCAAGTTGGCCACTTTGTCAACATGTGTATCTTACCTGACCGGCCAA 1620  
Qy 1621 CACGCTCTGTGTCACCTGGGCCAGCTGGTACTCTTGGGTGCTTAATGACACCTGTC 1680  
Db 1621 CACGCTCTGTGTCACCTGGGCCAGCTGGTACTCTTGGGTGCTTAATGACACCTGTC 1680  
Qy 1681 ACGATCGGCTGCGCCCGCCACCAACCAAGGATGCAACGCTGGAGACAGTATGGGACA 1740  
Db 1681 ACGATCGGCTGCGCCCGCCCAACCAACCAAGGATGCAACGCTGGAGACAGTATGGGACA 1740  
Qy 1741 CTGCCCCAATCTCCACAGGCTTCTCTCCAGATGTCCATCTGGCAGCTGGGCGAGAGC 1800  
Db 1741 CTGCCCCAATCTCCACAGGCTTCTCTCCAGATGTCCATCTGGCAGCTGGGCGAGAGC 1800  
Qy 1801 CAGCCCGTTAAGTGGCTGTGGCCAGCATAGGAGGAGTATTTTTCGGGCGCTCAGGCT 1860  
Db 1801 CAGCCCGTTAAGTGGCTGTGGCCAGCATAGGAGGAGTATTTTTCGGGCGCTCAGGCT 1860  
Qy 1861 AAGGCTGTGCTGAAGAGTTTCAAGGAGGAGCTGGCTGCCCTGGATAAGGAATTCAGATC 1920  
Db 1861 AAGGCTGTGCTGAAGAGTTTCAAGGAGGAGCTGGCTGCCCTGGATAAGGAATTCAGATC 1920  
Qy 1921 CGAATGCAAAAGCTGCACATGCCCTACGAGTACCTGCGGCCAGCGTGTGGAACACAGT 1980  
Db 1921 CGAATGCAAAAGCTGCACATGCCCTACGAGTACCTGCGGCCAGCGTGTGGAACACAGT 1980  
Qy 1981 GTGGCCATCTAAGCGTGCACCCCTTTTGGTTATTTTTCAGCCCCCATCACCAGCCACCAAG 2040  
Db 1981 GTGGCCATCTAAGCGTGCACCCCTTTTGGTTATTTTTCAGCCCCCATCACCAGCCACCAAG 2040  
Qy 2041 CTGACCCCTTCTGGTTATAGCCCTGCTCCCTCCCAAGTCCACCTCTTCCGATGTCCTC 2100  
Db 2041 CTGACCCCTTCTGGTTATAGCCCTGCTCCCTCCCAAGTCCACCTCTTCCGATGTCCTC 2100  
Qy 2101 CTTCTCTCAGGCGGACCTTTTCATGCTCTCTGACCCAGTCAACACATTTTACTCTAGA 2160  
Db 2101 CTTCTCTCAGGCGGACCTTTTCATGCTCTCTGACCCAGTCAACACATTTTACTCTAGA 2160  
Qy 2161 GGCATCACCTGGGACCTTACTCTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220  
Db 2161 GGCATCACCTGGGACCTTACT 2220  
Qy 2221 TCT 2280  
Db 2221 TCT 2280  
Qy 2281 TTTCAAGACTAGATAGGGGGATATAATACATTTACTCCACACCTTTTATGAATCAAT 2340  
Db 2281 TTTCAAGACTAGATAGGGGGATATAATACATTTACTCCACACCTTTTATGAATCAAT 2340  
Qy 2341 ATGATTTTTTTTGTGTTTAAAGACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400  
Db 2341 ATGATTTTTTTTGTGTTTAAAGACAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2400  
Qy 2401 GTGCGCATCACACGGCTCAGTGCAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAG 2460  
Db 2401 GTGCGCATCACACGGCTCAGTGCAGCTCTGAGCTCTGAGCTCTGAGCTCTGAGCTCTGAG 2460  
Qy 2461 TCAGCTCTCTGAGTGTGGGACTACAGCTCATGCCATCATGCCATCATGCCATCATATTTTT 2520  
Db 2461 TCAGCTCTCTGAGTGTGGGACTACAGCTCATGCCATCATGCCATCATGCCATCATATTTTT 2520  
Qy 2521 TATTTTCTGGGAGACGGGCGCTCTCTATGTTGCTAGGCTGGAATAGGATTTTGAACCC 2580  
Db 2521 TATTTTCTGGGAGACGGGCGCTCTCTATGTTGCTAGGCTGGAATAGGATTTTGAACCC 2580  
Qy 2581 AAATTGAGTTTAAATAATAAAGTTGTTTTCAGCTAAAGATGGAAGAACTAGGAC 2640  
Db 2581 AAATTGAGTTTAAATAATAAAGTTGTTTTCAGCTAAAGATGGAAGAACTAGGAC 2640  
Qy 2641 TGAATCTTTTAAATAATAATATGGCAAG 2671  
Db 2641 TGAATCTTTTAAATAATAATATGGCAAG 2671

## RESULT 2

ADJ74847  
ID ADJ74847 standard; DNA; 2671 BP.  
XX  
AC ADJ74847;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
Marker gene SEQ ID NO:99.  
XX  
XX bronchial asthma; chronic obstructive pulmonary disease;  
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
KW gene therapy; marker gene; gene; ds.  
XX  
OS Homo sapiens.  
XX  
FN EP1394274-A2.  
XX  
PD 03-MAR-2004.  
XX  
XX 04-AUG-2003; 2003EP-00254857.  
XX  
XX 06-AUG-2002; 2002JP-00229312.  
PR 20-MAR-2003; 2003JP-00077212.  
XX  
XX (GENO-) GENOX RES INC.  
XX  
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
XX  
XX WPI; 2004-193155/19.  
XX  
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by  
PT comparing the expression level of a marker gene in a biological sample  
PT from a subject with the expression level of the gene in a sample from a  
PT healthy subject.  
XX  
PS Claim 1; SEQ ID NO 99; 241pp; English.  
XX  
XX The present invention describes a method of testing for bronchial asthma  
CC or chronic obstructive pulmonary disease. The method comprises  
CC determining the expression level of a marker gene in a biological sample  
CC from a subject, comparing the expression level determined with the  
CC expression level of the marker gene in a biological sample from a healthy  
CC subject, and judging whether the subject has bronchial asthma or chronic  
CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
CC genes (S1) whose expression levels increase when respiratory epithelial  
CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
CC whose expression levels decrease when respiratory epithelial cells are  
CC stimulated with interleukin-13. Also described: (1) a reagent (I) for  
CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
CC (2) a kit for screening for a candidate compound for a therapeutic agent  
CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
CC an animal model for bronchial asthma or chronic obstructive pulmonary  
CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
CC method for producing an animal model for bronchial asthma or chronic  
CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
CC a marker gene or an antisense nucleic acid corresponding to a portion of  
CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
CC expression of the gene through an RNAi effect or an antibody recognising  
CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
CC probe has been immobilised to assay a marker gene. (I) has respiratory  
CC and antiasthmatic activities, and can be used in gene therapy. The method  
CC is useful for testing for or screening for a therapeutic agent for  
CC bronchial asthma or chronic obstructive pulmonary disease. The present  
CC sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 2671 BP; 580 A; 743 C; 718 G; 630 T; 0 U; 0 Other;

Query Match

100.0%; Score 2671; DB 12; Length 2671;

Best Local Similarity 100.0%; Pred. No. 0; Matches 2671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	AAGATGGGTCTCTACCGCATCCGCGTGTCCACTCGGGGCTCGCTCTATGCGCGTTCCAAC	60
DB	1	AAGATGGGTCTCTACCGCATCCGCGTGTCCACTCGGGGCTCGCTCTATGCGCGTTCCAAC	60
QY	61	AACAGGTGCAGCTGTGGCTGTGCGCCAGCAGCACGGGAGGCGGCTCGGGAAGCGACTG	120
DB	61	AACAGGTGCAGCTGTGGCTGTGCGCCAGCAGCACGGGAGGCGGCTCGGGAAGCGACTG	120
QY	121	TGSCCGCACGGGGCAAGGAGACAGNACTCAAGTGGGAAGTACCGGAGTATCTGGGGCGG	180
DB	121	TGSCCGCACAGGGGCAAGGAGACAGNACTCAAGTGGGAAGTACCGGAGTATCTGGGGCGG	180
QY	181	CTGCTGTTTGTGAATCTGGCGAAACGGCACCTCTTAAAGGACGAGCGCTGGTCTGCAAC	240
DB	181	CTGCTGTTTGTGAATCTGGCGAAACGGCACCTCTTAAAGGACGAGCGCTGGTCTGCAAC	240
QY	241	TGGATCTCTGTGACGGGCCCCGGAGCGGGGACGAGGTCAGGTTCCCTTTTACCCTGG	300
DB	241	TGGATCTCTGTGACGGGCCCCGGAGCGGGGACGAGGTCAGGTTCCCTTTTACCCTGG	300
QY	301	GTGAGGGCAACGGGCTCTGAGCTGCTGAGCTGCTGAAGGACACGGCGCAGCTGTGGGCGAGGAC	360
DB	301	GTGAGGGCAACGGGCTCTGAGCTGCTGAGCTGCTGAAGGACACGGCGCAGCTGTGGGCGAGGAC	360
QY	361	CCTCAGGGCTGTTCCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAAAGTAAGTTGTAC	420
DB	361	CCTCAGGGCTGTTCCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAAAGTAAGTTGTAC	420
QY	421	CGGTGGGAAACTGGAAGGACGGGTTAACTTCTGAATATGGCTGGGGCCAAACTATATGAC	480
DB	421	CGGTGGGAAACTGGAAGGACGGGTTAACTTCTGAATATGGCTGGGGCCAAACTATATGAC	480
QY	481	CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGCTGGCC	540
DB	481	CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGCTGGCC	540
QY	541	AAGGGCTCGCGACCTCCGCTATCAAGACTCTCTAAATGTTCTGACTGCTGGAAGGAT	600
DB	541	AAGGGGCTGGCGACCTCCGCTATCAAGACTCTCTAAATGTTCTGACTGCTGGAAGGAT	600
QY	601	CTAGATGACTTCAACCGGATTTTCTGGTGTGTGACAGCAAGCTGGCTGAGCGGCTGCGG	660
DB	601	CTAGATGACTTCAACCGGATTTTCTGGTGTGTGACAGCAAGCTGGCTGAGCGGCTGCGG	660
QY	661	GACTCTCGGAAGGAAGATGCTTATTTGGGTACCAAGTTCTTAAATGGCGGCAACCCCGTG	720
DB	661	GACTCTCGGAAGGAAGATGCTTATTTGGGTACCAAGTTCTTAAATGGCGGCAACCCCGTG	720
QY	721	GTGCTGAGGGCTCTGCTCACTTCTGCTCGCCTAGTGTCCCTCAGGCGATCGAGGAA	780
DB	721	GTGCTGAGGGCTCTGCTCACTTCTGCTCGCCTAGTGTCCCTCAGGCGATCGAGGAA	780
QY	781	CTGCAAGGCGGCTGAGGAAGGAGCTGGAGGAGGACACTCTGCGAAGCTGACTTCTCC	840
DB	781	CTGCAAGGCGGCTGAGGAAGGAGCTGGAGGAGGACACTCTGCGAAGCTGACTTCTCC	840
QY	841	CTGCTGGATGGGATCAAGGCAACGTCATTTCTGTGTAGCAGCAGCACTTGCTGCGCCT	900
DB	841	CTGCTGGATGGGATCAAGGCAACGTCATTTCTGTGTAGCAGCAGCACTTGCTGCGCCT	900
QY	901	CTAGTCAATGCTGAAATGAGCGCTGATGGGAAACTCTTGCCCATCGGTCAATCAGCTCCAG	960
DB	901	CTAGTCAATGCTGAAATGAGCGCTGATGGGAAACTCTTGCCCATCGGTCAATCAGCTCCAG	960
QY	961	CTGCGCGCACAGATCCCGACACCTCTTCTGCTTACCGATCCCGCATATGGCC	1020
DB	961	CTGCGCGCACAGATCCCGACACCTCTTCTGCTTACCGATCCCGCATATGGCC	1020
QY	1021	TGGCTTCTGGCCAAATGCTGGGTGCGCAGCTCTGACTTCCAGCTCCATGAGCTGCGAGTCT	1080
DB	1021	TGGCTTCTGGCCAAATGCTGGGTGCGCAGCTCTGACTTCCAGCTCCATGAGCTGCGAGTCT	1080









1380 CTATGCCAAGATGCGCTCGGGCTCTGGGAATCATCTATCGTATGTGGAAGGAATCGT 1439  
1812 CTATGCCAAGATGCGCTCGGGCTCTGGGAATCATCTATCGTATGTGGAAGGAATCGT 1871  
1440 GAGTCTCCACTATAAGACAGAGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTG 1499  
1872 GAGTCTCCACTATAAGACAGAGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTG 1931  
1500 TCAGAGATCACTGAATCGGGCTGCAAGGGGCCAGAGCCGAGGGTTCCTGTCTCTTT 1559  
1932 TCAGAGATCACTGAATCGGGCTGCAAGGGGCCAGAGCCGAGGGTTCCTGTCTCTTT 1991  
1560 ACAGGCTCGGGACACGTTTGCACCTTTGTACCATGTGTATCTTCACTGTCACCGGCCA 1619  
1992 ACAGGCTCGGGACACGTTTGCACCTTTGTACCATGTGTATCTTCACTGTCACCGGCCA 2051  
1620 ACA CGCTCTGTGCACTCTGGCCAGCTGGA CTGTTACTCTTGGTGCCCTAAATGCACTCTG 1679  
2052 ACAGGCTCTGTGCACTCTGGCCAGCTGGA CTGTTACTCTTGGTGCCCTAAATGCACTCTG 2111  
1680 CAGGATCGGGCTGCCCCGCCAACCAACCAAGGATGCAAGCTGGAGACAGTGGCGAC 1739  
2112 CAGGATCGGGCTGCCCCGCCAACCAACCAAGGATGCAAGCTGGAGACAGTGGCGAC 2171  
1740 ACTGCCCACTTCCACAGGCTTCTCTCCAGATGTTCATCATCTTGGCAGCTGGGCAGAGC 1799  
2172 ACTGCCCACTTCCACAGGCTTCTCTCCAGATGTTCATCATCTTGGCAGCTGGGCAGAGC 2231  
1800 CCAAGCCGTTATGTTGGCTGTGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTGAGCC 1859  
2232 CCAAGCCGTTATGTTGGCTGTGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTGAGCC 2291  
1860 TAAGGCTGTGCTGAAGAAGTTCAAGGAGGAGCTGGCTGCTGGATGAAGGAATTCAGAT 1919  
2292 TAAGGCTGTGCTGAAGAAGTTCAAGGAGGAGCTGGCTGCTGGATGAAGGAATTCAGAT 2351  
1920 CCGGAATGCAAGCTGACATGCTTACGAGTACCTGCGGCCAGCGTGGTGGAAACAG 1979  
2352 CCGGAATGCAAGCTGACATGCTTACGAGTACCTGCGGCCAGCGTGGTGGAAACAG 2411  
1980 TGTGGCCATTAAGCGTTCGCCACCTTTTGGTTATTTTCAGCCCCCATCAACCAAGCCACAA 2039  
2412 TGTGGCCATTAAGCGTTCGCCACCTTTTGGTTATTTTCAGCCCCCATCAACCAAGCCACAA 2471  
2040 GCTGACCCCTTCGTGTTATAGCCCTGCGCTCCCAAGTCCACCCCTTCCCATGTCCCA 2099  
2472 GCTGACCCCTTCGTGTTATAGCCCTGCGCTCCCAAGTCCACCCCTTCCCATGTCCCA 2531  
2100 CCCTCCCTAGAGGGCACCTTTTTCATGGTCTCTGCAACCCAGTGAACACATTTTACTCTAG 2159  
2532 CCCTCCCTAGAGGGCACCTTTTTCATGGTCTCTGCAACCCAGTGAACACATTTTACTCTAG 2591  
2160 AGGCATCACCTGGGACCTTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2219  
2592 AGGCATCACCTGGGACCTTACTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2651  
2220 CTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2279  
2652 CTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2711  
2280 ATTTCAAGACTAGAAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAA 2339  
2712 ATTTCAAGACTAGAAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAA 2771  
2340 TATGATTTTTTGTGTTTAAAGACAGAGTCTCACTTTTGACACCCAGCGCTGGAGTGCAG 2399  
2772 TATGATTTTTTGTGTTTAAAGACAGAGTCTCACTTTTGACACCCAGCGCTGGAGTGCAG 2831  
2400 TGGTGCCATCACACGCTCATGCGCTCAGGCTCTGGGCTCAATGATATCTTCCAC 2459  
2832 TGGTGCCATCACACGCTCATGCGCTCAGGCTCTGGGCTCAATGATATCTTCCAC 2891

2460 CTCAGCCTCCTGAGTAGCTGGGACTACAGGCTCATGCGCATCATGCCAGCTAATATTTT 2519  
2892 CTCAGCCTCCTGAGTAGCTGGGACTACAGGCTCATGCGCATCATGCCAGCTAATATTTT 2951  
2520 TTATTTTCGTGGAGACGGGCTCACTATGTTGCTAGCTGGAATAGGATTTTGAACC 2579  
2952 TTATTTTCGTGGAGACGGGCTCACTATGTTGCTAGCTGGAATAGGATTTTGAACC 3011  
2580 CAAATTTGAGTTTAAACAATAAATAAAGTTGTTTACGCTTAAAGATGGAAGAACTAGGA 2639  
3012 CAAATTTGAGTTTAAACAATAAATAAAGTTGTTTACGCTTAAAGATGGAAGAACTAGGA 3071  
2640 CTGAACCTATTTTAAATAAATAAATATTCGCAAAAG 2671  
3072 CTGAACCTATTTTAAATAAATAAATATTCGCAAAAG 3103

RESULT 5  
ABL60541  
ID ABL60541 standard; cDNA; 2844 BP.  
XX  
AC ABL60541;  
XX  
DT 27-AUG-2002 (first entry)  
XX  
DE Human lipid metabolism enzyme (LME)-5 cDNA (clone Id: 7484270CB1).  
XX  
KW Human; lipid metabolism enzyme; LME; cytostatic; neuroprotective; gene;  
KW nontropic; cerebrotrophic; antiparkinsonian; antialzheimer's; vaccine;  
KW antisclerotic; antimicrobial; anti-AIDS; cardiovascular; antiangiinal;  
KW gene therapy; protein therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 107..2161  
FT /tag= a  
FT /product= "lipid metabolism enzyme"  
FT /note= "LME-5"  
XX  
PN WO00229036-A2.  
XX  
PD 11-APR-2002.  
XX  
PF 05-OCT-2001; 2001WO-US031302.  
XX  
PR 06-OCT-2000; 2000US-0238388P.  
PR 13-OCT-2000; 2000US-0240616P.  
PR 02-NOV-2000; 2000US-0245719P.  
PR 08-NOV-2000; 2000US-0247503P.  
PR 17-NOV-2000; 2000US-0249503P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PA Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;  
PI Walla NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;  
PI Lal PG, Tribouley CM;  
XX  
XX WPI; 2002-315862/35.  
DR P-PSDB; ABB08005.  
XX  
PT Lipid Metabolism Enzymes and nucleic acids, useful for preventing,  
PT diagnosing and treating e.g. cancer, Alzheimer's disease and Creutzfeld-  
PT Jakob disease.  
XX  
PS Claim 5; Page 124-125; 127pp; English.  
XX  
CC The invention relates to human lipid metabolism enzymes (LMEs) and  
CC encoding polynucleotides. The LMEs can be expressed by standard  
CC recombinant technology. The LME polypeptides, polynucleotides and  
CC modulators may be used in the prevention, diagnosis and treatment of  
CC diseases associated with inappropriate LME expression such as cancer  
CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.





Db 2150 GTGGCCACTTAAGCGTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCACCAAGCCACAAG 2209  
Qy 2041 CTGACCCCTTCGTGGTTATAGCCCTGCCCTCCCAAGTCCACACCTCTTCCCAATGCCAC 2100  
Db 2210 CTGACCCCTTCGTGGTTATAGCCCTGCCCTCCCAAGTCCACACCTCTTCCCAATGCCAC 2269  
Qy 2101 CTTCCCTTAGAGGGGACCTTTTCATGGTCTCTGCACCCAGTGAACACATTTTACTCTAGA 2160  
Db 2270 CTTCCCTTAGAGGGGACCTTTTCATGGTCTCTGCACCCAGTGAACACATTTTACTCTAGA 2329  
Qy 2161 GGCAACCTCGGACCTTACTCTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220  
Db 2330 GGCAACCTCGGACCTTACT 2389  
Qy 2221 TCT 2280  
Db 2390 TCT 2449  
Qy 2281 TTTCAGACTTAGAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAT 2340  
Db 2450 TTTCAGACTTAGAATAGGGGGATATAATACATATTACTCCACACCTTTTATGAATCAAT 2509  
Qy 2341 ATGATTTTTTTTGTGTGTTTAAGACAGAGTCTCATTGACACCCAGGCTGGAGTGCAGT 2400  
Db 2510 ATGATTTTTTTTGTGTGTTTAAGACAGAGTCTCATTGACACCCAGGCTGGAGTGCAGT 2569  
Qy 2401 GGTGCCATCACACGGCTCACTGCAGGCTCAGGCTCAGGCTCAAAATGATCTCCACCC 2460  
Db 2570 GGTGCCATCACACGGCTCACTGCAGGCTCAGGCTCAGGCTCAAAATGATCTCCACCC 2629  
Qy 2461 TCAGCCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 2520  
Db 2630 TCAGCCTCTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCT 2689  
Qy 2521 TATTTTCGTGGAGACGGGGCTCATTATGTTGCTAGGCTGGAAATAGGATTTTGAACCC 2580  
Db 2690 TATTTTCGTGGAGACGGGGCTCATTATGTTGCTAGGCTGGAAATAGGATTTTGAACCC 2749  
Qy 2581 AAATTGAGTTTACAAATAATAAAGTTGTTTACGTTAAGATGGAAGAAGTCTAGGAC 2640  
Db 2750 AACTTGAGTTTACAAATAATAAAGTTGTTTACGTTAAGATGGAAGAAGTCTAGGAC 2809  
Qy 2641 TGAATATTTTAAATAAATAATTTGG 2665  
Db 2810 TGAGCTATTCTTAATGAAGATCG 2834

RESULT 6

ABT42155  
ID ABT42155 standard; DNA; 2048 BP.  
XX AC ABT42155;  
XX DT  
XX 26-JUN-2003 (first entry)  
DE Toxicity modelling related rat gene SEQ ID No 1857.  
XX Toxic effect; gene expression profile; renal toxicity; toxicity marker;  
KW database; drug screening; toxicity assay; rat; ds.  
XX OS Rattus norvegicus.  
XX PN W020295000-A2.  
XX PD  
XX 28-NOV-2002.  
XX 22-MAY-2002; 2002WO-US016173.  
XX PF  
XX 22-MAY-2001; 2001US-0292335P.  
PR 13-JUN-2001; 2001US-0297523P.  
PR 19-JUN-2001; 2001US-0298925P.  
PR 10-JUL-2001; 2001US-0303807P.  
PR 10-JUL-2001; 2001US-0303808P.

PR 10-JUL-2001; 2001US-0303810P.  
PR 28-AUG-2001; 2001US-0315047P.  
PR 27-SEP-2001; 2001US-0324928P.  
PR 22-OCT-2001; 2001US-0330462P.  
PR 01-NOV-2001; 2001US-0330867P.  
PR 21-NOV-2001; 2001US-0331805P.  
PR 06-DEC-2001; 2001US-0336144P.  
PR 19-DEC-2001; 2001US-0340873P.  
PR 21-FEB-2002; 2002US-0357842P.  
PR 21-FEB-2002; 2002US-0357843P.  
PR 21-FEB-2002; 2002US-0357844P.  
PR 15-MAR-2002; 2002US-0364134P.  
PR 08-APR-2002; 2002US-0370144P.  
PR 08-APR-2002; 2002US-0370206P.  
PR 08-APR-2002; 2002US-0370247P.  
PR 17-APR-2002; 2002US-0372794P.  
PR 21-APR-2002; 2002US-0371679P.

(GENE-) GENE LOGIC INC.

Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;

WPI; 2003-148464/14.

Predicting at least one toxic effect of a compound, useful for toxicity modeling, comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database.

Example 4; Page; 446pp; English.

The invention relates to a novel method of predicting at least one toxic effect of a compound. The method comprises a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising at least part of the data or information given in the specification. The methods are useful for predicting at least one toxic effect of a compound, predicting the renal progression of a toxic effect of a compound, predicting the renal toxicity of a compound, or identifying toxicity markers in tissues or cells exposed to known renal toxin. The genes are useful as toxicity markers in drug screening and toxicity assays, in monitoring disease or physiological states, or disease progression. This polynucleotide represents a rat DNA sequence relating to the toxic effect database described in the specification. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the World Intellectual Property Organization

Sequence 2048 BP; 482 A; 537 C; 542 G; 487 T; 0 U; 0 Other;

Query Match 48.9%; Score 1306; DB 10; Length 2048;  
Best Local Similarity 78.3%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 435; Indels 3; Gaps 1;  
Qy 1 AAGATGGGTCTCTACCGCATCCGCGTGTCCACTGGGGCTCGCTCTATGCGGTTCACAC 60  
Db 17 AAGATGGGTCTCTACCGCATCCGCGTCTCCACGGAGATCCCAAGTACGGGGCTCCAC 76  
Qy 61 AACAGGTGCGAGTGTGGTGTGCGCCAGCAGCGGGAGCGCGCTCGGGAAGCGACTG 120  
Db 77 AACGAGGTCTACCTGTGTGGTTGGTGTGACACAGCATGGAGAGGCATCTCTCGGGAAGCTGCTA 136  
Qy 121 TGGCCCGCAGCGGGCAAGGAGACAGAACTCAAGTGGAACTACCGAGTATCTGGGGCCG 180  
Db 137 CGACCCTGTGGGACTCGGAAGCAGAAATTCAAAGTGAATGTGTGAGATACCTTGGGCCA 196  
Qy 181 CTGCTGTTTGTGAAGTTCGCGCAACCGCACCTCTCTTAAGGACGACCGCTGCTTCTGCAAC 240  
Db 197 CTGCTGTTTGTGAAGTTCGCGCAACCGCACCTCTCTTAAGGACGACCGCTGCTTCTGCAAC 256  
Qy 241 TGGATCTCTGTGAGGG 297  
Db 257 TGGATTTCTGTGAAGGG 316

Qy	298	TGGGTGGAGGGCAACGGCGTCTCTGAGCCTGCCTGAAAGCACCGGCCGACCTGTGGCGAG	357
Db	317	TGGGTTTCAGGGCAGAAGCATCTGAGCCTCCCTGAGGCACCTGCTGCACCGTGGTTGAA	376
Qy	358	GACCTCAGGGCCTGTTCCAAACAACGGGAAGAGAGCTGGAGAGAGAGAGAAAGTTG	417
Db	377	GATTCTCAAGGACTGTGTCAGGAACAATAGGAAGAGAGGAGCTTTGAAGAGAGAGGAGTCTG	436
Qy	418	TACCGTGGGGAAACTGGAAGGACGGGTAAATCTGAATATGGCTGGGGCCAAACTATAT	477
Db	437	TACAGTGGGGCAACTGGAGATGGCTCAATCTGTAATGTGGCGCGGCCAGTATATCT	496
Qy	478	GACCTCCCTGTGGATGAGCGAATTTCTGGAAACAAGAGAGTTGACTTTGAGGTTTCGCTG	537
Db	497	GACCTCCCTGTAGACCAACGATTTCTGAGAGGACAAAAGAAATGAATTTGAAGCTTTCACAG	556
Qy	538	GCCAAAGGGCTGGCGGACCTCGCTATCAAAAGACCTCTTAATGTTCTGACTTCTGCTGAAG	597
Db	557	GTTATAGGGGTAAATGATATCTGTTGTCAACTTTCCTATAAACACTGTGACCTGCTGGAAA	616
Qy	598	GATCTAGATGACTTCAACCGGAATTTCTGTGTGGTCAGAGCAAGCTGGCTGAGCGGTG	657
Db	617	AGCCTAGATGACTTCAACTGCGTTTTCAAGAGTGCCTATACCAAAATGGCTGAGCGGTT	676
Qy	658	CGGACTCTCTGGAAGGAAGATGCTTATTTGGGTACCAAGTTTCTTAATGCGGCCAACCC	717
Db	677	CGAAACTCTCTGGAAGGAAGATGCGTCTCTTTGGGTACCAATTTCTCAATGGTGTCAACCC	736
Qy	718	GTGTTGTCTGAGCGCCTCTGCTCACTTCTCTGCTCGCCTAGTGTTCCTCAGAGCATGGAG	777
Db	737	ATGTTGTCTGAAGCGCTCTACTTGTCTCTCGCCCGCTGGTATTTCCCTCAGGHAATGGAG	796
Qy	778	GAACTGACGCCCACTGCTGGAGAAAGGAGCTGGAGGGAGGCACACTGTTTCGAAGCTGACTTC	837
Db	797	AAGCTACAGGCCCACTGCTGAACAAGGAGCTCCAGAAAGGCACCTCTGTTTGAAGCGGATTC	856
Qy	838	TCCCTGTGATGGATCAAGGCCCAAGTCAATTTCTGTAGCCAGCAGCACCTGGCTGCC	897
Db	857	TTCCCTTCTGGAATGGGATCAAGGCCCAATGTCACTCCTTTGTAGCCACAGCATCTGGCTGCC	916
Qy	898	CCTCTAGTCACTGTGAATTTGACGCTGATGGGAAACTCTTGCCCATGGTTCATCCAGCTC	957
Db	917	CCTCTCTCATGCTGAAGCTGATGCTGTATGGACAACTCTTGCCCATAGCCATCCAGCTT	976
Qy	958	CAGCTGCCCGCACAGGATCCCCACCACTCCCTTTCTTGCTACGGATCCCCCAATG	1017
Db	977	GAACTGCCCAAAACTGGGTCTACTCCACCACTATTTTTCAGCGCCTCGGATCCCCCAATG	1036
Qy	1018	GCCTGGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCCAGCTCCATGAGCTGCAG	1077
Db	1037	GACTGGCTCTTAGCCCAATGTGGGTCCGGAGCTCCGACTTTACAGCTCCATGAGCTGCAG	1096
Qy	1078	TCTCATCTTCTGAGGGACACTTCATGGCTGAGGTCAATGTTGTGGGCCACCATGAGGTGC	1137
Db	1097	GCTCATCTTCTGAGGGACACTTGAATGGCTGAGCTCTTTGCTGTGGGCCACCATGAGGTGC	1156
Qy	1138	CTGCCGTGATATACATCTTCTCAAGCTTATAATTCGCCACCTGCGATACACCTGGAA	1197
Db	1157	CTGCTTTCCGTGACACCTGTTTTTAAAGCTTCTAGTTCTCTCATCTGCTTTTACACCATGGAA	1216
Qy	1198	ATTAACTCTGGGCCAGGACTGGCTGGTCTCTGACATGGGAATTTTTCGACCCAGATAATG	1257
Db	1217	ATTAAATGTCCGGGCCAGGAGTGACCTGATCTCAGAGAGAGGCTTTTTTTGACAAGGCAATG	1276
Qy	1258	AGCACTGGTGGGGAGGCCACGTGCAGCTGTCTCAAGCAAGCTGGAGCCTTCTTAAACCTAC	1317
Db	1277	AGCACAGTGGGGAGGCCACTTGATCTTCTCAAGCAAGCTGGAGCCTTCTTGACCTAT	1336
Qy	1318	AGCTCCTTCTGTCCCTCTGATGACTTGGCCGACCGGGGGTCTCTGGGAGTGAAGTCTTCC	1377
Db	1337	TGCTCATTTGTGTCCTCCCGATGACTTTGGCTGAGCGAGGACTTTTGAATATCGAGACTTGC	1396

Qy	1378	TTCTATGCGCCAAAGATGCGCTCGCGCTCTGGGAAATCATCTATCGGTATGTGGGAAGAAATC 1437
Db	1397	TTCTATGCTAAAGACGCGCTCGGCACTCTGGCAGATCATGAATCGTACGTGTGGGAAATG 1456
Qy	1438	GTGAGTCTCCACATATAGACAGACGCTGGCTGTGAAGACGACCCAGACGTGCAGACCTGG 1497
Db	1457	TTCAATCTCCACTACAAGACCGCAAAAGCTGTGCAAGACGACTATGAATGCGACAGCTGG 1516
Qy	1498	TGTCGAGAGATCACTGAAATCGGGCTGCAAGGGGCCCCAGGACCGAGGGTTTCCTGTCTCT 1557
Db	1517	TGTCGAGAGATCACTGACATTTGCTCTCAAGGGGCCCCAGGACGAGGCTTCCTACCTCT 1576
Qy	1558	TTACAGGCTCGGACACAGGTTTGCCACTTTGTGCACCATGTGTATCTTACACTGTGCACCGC 1617
Db	1577	CTTCAGTCCCGGCTCAGGCTTGCTACTTCAATCAACATGTGCATCTTCACGTGCACCGCA 1636
Qy	1618	CAACAGCCTCTGTGCACCTGGGCGAGCTGGTACTCTTTGGTGGCTTAATGCACCC 1677
Db	1637	CAGCACTCTTCCGTCCATCTTTGGCCAGCTGGATTGGTTCTACTGGGTTCTTAATGCACCC 1696
Qy	1678	TGCACAGTGGGCTTGCCCCGCCCAACACCAAGATGCAACGCTGGAGACAGTGATGGCG 1737
Db	1697	TGCACCATGGGCTGCAACCCACCAACGAGAGCAACATGGAGAGCTGATGGCT 1756
Qy	1738	ACACTGCCAACTTCACACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCAGA 1797
Db	1757	ACACTGCCAAACCTAATCAGTCTACTCTCCAGATAAATGTCGTTGGCTCTCTGGGCAGA 1816
Qy	1798	CGCCAGCCGTTATGTGGCTGTGGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTGAG 1857
Db	1817	CGCCAGGCTGTTATGTGGTCCCTGGGCCAGCATTCAGAGGAAACACTTCCAAACCTGAG 1876
Qy	1858	CCTAAGGCTGTCTGGAAGATTTCAGGAGGAGCTGGCTGCCCTGGATAAGGAAATTGAG 1917
Db	1877	GCCAGGCTGTCTGAAGAGTTTCAGAGAGAACTGGCTGCCCTTGGATAAGGAAATTGAG 1936
Qy	1918	ATCCGGAATGCAAGCTGGACATGCCCTACGAGTACCTCGGGCCCGCAGCGTGGTGGAAAA 1977
Db	1937	ATTGCTAATAAGAGCTTGACATACCTTATGAGTACCTCGGCCCCAGCATGGTGGAAAA 1996
Qy	1978	AGTGTGCCCATCTAAGCTGCGCACCCCTTTGGTTATTT 2015
Db	1997	AGCGTGGCCATATGAGCATCCCGCAGACTCCTGCTTGT 2034
RESULT 7		
ADJ75763		
XX	ID	ADJ75763 standard; DNA; 1992 BP.
XX	AC	ADJ75763;
XX	AC	
DT	20-MAY-2004	(first entry)
XX	DE	Marker gene SEQ ID NO:1015.
XX	DE	
XX	OS	bronchial asthma; chronic obstructive pulmonary disease;
KW	KW	respiratory epithelial cell; interleukin-13; respiratory; antiaesthetic;
KW	KW	gene therapy; marker gene; gene; ds.
XX	XX	
OS	Mus	musculus.
XX	OS	
XX	FN	EPI394274-A2.
XX	FN	
PD	03-MAR-2004.	
XX	XX	
PF	04-AUG-2003; 2003EP-00254857.	
XX	XX	
PR	06-AUG-2002; 2002JP-00229312.	
PR	20-MAR-2003; 2003JP-00077212.	
XX	XX	
PA	(GENO-) GENOX RES INC.	
XX	XX	
PI	Ohtani N, Sugita Y, Yamaya M, Kubo H, Nacai H, Izuwara K;	

XX	WPI; 2004-193155/19.
DR	Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX	comparing the expression level of a marker gene in a biological sample
PT	from a subject with the expression level of the gene in a sample from a
PT	healthy subject.
PT	
XX	Claim 14; SEQ ID NO 1015; 241bp; English.
PS	
XX	The present invention describes a method of testing for bronchial asthma
CC	or chronic obstructive pulmonary disease. The method comprises
CC	determining the expression level of a marker gene in a biological sample
CC	from a subject, comparing the expression level determined with the
CC	expression level of the marker gene in a biological sample from a healthy
CC	subject, and judging whether the subject has bronchial asthma or chronic
CC	obstructive pulmonary disease. The marker gene comprises: (a) a group of
CC	genes (S1) whose expression levels increase when respiratory epithelial
CC	cells are stimulated with interleukin-13; or (b) a group of genes (S2)
CC	whose expression levels decrease when respiratory epithelial cells are
CC	stimulated with interleukin-13. Also described: (1) a reagent (I) for
CC	testing for bronchial asthma or chronic obstructive pulmonary disease;
CC	(2) a kit for screening for a candidate compound for a therapeutic agent
CC	to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
CC	an animal model for bronchial asthma or chronic obstructive pulmonary
CC	disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
CC	method for producing an animal model for bronchial asthma or chronic
CC	obstructive pulmonary disease; (6) a therapeutic agent for bronchial
CC	asthma or chronic obstructive pulmonary disease, comprising the compound,
CC	a marker gene or an antisense nucleic acid corresponding to a portion of
CC	the marker gene, a ribozyme, a polynucleotide that suppresses the
CC	expression of the gene through an RNAi effect or an antibody recognising
CC	a protein encoded by a marker gene; and (7) a DNA chip for testing for
CC	bronchial asthma or a chronic obstructive pulmonary disease, on which a
CC	probe has been immobilised to assay a marker gene. (1) has respiratory
CC	and antihistaminic activities, and can be used in gene therapy. The method
CC	is useful for testing for or screening for a therapeutic agent for
CC	bronchial asthma or chronic obstructive pulmonary disease. The present
CC	sequence is used in the exemplification of the present invention.
XX	
SQ	Sequence 1992 BP; 455 A; 537 C; 543 G; 457 T; 0 U; 0 Other;
	Query Match 47.6%; Score 1272; DB 12; Length 1992;
	Best Local Similarity 77.8%; Pred. No. 0;
	Matches 1549; Conservative 0; Mismatches 440; Indels 3; Gaps 1;
Qy	4 ATGGGTCTTACCGCATCCGCTGTCCACTGGGGCTCGCTATATGCCGTTCCAACAAC 63
Dd	1 ATGGGTGTCTACCGCATCCGCTGTCCACTGGGGACTCCGTGTACCGGGCTCCAACAAC 60
Qy	64 CAGTGCACTGTGGCTGTGCAGCAGCGGGAGGGCGCTCGGAACGACTGTGG 123
Dd	61 GAGGTCTACTGTGGTTGATTCGACAGCATGGGGAGGATCTCTCGGAACGACTGTTCCGA 120
Qy	124 CCGGCACGGGGCAAGAGACAGAACTCAAGGTGGAAATACCGGAGTATCTGGGGCCGCTG 183
Dd	121 CCTGTGCGNACTCGAGGCGAATTCAGGTGGATGTGTCAGATACTTGGGCCACTG 180
Qy	184 CTGTTTTGAAACTCGCAGAACCGGACCTCTTAAGGACGACGCTGGTCTGCAACTGG 243
Dd	181 CTGTTTTGAGAGTGCAGAAATGGCATATTCTCAAAGAGGACGCGCTGGTCTGCAACTGG 240
Qy	244 ATCTCTGTCAAGGGCCCCGGAGCCC--GGGACGAGGTTCAGTTCCCTTGTACCGCTGG 300
Dd	241 ATTCTGTGAAGGGCCCCGGAGCACAGGGATCCGAGTACAGTTCCCTGTGTAACGATGG 300
Qy	301 GTGGAGGGCAACGGCGTCTGAGCTTCTGAAAGGACACGGGCGGACATGTGGGGGAGGAC 360
Dd	301 GTTCAGGGCACCAAGATCTCTGAACCTCCCTGAGGGACATGTGCTGACCGTGTGTAAGAC 360
Qy	361 CCTCAGGGCTGTTCAGAAAACACGGGAAAGAAGTGTGGAAGAGAGAAAGTGTATC 420
Dd	361 TCTCAAGGGCTGTTCAGAAACACAGGAGGAGGAACTGGAAGAAAGAGGAGTCTGTAC 420



Db 781 TTGAAGACCCAGCTGGAGAAAGAACTCCAGGCTGGATCTCTGTTTGAAGTGAATTTCTCC 840  
Qy 841 CTGCTGGATGGATCAAGGCAACGTCATTCTCTGTAGCAGCAGCACTGGCTGGCCCT 900  
Db 841 TTTCTGGATGGATCAAGGCAACGTCATTCTCTGTAGCAGCAGCACTGGCTGGCCCT 900  
Qy 901 CTAGTCATGCTGAAATTTGACGCTGTATGGGAACTCTTGGCCATGGTTCATCAGCTCCAG 960  
Db 901 TTGGTCATGCTGAAATTTGACGCTGTATGGGAACTCTTGGCCATGGTTCATCAGCTCCAG 960  
Qy 961 CTGCCCCGACAGGATCCCAACCACTCCCTCTTTCTTGGCTACGATCCCAATGGCC 1020  
Db 961 CCACCTTGACAGGATGTCCCCACCTCTGCTCTTTCTGCCCCGATCCCAATGGCC 1020  
Qy 1021 TGGCTTCTGSCCAAAATGCTGGGTCGACGCTCTGACTTCCAGCTCCAGCTCCAGCTCT 1080  
Db 1021 TGGCTTCTGSCCAAAATGCTGGGTCGACGCTCTGACTTCCAGCTCCAGCTCCAGCTCT 1080  
Qy 1081 CATCTTCTGAGGGGACACTTTGATGGCTGAGGTCATTTGTTGGCCACCATGAGGTCCTG 1140  
Db 1081 CATCTGCTGAGGGGACACTTTGATGGCTGAGGTCATTTGTTGGCTGAGGTCATTTG 1140  
Qy 1141 CCGTCGATACATCTTCTTCAAGCTTATTAATTCGCCACCTGCGATACACCTGGAAT 1200  
Db 1141 CCTAGCCTCCATCTATCTACAAGCTCTGATCCCCACCTTCCGCTACACCATGGCGATC 1200  
Qy 1201 AACGTCGGGCCAGGACTGGGCTGGTCTCTGACATGGGAATTTTCGACAGATAATGAGC 1260  
Db 1201 AACGTCGGGCCAGGACTGGTCTGGTCTCCGAATGGGGAATTTTGACCTGGTGGAGC 1260  
Qy 1261 ACTGCTGGGGGAGGCCACGCTGACGCTGCTCAAGCAAGCTGGAGCCTTCTCACTACAGC 1320  
Db 1261 ACTGCTGGGAGGCCACGCTGACATCTTCAGAGAGCCATGCTGTTGACCTATCAT 1320  
Qy 1321 TCCTTCTGCTCCCTGATGACTGGGCGACCGGGGCTCTGGGAGTGAAGTCTTCCTTC 1380  
Db 1321 TCCTTCTGCTCCCTGATGACTGGGCGACCGGCTCTGGGAGTGAAGTCTTCCTTC 1380  
Qy 1381 TATGCCCAAGATCGCTGGGCTCTGGGAATCATCTATCGGTATGTGGAAGAACTGTCG 1440  
Db 1381 TATGGC---GATGCCATGAGGCTGTGGGGAATCATGACCGGTACATGGAGGGATGGTT 1437  
Qy 1441 AGTCTCCACTATAAGACAGACGCTGGCTGTGAAAGACGACCCAGCTGACACCTGGTGT 1500  
Db 1438 GGGCTTTTCTACATAGTACCAAGCCATGAAGATGATCTAGAGCTGACGGCTGGTGC 1497  
Qy 1501 CGAGAGATCATGAATTCGGGCTGCAAGGGGCCAGGACCGAGGGTTCTGTCTCTTTA 1560  
Db 1498 AGAGAGATGACTGAGACTGGACTGACAGAGGGGCCAAGACAGGGGTTCTCTATCTCTTA 1557  
Qy 1561 CAGCTCGGACACAGGTTTGCCTTTGTCACCATGTATCTTCACTGCACCGGCCAA 1620  
Db 1558 GAGTCCCGGGCTAGCTCTGCCATTTGTCAACATGTGATCTTCAATGACAGGTGAG 1617  
Qy 1621 CAGCCTCTGTGCACTCGGCGCAGCTGGAATGCTGCTCTTGGGTGCTTATGACCCCTGC 1680  
Db 1618 CATGCTTCTAACCACTGGGCGCAGCTGGAATGCTGCTCTGATCCCTATGCCCCATGC 1677  
Qy 1681 ACAGTGGCTGCCCCCGCCAAACCAAGATGCAACGCTGGAGACAGTGTATGGGAC 1740  
Db 1678 ACCATGCAAGAGCCCCCACCACCTCTCTAAGGATGTGACAGAGAAGGATATAGTGGACTTA 1737  
Qy 1741 CTGCCCCAATCTCCACAGGCTTCTCTCCAGATGTCATCTTGGCAGCTGGGCGACAGC 1800  
Db 1738 CTGCCCCAATCTCCACAGGACCGTATGCAAAAGACCTTCAAAAGTTCTTGGCAGAGC 1797  
Qy 1801 CAGCCCTGTATGTGGCTGTGGGCGACATGAGGAGGATATTTTTCGGGCCCTTGAGCCT 1860  
Db 1798 CAGCCTGTATGGT---AGAGCAACATGAGGAGAAATATTTCTCTGTCTGAGGCC 1854  
Qy 1861 AAGCTGTCTGAAGAGTTCAGGAGAGCTGGCTCCCTGGATTAAGGAAATTTGAGATC 1920  
Db 1855 CAAGCTGTGTGAGACAAATTCAGGAGGAACTGGCTTCCATGGACAGGAGATTTGAGGTC 1914

Qy 1921 CGGAATGCAAAAGCTGGACATGCCCTTACAGTACCTTGGGCCCGCAGCGTGTGGAACAGT 1980  
Db 1915 CGGAATGCAATGCTCTGGACCTGCTGTGAGTACCTTTGACCCAGCATGTTAGAGAACAGC 1974  
Qy 1981 GTGGCCATCTAAGCTGCGCACCTTTGGTTATTTTCAGCCCCCATCACCC 2030  
Db 1975 GTGACCATCTGAGAGGCTTGGCCCGCTCAGCTCCAAAGCTCCACATCC 2024

RESULT 9

AD509995  
ID ADS09995 standard; DNA; 2302 BP.

XX  
AC ADS09995;

DT 16-DEC-2004 (first entry)

XX Human therapeutic DNA - SEQ ID 232.

DE antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnary;  
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

OS Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
PI Wang D, Chen R, Zhao Qa, Wang J, Ghosh M, Xue AJ, Wang G, Zhou P;  
XX WPI; 2004-668857/65.  
DR P-PSDB; ADS10679.

XX New polynucleotide, useful in preparing a composition for diagnosing or  
PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
PT aplastic anemia or cancer for promoting wound healing.

XX Claim 1; SEQ ID NO 232; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianaemic, cytostatic and vulnary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anaemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic DNA of  
CC the invention. The current sequence is not shown explicitly within the  
CC specification but can be accessed from the WIPO web-site.

XX Sequence 2302 BP; 538 A; 623 C; 608 G; 533 T; 0 U; 0 Other;

Query Match 38.6%; Score 1030.4; DB 13; Length 2302;  
Best Local Similarity 71.0%; Pred. No. 2e-261;  
Matches 1441; Conservative 0; Mismatches 571; Indels 18; Gaps 5;

Qy 4 ATGGGTCTTACCGCATCCGCTGTCCACTGGGCGCTCGCTCTATGCCGTTCCACAC 63

Db 1 ATGGGCAAGTACACGCTCCGCTAGCACCGGGGATTGCTCTCGGGGCTCTCCCAAC 60

Qy 64 CAGGTCCAGCTGTGGCTGTGCGCCAGCAGCGGGAGCGCGCTCGGGAAGCAGCTGTGG 123

Db 61 CTGGTCAGCTATGGCTGTGGCGGAGCACCGGGAGGACACCTAGGGAAGCAGCTGCCA 120







Db 1376 CTCTGTCTCTGACGACCTGGCTGACCGGGGCTGCTGGACTCCAGGTGCTCTCTAT 1435  
Qy 1384 GCCAAGATGCGCTGGCGCTCTGGGAATCATCTATCGGTATGTGGAAGAAATGCGAGT 1443  
Db 1436 GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGAGGGGATCGTCCAC 1495  
Qy 1444 CTCACATATAAGACACAGCTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGCA 1503  
Db 1496 CTCTTCTACARAGGATGACATAGTAGAAGGGGACCTGAGCTGCAGGCTGGTGCGG 1555  
Qy 1504 GAGATCACTGAATCGGGCTGCAAGGGGCCCGAGGCTTCTCTCTCTTTACAG 1563  
Db 1556 GAGATCAAGGAGTGGGGCTGTGCCAGGCCCGAGGCTTCTCTCTCTCTCTCTCTCT 1615  
Qy 1564 GCTCGGGACAGGTTGGCCACTTTGTTCACATGTGTATCTTCACTGCAACCGGCCAAGAC 1623  
Db 1616 TCCAGAGTCAACTCTGCCATTTCTTCAACATGTGCTTCACTGCACTGCCAGCAT 1675  
Qy 1624 GCCTCTGTGCACTGGGCCAGCTGGACTGTGTAATCTTGGGTGCTTAATGCACTGCA 1683  
Db 1676 GCGGCATCAACAGGGCCAGCTGGACTGTGTAATCTTGGGTGCTTAATGCACTGCA 1735  
Qy 1684 ATGCGGCTCCCGCCCAACACCAAG---GATGCAACCGCTGGAGACAGTGTGCGCA 1740  
Db 1736 ATGCGGATGCCCGCCACCAACCAAGGAGATGTGACATGGCCACAGTGTGGGTCA 1795  
Qy 1741 CTGCGCAACTTCCACAGGCTTCTTCCAGATGTTCATCACTTGGCAGCTGGGCAAGC 1800  
Db 1796 CTACCTGATGTCCGGCAGGCTGTCTTCAATGGCCATCTCATGGCATVATGATGCGCG 1855  
Qy 1801 CAGCCGTTATGCTGGCTGGCCAGCATGAGGAGTATTTTCGGGCTTCTGAGCT 1860  
Db 1856 CAGCCAGACATGCTGCTTGGGGCCACCAAGAAATATTTCTCAGGCCCCAAGCCC 1915  
Qy 1861 AAGGCTGTCTGAAGAAGTTTCAGGGAGGAGCTGGCTGCTGATGAAGAAATTCAGATC 1920  
Db 1916 AAGCTGTGCTAACCATTCCGACAGATTTCGAAAGCTGAAAGAGATTACAGCC 1975  
Qy 1921 CGGAATGCAAGCTGGACATGCCCTACGATGCTTACGATGCTGGGCGCCAGGCTGGTGA 1980  
Db 1976 CGGAATGACAACTTGACTGGCCCTATGAAATATCTGAGCCAGCTGYATAGAACAGT 2035  
Qy 1981 GTGGCCATCTAGC 1994  
Db 2036 GTCCACATCTGAC 2049

RESULT 11  
ADQ39009  
ID ADQ39009 standard; DNA; 2867 BP.  
XX  
AC ADQ39009;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 672.  
XX  
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
KW cardiant; gene therapy; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2004058052-A2.  
XX  
PD 15-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-US040978.  
XX  
PR 20-DEC-2002; 2002US-0434778P.  
PR 10-MAR-2003; 2003US-0453135P.  
PR 30-APR-2003; 2003US-0466412P.  
PR 23-SEP-2003; 2003US-0504955P.  
XX

(APPL-) APPLERA CORP.  
Cargill M, Devlin J, Iakoubova O;  
WPI; 2004-533949/51.  
P-PSDB; ADQ39837.  
Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.  
Claim 7; SEQ ID NO 672; 145pp; English.  
The invention relates to a novel method for identifying an individual who has an altered risk for developing myocardial infarction. The method comprises detecting a single nucleotide polymorphism (SNP) in any one of the nucleotide sequences given in the specification in the individual's nucleic acids, where the presence of the SNP is correlated with an altered risk for myocardial infarction in the individual. The invention further comprises: an isolated nucleic acid molecule comprising at least 8 contiguous nucleotides where one of the nucleotides is an SNP given in the specification or its complement and encoding any one of the amino acid sequences given in the specification; an isolated polypeptide comprising an amino acid sequence given in the specification; an antibody that specifically binds to the polypeptide or its antigen-binding fragment; an amplified polynucleotide containing an SNP given in the specification and which is between about 16 and 1000 nucleotides in length; a kit for detecting an SNP in a nucleic acid, comprising the polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a nucleic acid molecule; a method of detecting a variant polypeptide; and a method for identifying an agent useful in treating or preventing myocardial infarction. The novel detection method has cardiant activity. The nucleic acids of the invention may be used in gene therapy. The method is useful in identifying an individual who has an increased or decreased risk for developing myocardial infarction and for preparing a composition for treating or preventing myocardial infarction. This polynucleotide sequence represents a human myocardial infarction-associated gene containing one or more SNPs of the invention. Note: This sequence was not shown in the specification. The sequence has come from an electronic sequence listing downloaded from the WIPO website.  
Sequence 2867 BP; 668 A; 826 C; 764 G; 598 T; 0 U; 11 Other;  
Query Match 38.1%; Score 1016.4; DB 13; Length 2867;  
Best Local Similarity 69.4%; Pred. No. 1.1e-257;  
Matches 1384; Conservative 8; Mismatches 599; Indels 3; Gaps 1;  
Qy 4 ATGGGTCTCTACCGCATCCGGCTGTCCACTGGGGCTCGCTCTATGCCGTTCCACAC 63  
Db 555 ATGGGCGCTACCGCATCCGGCTGGCCACCGGGGCTGGCTCTCTCCGGGTGCTACAC 614  
Qy 64 CAGGTGACGTGTGGCTGGTCCGCGCAGCACGCGGAGCGGCGCTCGGAAGCGACTGTGG 123  
Db 615 CGGTGACGCTTTGGCTGGTCCGCGCAGCGCGGAGCGGAGCTGAGCTGAGCTGCGG 674  
Qy 124 CCGCAGCGGGCAAGAGACAGAACTCAAGTGGGAAGTACCGGAGTATCTGGGGCGGTG 183  
Db 675 CCGCGCGGGCGAGGAGGAGGAGTTTGCATCATGCTTGCAGAGGAGCTTGGGGCTCTG 734  
Qy 184 CTGTTTGTAACTCGCGCAAGCGGACCTCTTAAGGAGCAGCGCTGCTTCTGCACTGG 243  
Db 735 CAGTTCTGTGAGGCTGCGCAAGCACCATCTGGTGTGTGGACGAGCGCTGTTCTGCGCCG 794  
Qy 244 ATCTCTGTGAGGGGCCCGGAGCGGGGACGAGGTTCAGGTTCCCTTGTTCACGCTGGGTG 303  
Db 795 ATCAGGTGCAAGGGCCCTGGAGCTGTGCGGAGGTGGCTTCCCGTGTACCGCTGGGTG 854  
Qy 304 CAGGCAACCGCGCTCTGAGCCTTGCAAGCAACCGGCCCGCACCTGTGGGCGAGACCT 363  
Db 855 CAGGCGAGGACATCTCTGAGCTTGCAGGAGGCGCCCGCCGCTGCCAGGACAACTGT 914  
Qy 364 CAGGCGCTGTTCCAGAAACACCGGAGAACAGCTGGGAAGAGAGAGAGTTGTACCGG 423

Db 915 TTGGACATGTTCCAGAAAGCATCGAGAGAGAACTGAAAAGACAGACAGCAGATCTTACTGC 974  
Qy 424 TGGGGAACCTGGAGGACGGGTTAAATTCGAAATATGGCTGGGGCCAAACTATATGACCTC 483  
Db 975 TGGGCCACCTGGAGAGAGGGTTACCCCTGACCATCGCTGCAGACCGTAAGATGATCTA 1034  
Qy 484 CTTGTGGATGAGCGATTTCTTGGAGAGCAAGAGAGTTGACTTTTGAGGTTTGGCTGGCCAAAG 543  
Db 1035 CCTCCAAATATGAGATTCCATGAGGAGAGAGGCTGGACTTTTGAATGGACACTGAAGGCA 1094  
Qy 544 GGCTGGCCGACCTCGTATCAAAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGATCTA 603  
Db 1095 GGGGCTCTGGAGATGGCCCTCAAACRTGTTTACACCCCTCGAGCTCTCTGGAATCCCTTA 1154  
Qy 604 GATGACTTTAAACCGGATTTCTCGTGGTGCAGAGCAAGCTGCTCAGCGCGTGGCGGAC 663  
Db 1155 GAAGACTTTGATCAGATCTTCTGGGGCCAGAGAGTGGCTGGCTGAGAGGTTTCCGCCAG 1214  
Qy 664 TCCTGGAAGGAAGATGCTTTATTTGGGTACACAGTTTCTTAATGGCCCAACCCCGTGGTG 723  
Db 1215 TGTGGCAGGATGATGAGTTGTTTCACTACAGTTCTCTCAATGGTGCCCAACCCCATGCTG 1274  
Qy 724 CTGAGGGCTCTGCTCAGCTTCTGCTCGCTAGTGTTCCTCCAGGCATGAGGAACCTG 783  
Db 1275 TTGAGACGGCTCGACCTCTCTGCCCTCCAGGCTAGTGTGCTGCCCTCRGGGATGGAAGAGCTT 1334  
Qy 784 CAGGCCAGCTGGAGAGGAGCTGGAGGAGGACACTGTTGAAAGCTGACTTCTCCCTG 843  
Db 1335 CRGGCTCACTGGAGAAAGAACTTCAGATGGTTCCCTGTTTGAAGTGAATTCATCCTT 1394  
Qy 844 CTGGATGGATCAAGGCCAACGTCATTCTCTGTAGCCAGCAGACCTGGCTGCCCTCTTA 903  
Db 1395 CTGGATGGAATTCAGCCCAAGTATCCGAGGAGAGAGCAATACCTGGCTGCCCCCTC 1454  
Qy 904 GTCATGCTGAAATGCGCTGATGGGAACTCTTGGCCATGTCTATCCAGCTCCAGCTG 963  
Db 1455 GTTATGCTGAAGATGGAGGCCAATGGGAAGCTCGAGGCCATGGTCTATCCAGATTCAGCCT 1514  
Qy 964 CCCGACAGAGTCCCCACACCTCCCTTTTCTTGCTACGATCCCCCAATGGCTGG 1023  
Db 1515 CCARCCAGCTCTCCAAACCCCAACACTGTTCTGGCTCAGACCCCCCACTTGGCTGG 1574  
Qy 1024 CTTCTGGCCAAATGCTGGTGCAGCTCTGACTTCCAGCTCCATGAGCTGCAGTCTCAT 1083  
Db 1575 CTCCTGSCAAAGTCTGGTCCGAAATTCAGATTTCCAACTGCACGAGATCCAGTATCAC 1634  
Qy 1084 CTTCTGAGGGGACACTGTAGTGGCTGAGTCAATTTGTTGGCCACCATGAGTGGCTGCCG 1143  
Db 1635 TTGCTGAACACKCACTGCTGGTGGCTGAGTCAATGCTGCGCCACCATGCGGTGCTCCCA 1694  
Qy 1144 TCGATACATCTTCTCAAGCTTATAATTTCCACCTGGATACACCTTGGAAATTAAC 1203  
Db 1695 GGACTGACCCCATCTTCAAGTTCCTGATCCCCCATATCCGCTACACCATGGAATCAAC 1754  
Qy 1204 GTCCGGCCAGGACTGGGCTGCTCTGACATGGGAATTTTCGACCAGATAATGAGCACT 1263  
Db 1755 ACCGGGCCCGGACCACTCATCTCAGATGGAGGAATTTTGTAAAGGCAGTGAGCA 1814  
Qy 1264 GGTGGGGGACGACGTGAGCTGCTCAAGCAAGCTGGAGCCCTTCTTAACCTACAGTCC 1323  
Db 1815 GGTGGAGGGGGCCATGTACAGTTGCTCCGTGGCGGCGAGCTCAGCTGACCTACTGCTCC 1874  
Qy 1324 TTCTGTCCCTCATGACTTTGGCGGACCGGGGCTCCTGGAGTGAAGTCTTCTCTCTAT 1383  
Db 1875 CTCTGTCTCTGACGACCTGGCTGACCGGGGCTGCTGGGACTCCAGGTGCTCTCTAT 1934  
Qy 1384 GCCAAGATCGCTGCGGCTCTGGGAATCATCTATCGGTATGTGGAAGGAATCGTAGT 1443  
Db 1935 GCCCATGATGTTTACGGCTCTGGAGATCATTTGCCAGGTATGTGGAGGGGATCGTCCAC 1994  
Qy 1444 CTCACATTAAGACAGCTGGCTGTGAAAGACGACCCAGCTGCGACCTGGTGTGGA 1503  
Db 1995 CTCTTTCTACCARAGGATGACATAGTGAAGGGGACCCCTGAGCTGCAGGCTGGTGTGCGG 2054

Qy 1504 GAGATCACTGAATACTGGGCTGCAAGGGGCCAGGACCGAGGGTTTCCTCTCTTTACAG 1563  
Db 2055 GAGATCAGGAGGTGGGGCTGTGCCAGGCCAGGACCGAGGTTTCCTCTCTCTTCCAG 2114  
Qy 1564 GTCGGGACAGGTTTGGCCACTTTTGCACCATGTGTATCTTTCACCTGCACCGGCCAACAC 1623  
Db 2115 TCCCAGAGTCAACTCTGCCATTTTCTCACCATTGCGCTTTCACGCTGCATGCCCCAGCAT 2174  
Qy 1624 GCCTCTGTGCACCTGGGCCAGCTGGACTGGTACTCTTTGGGTGCCTAATGCACCCCTGCACG 1683  
Db 2175 GCCGCATCAACACAGGCCAGCTGGACTGGTATGCTTGGGTCCCTAATGCTCCATGCACA 2234  
Qy 1684 ATGCGGCTGCCGCCGCCCAACCAAG---GATGCAACGCTGGAGACAGTGTATGGCGACA 1740  
Db 2235 ATGCGGATGCCGCCGCCCAACCAAGCAAGGAAAGATGTGACGATGGCCACAGTGTGGGTCA 2294  
Qy 1741 CTGCCCACATTCACACAGGCTTCTCTCCAGATGTCCATCATCTTGGCAGCTGGCAGACGC 1800  
Db 2295 CTACCTGATGTCCGGCAGGCTGTCTTCAAATGGCCATCTCATGGCATTTGATGCTGCCGC 2354  
Qy 1801 CAGCCGTTATGCTGGCTGGGCCAGCATGAGGAGGAGTATTTTTCGGGCCCTGAGCCT 1860  
Db 2355 CAGCCAGACATGGTGGCTCTGGGCCACCAAGAAATAATTTCTCAGGCCCAAGGCC 2414  
Qy 1861 AAGGCTGTGCTGAAGAAGTTTCAGGGAGGAGCTGGCTGCCCTCGATAAGAAATTTGAGATC 1920  
Db 2415 AAGGCTGTGCTAAACCAATTTCCGAAACAGATTTGGAAGAGCTGAAAAGGAGATTACAGCC 2474  
Qy 1921 CGAATGCAAGCTGGACATGCCCTACGAGTACCTGCGGCCAGCGTGGTGGAAACAGT 1980  
Db 2475 CGAATGAGCAACTTGAATGAGTGGCCCTATGAATATCTGAAGCCAGCTGTATAGAGAACGT 2534  
Qy 1981 GTGGCCATCTAAGC 1994  
Db 2535 GTACCATCTGAGC 2548

RESULT 12  
AAC58018  
ID AAC58018 standard; DNA; 2343 BP.  
XX AC AAC58018;  
XX AC  
XX DT 25-JAN-2001 (first entry)  
XX XX  
DE Arachidonic acid metabolism related genomic biallelic marker #652.  
XX Human; biallelic marker; arachidonic acid metabolism; genotyping;  
KW detection; hybridisation; phenotype; SNP; polymorphic base;  
KW single nucleotide polymorphism; hybridisation assay; sequencing assay;  
KW specific amplification assay; identification; ERBM; 12-LO-RBM;  
KW elcabanoid-related biallelic marker; 12-LO-related biallelic marker; ds.  
XX Homo sapiens.  
OS  
XX XX  
XX PN WO200047771-A2.  
XX XX  
PD 17-AUG-2000.  
XX PF 11-FEB-2000; 2000WO-IB000184.  
XX PR 12-FEB-1999; 99US-0119917P.  
XX PR 23-MAR-1999; 99US-00275267.  
XX PR 07-MAY-1999; 99US-0133200P.  
XX (GEST ) GENSET.  
PA Blumenfeld M, Bougueleret L, Chumakov I;  
XX WPI; 2000-571881/53.  
XX P-PSDB; AAB24019.  
XX XX

PT Novel biallelic markers useful for detecting conditions and genotypes  
PT associated with arachidonic acid metabolism.  
XX  
PS Claim 70; Page 797-799; 802pp; English.

XX The present invention describes polynucleotides including biallelic  
CC markers derived from genes involved in arachidonic acid metabolism and  
CC from genomic regions flanking those genes. Methods from the present  
CC invention may be used to select individuals for clinical trials and  
CC predict responses to treatment with drugs. The polynucleotides may be  
CC used in hybridisation assays, sequencing assays and specific  
CC amplification assays for identifying an eicosanoid-related biallelic  
CC marker (EREM) or 12-LO-related biallelic marker, and for amplifying a  
CC segment of nucleotides containing an BRM. The polynucleotides are useful  
CC in diagnostic kits. The markers may be used to detect conditions and  
CC genotypes associated with arachidonic acid metabolism. AAC57367 to  
CC AAC58018 and AAB24019 and AAB24020 represent sequences used in the  
CC exemplification of the present invention. N.B. Polymorphic bases (single  
CC nucleotide polymorphisms also known as SNPs) in the polynucleotide  
CC sequences from the present invention have been given as their  
CC corresponding degenerate bases e.g. a polymorphic base of C or T has been  
CC given as Y

XX Sequence 2343 BP; 511 A; 688 C; 636 G; 495 T; 0 U; 13 Other;

Query Match 37.9%; Score 1013.6; DB 3; Length 2343;  
Best Local Similarity 69.2%; Pred. No. 5.7e-257;  
Matches 1380; Conservative 11; Mismatches 600; Indels 3; Gaps 1;

QY 4 ATGGGTCTCTACCGCATCCCGTGTCCACTGGGGCTCGCTATGTCGGGTTCCACACAC 63  
DB |||||  
QY 64 CAGGTGCAGCTGTGGTGTGCGCCAGCACGGAGCGCGCTCGGGAAGCGACTGTGG 123  
DB |||||  
QY 100 CGGTGCAGCTTGGTGTGCGGACCGCGGGAGCGGAGCTGGAGCTGCAGCTGCGG 159  
DB |||||  
QY 124 CCCGACCGGGGCAAGGAGACAGAACTCAAGGTGGAGTAGTCCGAGGTATCTGGGGCGGCTG 183  
DB |||||  
QY 160 CCGGCGCGGGCGAGGAGGAGGTTGATCATGACGTTGACAGAGACTTGGGGCTCCTG 219  
DB |||||  
QY 184 CTGTTTGTGAACCTGGCGAAGACGGACCTCTTAAGGACGAGCGCTGTCTGCAACTGG 243  
DB |||||  
QY 220 CAGTTTGTGAGGCTGCGCAAGCACCACTGGCTGGTGGAGACGCGGTGTTCTGCGACCG 279  
DB |||||  
QY 244 ATCTCTGTCAGGGCCCGGAGCGGGGACGAGTCAAGTTCCTTTGTTACCGCTGGGTG 303  
DB |||||  
QY 280 ATCAGGTCAGGGCCCTGGAGCTCGCGGAGGTGGCCCTTCCGTGCTACCGCTGGGTG 339  
DB |||||  
QY 304 GAGGGCAACGGGCTCTGAGCCTGCTGAAAGGACCGCGCGCACTGTGGGCGAGGACCT 363  
DB |||||  
QY 340 CAGGGCGAGGACATCTGAGCCTGCCCCGAGGGCACCGCCCGCTGCCAGGACAAATGCT 399  
DB |||||  
QY 364 CAGGGCTCTTCAGAAACACCGGAGAGAGCTGGAAAGAGAGAGAGAGTGTACCGG 423  
DB |||||  
QY 400 TTGGACATGTTCCAGAAAGATCGAGAGAGAGAACTGAAAGACAGACAGCATCTACTGC 459  
DB |||||  
QY 424 TGGGGAACCTGGAAGACGGGTTAATCTGAATATGCTGGGGCCCAAACTATATGACCTC 483  
DB |||||  
QY 460 TGGGCCCTCTGGAAGAGAGGGTTACCCCTGACCATCGCTGACAGCGTAAGGATGATCTA 519  
DB |||||  
QY 484 CCTGTGGATGAGCGATTTCTGGAAGACAAAGAGAGTTGACTTTTGGGTTTTCGCTGGCCAA 543  
DB |||||  
QY 520 CCTCCAAATATGAGATTCCATGAGGAGAGAGGCTGGAATTTGATGGACACTGAAGGCA 579  
DB |||||  
QY 544 GGGCTGGCGCACTCGCTATCAAGACTCTCTAAATGTTCTGACTGTCTGGAAGAGATCTA 603  
DB |||||  
QY 580 GGGGCTCTGGAGATGGCCCTCAACRTGTTTACACCCCTCTGAGCTCTCTGGAATGCTCTA 639  
DB |||||  
QY 604 GATGACTTCAACCGGATTTCTGGTGTGCTCAGAGCAAGCTGGCTGAGCGCTGGGGAC 663  
DB |||||  
QY 640 GAAGACTTTGATCAGATCTTCTGGGGGCCAAGAGAGTGGCCCTGGCTGAGAAGGTTTGGCCAG 699  
DB |||||

QY 664 TCCTGGAAGGAAGATGCCCTTATTTGGGTACCAAGTTTCTTAATGGCGCCACCCCGTGGTG 723  
DB |||||  
QY 700 TGTGGCAGGATATGAGTTGTTTCACTACCAAGTTTCTCAATGGTGCCCAACCCCATGCTG 759  
DB |||||  
QY 724 CTGAGCGCTCTGCTCACCTTCTCTGCTGCTAGTGTTCCTCCAGGATGAGGAAGTGG 783  
DB |||||  
QY 760 TTGAGTCTGAGCTCTGCTCTGCTCTCAAGCTAGTGTGCTCGGATGGAAGAGCTT 819  
DB |||||  
QY 784 CAGGCCCTGAGCTGGGAAGGAGCTGGAGGAGGACACATGTTTGAAGCTGACTTCTCCCTG 843  
DB |||||  
QY 820 CRGGCTCAACTGGAGAAAGAACTTCAGAAATGTTTCCCTGTTTGAAGCTGACTTCTATCCT 879  
DB |||||  
QY 844 CTGGATGGATCAAGGCCCAACGTCATCTCTGTAGCAGCAGCAGCAGCTGGCTGCCCTCTA 903  
DB |||||  
QY 880 CTGGATGGAAATTCACAGCCAACTGATCCGAGGAGAGAACTATCTGGCTGCCCTCTC 939  
DB |||||  
QY 904 GTCATGCTGAAATTCAGCCTGATGGGAAATCTTTGGCCCATGTCATCCAGCTCCAGCTG 963  
DB |||||  
QY 940 GTTATGCTGAGATGGAGCCCAATGGGAAGCTGAGAGCCCATGCTCATTCAGATTCAGCCT 999  
DB |||||  
QY 964 CCCCGCACAGGATCCCAACCACTCTCCCTTTTCTTGGCTTACGGATCCCCCAATGGCTCG 1023  
DB |||||  
QY 1000 CCCARCCCGAGCTCTCCAAACCCCAACACATGTTCTGCTGCCCTCAGACCCCSACTTGGCTGG 1059  
DB |||||  
QY 1024 CTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCCAGCTCCAGCTCAGCTCAGTCTCAT 1083  
DB |||||  
QY 1060 CTCCTGGCAAGTCTCTGGGTCCGAAATTCAGATTTTCCAACTGCACAGATCCAGTATCAC 1119  
DB |||||  
QY 1084 CTTCTGAGGGGACACTTGCAGCTGAGTTCATGTTGTGGCCACCATGAGTGGCTGCCG 1143  
DB |||||  
QY 1120 TTGCTGAAACACACACTCTGGTGGCTGAGTCTATGCTGTCGCCCACTATGGGTGGCTCCCA 1179  
DB |||||  
QY 1144 TCGATACATCTCTTCAAGCTTATAATTCGCCACCTGCCATACACCTCGTGAATTAAC 1203  
DB |||||  
QY 1180 GGACTGCACCCCATCTTCAAGTTCTGATCCCCCATATCCGCTACACCATGGAATCAAC 1239  
DB |||||  
QY 1204 GTCCGGGCGAGACTGGGGCTGTCTGACATGGGAATTTTCGACAGATATAGCACT 1263  
DB |||||  
QY 1240 ACCCGGGCCGACCCAACTCATCTCAGATGAGGAATTTTGTAAAGCAGTGAAGACA 1299  
DB |||||  
QY 1264 GGTGGGGAGGCCAGCTGCTCAAGCAAGCTGGAGCTTCTTAACTACAGCTCC 1323  
DB |||||  
QY 1300 GGTGAGGGGGCCATGTATACAGTTGCTCCGTGGGGGAGCTCAGTGAACCTACTGCTCC 1359  
DB |||||  
QY 1324 TTCTGTCCCTCTGATGACTTGGCCGACCGGGGGCTCTTGGGAGTGAAGTCTTCTCTAT 1383  
DB |||||  
QY 1360 CTCTGTCTCTGACGACTGGCTGACCGGGGGCTGTCTGGGACTCCAGGTGCTCTCTAT 1419  
DB |||||  
QY 1384 GCGCAAGATGCGCTGCGGCTCTGGGAATCATCTATTCGGTATGTGGAGGAATCTGTAGT 1443  
DB |||||  
QY 1420 GCGCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGATCATTTGGAGGGATTCGTCCAC 1479  
DB |||||  
QY 1444 CTCACATATAGACAGAGCTGGCTGTGAAGACGACCCAGAGCTCAGACCTGGTGTGCA 1503  
DB |||||  
QY 1480 CTCCTTCTACAPAGGAGATGACATAGTGAAGGGGGACCTTGAGCTCAGGCTGGGTGTCG 1539  
DB |||||  
QY 1504 GAGATCACTGAAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCTGTCTCTTTACAG 1563  
DB |||||  
QY 1540 GAGATCAGGAGGTGGGCTGTGCCAGGCCAGGACCGAGGTTTCCCTGTCTCTTCCAG 1599  
DB |||||  
QY 1564 GCTCGGGAACAGGTTTGCACCTTGTCAACATGTGTATCTTTCACCTGACCGGGCCAAAC 1623  
DB |||||  
QY 1600 TCCAGAGTCAACTCTGCCATTTCTCACCATTGTGCGTCTTTCAGCTGCACTGCCCAGCAT 1659  
DB |||||  
QY 1624 GCCTGTGCACTGGGCGAGCTGAGCTGGTACTTCTGGGTGCTCTTAAGTCACTCCCTGCA 1683  
DB |||||  
QY 1660 GCGGCATCAACCCAGGGCGAGCTGGACTGGTATGCTGGGTCCCTTAATGTCTCATGCA 1719  
DB |||||  
QY 1684 ATGCGGCTGCCCGCCCAACCAACCAAG--GATGCAACGCTGGAGACAGTGTATGCGGACA 1740  
DB |||||  
QY 1720 ATGCGGATGCCCGCCCAACCAACCAAGGAGATGTGACGANGGCCACAGTGTATGGGTCA 1779  
DB |||||  
QY 1741 CTGCCCAACTTTCACACAGGCTTCTCTCCAGATGTCTCATCTTGGCAGCTGGGCGAGACGC 1800  
DB |||||

Db 1780 CTACCTGATGTCGGGAGGCTGCTCTCAATGGCCATCTCATGGCATCTGAGTCGCGC 1839  
QY 1801 CAGCCGTTATGCTGCTGGGCGCAGCATGAGGAGGATATTTTCGGGCGCTGAGCCT 1860  
Db 1840 CAGCCAGACATGCTGCTCTGGGGCCACCAAGAGAAATATTTCTCAGGCCCCAAGCCC 1899  
QY 1861 AAGGCTGTGCTGAAGAAGTTTCAGGAGGAGCTGGCTGCCCTGGATTAAGAAATTTGAGATC 1920  
Db 1900 AAGCTGTGCTAAACCAATTCGAAACAGATTGGAAAAGGTRGAAAAGAGATTACAGCC 1959  
QY 1921 CGAATGCAAAAGCTGACATGCGCTACGAGTACCTCGGCGCCAGCGTGGTGGAAAACAGT 1980  
Db 1960 CGAATGAGCAACTGACTGGCCCTATGAATATCTGAAGCCAGCTGCATAGAGAACAGT 2019  
QY 1981 GTGCCATCTAAGC 1994  
Db 2020 GTCCATCTGAGC 2033

RESULT 13

ADSO9996  
ID ADS09996 standard; DNA; 2218 BP.

XX AC

XX ADS09996;

XX 16-DEC-2004 (first entry)

XX Human therapeutic DNA - SEQ ID 233.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
XX inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
XX aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

XX Homo sapiens.

XX WO2004080148-A2.

XX 23-SEP-2004.

XX 30-SEP-2003; 2003WO-US030720.

XX 02-OCT-2002; 2002US-0416186P.

XX (NUVE-) NUVELO INC.

XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;  
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
XX WPI; 2004-668857/65.  
XX P-PSDB; ADS10680.

XX New polynucleotide, useful in preparing a composition for diagnosing or  
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
XX aplastic anaemia or cancer for promoting wound healing.

XX Claim 1; SEQ ID NO 233; 718pp; English.

XX The invention relates to a novel isolated polynucleotide and the encoded  
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,  
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may  
XX be useful in preparing a composition for diagnosing or treating  
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
XX disorders, such as aplastic anaemia or cancer, as well as for promoting  
XX wound healing. The molecules may also be utilised during gene therapy  
XX procedures. The current sequence is that of a human therapeutic DNA of  
XX the invention. The current sequence is not shown explicitly within the  
XX specification but can be accessed from the WIPO web-site.

XX Sequence 2218 BP; 511 A; 600 C; 585 G; 522 T; 0 U; 0 Other;

Query Match 34.4%; Score 918.6; DB 13; Length 2218;  
Best Local Similarity 68.0%; Pred. No. 7.3e-232;

Matches 1379; Conservative 0; Mismatches 549; Indels 101; Gaps 3;  
QY 4 ATGGGCTCTCTACCGCATCGCGTGTCCACTGGGGCTCGCTCTATGCGGGTCCCAACAC 63  
Db 1 ATGGGCAAGTACACGGTCCGGTAGCCACCGGGGATTTGCTCTGGCGGGCTCTCCCAAC 60  
QY 64 CAGGTGCAGCTGTGGCTGGTCCGCCAGCACCGGGAGGGCGCTCCGGGAAGCAGCTGTGG 123  
Db 61 CTGGTGCAGCTATGCTGGTGGCGAGCACCGGGAGGAGACCTAGGGAAGCAGCTGCCA 120  
QY 124 CCGCACGGGGAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCGGCTG 183  
Db 121 CCGGTGTGGGGAAGGAGGAGAGTGTGAGATCGACGCTCCCTCGCACCTGGGGCGCCTC 180  
QY 184 CTGTTTGTGAAGTCCGCAACCGCACCTCTCTTAAGGACGAGCGCTGGTTCGCAACTGG 243  
Db 181 CTGATGGTGAAGTCCGCAACACAACTGCTGTTGAGTCTCGACTGGTTCGCAAGTGG 240  
QY 244 ATCTCTGTGCAGGGCCCGGAGCCCGGGGACGAGGTCAAGTTCCTTGTTCACCGCTGGGTG 303  
Db 241 ATCTCAGTGCAGGGCCCGGGGACCCAAAGCGAGGCGCTTTTCCCTGCTACCGCTGGGTG 300  
QY 304 GAGGCAACGGCGTCTGAGCCTGCTGAGGACCGGCGGACACTGTGGGGAGGACCT 363  
Db 301 CAGGGCCACGGAATTTATCTGCCCTGCTGAGGGA----- 334  
QY 364 CAGGGCTGTTCCAGAAACACCGGGAAGAGAGCTGGAAAGAGAGAGTGTGTACCGG 423  
Db 335 -----GG 336  
QY 424 TGGGGAACCTGGAAGACGGGTAAATCTGAATATGGCTGGGGCCAAACTATATGACCTC 483  
Db 337 TGGGCTCTCTGGAAGATGGGTAAATCTGCTATAGCAGGGAATAGGCAACCGGACCTT 396  
QY 484 CTTGTGATGACCGATTTCTGGAAGACAGAGATTGACTTTGAGGTTTCGCTGGCCAG 543  
Db 397 CCTAGGGAAGGAGTTCCTCGAGGATAGGATTTAGACTTTAATGTCTCCCTAGCAAAA 456  
QY 544 GGGCTGGCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGATCTA 603  
Db 457 GGGTTGAAGGACTTGGCCATTAAGGGGACACTGGATTTCTATAAATTTGTGAAAGGCTG 516  
QY 604 GATGACTTCAACCGGATTTTCTGGTGTCTAGACAGCAAGCTGGCTGAGCGCTGGGGAC 663  
Db 517 GAAGATTTCAAAAAAATATTTCCACATGSAAGACTGTCTCCGGCTGAGCGGTATGAT 576  
QY 664 TCCTGGAAGGAAGATGCTTATTTGGGTACAGTTTCTTAATGGGCGCCAAACCGCTGGTG 723  
Db 577 TCTTGAAGAATGATGCTCTTTGGGTACCAAGTTTCTCAATGGTGCAGAACCCCATGCTC 636  
QY 724 CTGAGGCGCTCTGCTCACCTTCTGCTGCTAGTGTTCCTCCAGGCAATGAGGAAGCTG 783  
Db 637 CTGAGGTGTTCTTCAAGGCTCCAGCGTCCCTGGTGTGCTGCTCCAGGGAATGAAGACTTG 696  
QY 784 CAGGCGCAGCTGGGAAGGAGCTGGAGGGAGGACACATGTTTCGAAGCTGACTTCTCCCTG 843  
Db 697 AAGACCCAGCTGGAGAAGAACTCCAGGCTGGATCTCTGTTTGAAGTGAATTTCTCTTG 756  
QY 844 CTGGATGGGATCAAGGCCAAACCTCATTTCTGTAGCAGCAGCACCTGCTGCCCTCTA 903  
Db 757 CTGGATGGAGTCAAGCTAAATGTATCATATTTTAAAGCAGCAATGCGTGGCAGCCCCCTTG 816  
QY 904 GTCATGCTGAATTCAGGCTCATGGGAACCTTGGCCCATGCTCATCCAGCTCCAGCTG 963  
Db 817 GTCATGCTGAAGCTTCAGGCTGATGAGGACTCTTACCCATGCTATCCAGCTCCAGCCA 876  
QY 964 CCGCGCACAGGATCCCCACACCTCCCTTTTCTTGCTCATCGGATCCCCCAATGGCCTGG 1023  
Db 877 CTTGACACGGATGTCCTCCCACTCTGCTCTTTTCTGCTCATCCCCCATGGCCTGG 936  
QY 1024 CTTCTGGCCAAATGCTGGGTGGGAGCTCTGACTTCCAGCTCGATGAGCTGAGTCTCAT 1083  
Db 937 CTCCTGGCCAAAGACCTGGGTCCGGAGCTCTGATTTCCAGCTGCAGCAGTTACAGTCACAT 996





Db	1896	-----GTA	869	GGTTGGGCTTTTCTACAATAGTGA	810
Qy	424	TGGGGAACCTGGAGGACGGTTAAATTC	1497	GTGTCAGAGATCACTGAAATCGGCTG	1556
Db	1889	TGGGGCTCTCTGGAAAGATGGTTAAATCC	809	GTGTCAGAGAGATGATGAGACTGGACT	750
Qy	484	CTGTGTGATGAGCGATTTCTTGGGAACA	1557	TTTACAGGCTCGGGACCAAGGTTTGCA	1616
Db	1829	CCTAGGACGAGCGATTCCTCGAGGATAG	749	CTTAGAGTCCCGGGCTCAGCTCGCCAC	690
Qy	544	GGGCTGGCCGACCTCGCTATCAAAAGACT	1617	CCAAACAGCGCTCTGTGCACCTGGGCG	1676
Db	1769	GGGTTGAAGGACTTGGCCATTAAAGGGGA	689	TCAGCATGCTTCTAAACACCTGGGCGA	630
Qy	604	GATGACTTCAACCGGATTTCTGGTGTGTC	1677	CTGCACGATGCGGCTGCGCCCGCCCA	1736
Db	1709	GAAGATTTTCAAAAATAATTTCCACATG	629	ATGCACCATGCAAGAACCCCGCCCAT	570
Qy	664	TCCTGGAAGGAAGATGCTTATTTGGGTAC	1737	GACACTGGCCCAACTTCCACAGGCTTCT	1796
Db	1649	TCCTGGAGAAATGATGCTTCTTTGGGTAC	569	CTTACTTGCCCAATCTCCACAGGCACG	510
Qy	724	CTGAGGCGCTCTGCTCACCCTTCCTGCTG	1797	AGCCAGCGCCCTTATGCTGGCTGTGGC	1856
Db	1589	CTGAGGTGTTCTTCAAGGCTCCAGGCTGC	509	ACGCCAGCGCTGTCTAT-----GCAT	465
Qy	784	CAGGCCACCTGAGAGAGCTGGAGGAGGCA	1857	GCCTAAGGCTGTGCTGAAGAAGTTCA	1916
Db	1529	AAGACCCAGCTGGAGAAAGAACTCCAGG	464	GCCCAAGCTGTCTGAGACAAATTCAG	405
Qy	844	CTGGATGGGATCAAGGCCAACGTCATTCT	1917	GATCCGGAATCAAAAGCTGGACATGCC	1975
Db	1469	CTGGATGGAGTCAAGCCTAATGTCTATCAT	404	GGTCCGGAATGAGTCTGAACTTGCCTG	345
Qy	904	GTCACTGTGAAATTTGAGCCTGATGGA	1976	ACAGTGTGCCCATCTTAAG	1993
Db	1409	GTGCTGTGAAGCTTGAGCCTGATGAGGACT	344	ACAGGCTGACCATCTGAG	327
Qy	964	CCCGCACAGGATCCCAACACCTCCCTTTCT	RESULT 15		
Db	1349	CCTTGACACGAGTGTCCCCACCTCTGCTCT	ADSL1348/c		
Qy	1024	CTTCTGCCCCAAATGCTGGGTGCGCAGCT	ID ADS11348	standard; DNA; 2227 BP.	
Db	1289	CTCCTGGCCAAAGCTTGGTCCGGAGCTCTG	AC	ADSL1348;	
Qy	1084	CTTCTGAGGGGAACATTTGATGGCTGAGGT	XX	16-DEC-2004 (first entry)	
Db	1229	CTGCTGAGGGGACACTTGATTTGCTGAGGT	DE	Human therapeutic contig DNA - SEQ	1585.
Qy	1144	TCGATACATCTTCTTCAGCTTATATTTCC	XX	antiinflammatory; neuroprotective;	antianaemic; cytostatic; vulnerary;
Db	1169	AGCCTCCATCTATCTACAAAGCTCTGATC	KW	inflammatory; haematopoiesis; immu	neurodegenerative; stem cell;
Qy	1204	GTCCGGCCAGGACTGGGCTGTCTCTGACAT	KW	aplastic anaemia; cancer; wound hea	ling; gene therapy; ds; gene.
Db	1109	ACGCTGGCCAGAGTAGTCTTGCTCCGAAT	XX	Homo sapiens.	
Qy	1264	GGTGGGGAGGCCACGTGACGTGCTCAAGCA	XX	WO2004080148-A2.	
Db	1049	GGTAGTGAAGCCACGTGGACATTCCTTCA	PN	23-SEP-2004.	
Qy	1324	TTCTGTCCCTCATGATCTGGCCGACCGGG	XX	30-SEP-2003; 2003WO-US030720.	
Db	989	CTCTGTCTCTCATGACCTGGCTGACCGGT	PF	02-OCT-2002; 2002US-0416186P.	
Qy	1384	GCCCAAGATCGCTGCGGCTCTGGGAAATC	XX	(NUVE-) NUVELO INC.	
Db	929	GGCTAAGATGCCATCAGGCTGTGGGNAAT	XX	Tang YT, Asundi V, Ren F, Zhang J,	Wehrman T, Wang Z, Ma Y;
Qy	1437	CGTAGTCTCCATATTAAGACACGCTGGTG	PI	Wang D, Chen R, Zhao Qa, wang J,	Ghosh M, Xue AJ, Weng G, Zhou P;
			XX	WPI; 2004-668857/65.	
			DR	P-PSDB; ADS11946.	
			XX	New polynucleotide, useful in prepar	ing a composition for diagnosing or
			PT	treating inflammatory, neurodegener	ative or stem cell disorders, e.g.,

PT aplastic anemia or cancer for promoting wound healing.  
XX Example 2; SEQ ID NO 1585; 718bp; English.  
PS  
XX

CC The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianemic, cytostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic contig  
CC DNA of the invention. The current sequence is not shown explicitly within  
CC the specification but can be accessed from the WIPO web-site.  
XX

XX Sequence 2227 BP; 527 A; 589 C; 600 G; 511 T; 0 U; 0 Other;  
SQ

Query Match 33.8%; Score 901.6; DB 13; Length 2227;  
Best Local Similarity 68.3%; Pred. No. 2.3e-227;  
Matches 1364; Conservative 0; Mismatches 529; Indels 105; Gaps 4;

QY 4 ATGGGCTCTACCGCATCCCGCTGTCCACTGGGGCTCGCTCTATGCCGGTTCCAAACAAC 63  
DB 2227 ATGGGCAAGTACACGCTCCGCTAGCACCGGGGATTTGCTCTGGGGGCTCTCCCAAC 2168  
QY 64 CAGGTGAGCTGTGGCTGTGGCGGACGACGGGAGCGCGCTCGGGAAGCAGCTGTGG 123  
DB 2167 CTGGTCAGCTATGGCTGTGGCGGACGACGGGAGGCGACCTAGGGGAAGCAGCTGCCA 2108  
QY 124 CCGCACGGGCAAGGAGACAGAACTCAAGTGGAAAGTACCGGAGTATCTGGGGCGCTG 183  
DB 2107 CCGGTGTGGGAAAGAGGACAGAGTTGAGATCGACGTCCCTCGACCTGGGGCGCTC 2048  
QY 184 CTGTTTGTGAAACTGCGCAAAACGGCACCTCTCTTAAGGACGACGCCCTGGTTCTGCAACTG 243  
DB 2047 CTGATGTTGAAGCTGCGCAAAACAAACGCTGCTGTGAGTCTGACTGGTTCTGCAAGTG 1988  
QY 244 ATCTGTGCGAGGCGCCGAGCGCGGGAGGAGTCAAGTTCCTTGTACCGCTGGGTG 303  
DB 1987 ATCTGAGTGCAGGCGCGGGAGCCCAAGGCGCGCGCTTTTTCCTCCCTGTACCGCTGGGTG 1928  
QY 304 GAGGGCAACGGCTCTGAGCCCTGCTGAAGGCAACCGCGGACCTGTGGGCGAGGACCT 363  
DB 1927 CAGGGCCACGGAATATCTGCCCTGCTGAGG----- 1897  
QY 364 CAGGGCTGTGTTCCAGAAACACACGGGAAGAGAGCTGGAAGAGAGAAAGTTGTACCGG 423  
DB 1896 -----GTACTGG 1890  
QY 424 TGGGAAACCTGGAGACGGTTAAATCTGAATATGGCTGGGCGCAAACTATATGACCTC 483  
DB 1889 TGGGGCTCTGGAAAGATGGGTTAAATCTGCTTATAGCAGGGAATAGGCAACCGGACCTT 1830  
QY 484 CTTGTGATGAGGATTTCTGGAAGACAGAGATTTGACTTTGAGCTTTGGCTGGGCGCAAG 543  
DB 1829 CCTAGGGAAGAGGATTTCTCGAGGATAAGGATTTAGACTTTAATGTCTCCCTAGCAAAA 1770  
QY 544 GGGCTGGCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTTGCTGGAAGGATCTA 603  
DB 1769 GGGTTGAAGGACTTGGCCATTAAAGGGACACTGGATTTCTAATAATTTGTGAAAGGCTG 1710  
QY 604 GATGACTTCAACCGGATTTTCTGGTGTGTGTGTCAGAGCAAGCTGGCTGAGCGCGTGGGGAC 663  
DB 1709 GAAGATTTCAAAAAAATTTCCACATGGAAGACTGTCTGGCTGAGCGGGTTTATGAT 1650  
QY 664 TCTGGAAGGAGATGCTTATTTGGTACCAAGTTTCTTAATGGCCCAACCCCGTGGT 723  
DB 1649 TCTTGAAGAAATGATGCTTCTTTGGGTACCAAGTTTCTCAATGGTCAAAACCCCATGCTC 1590  
QY 724 CTGAGCGCTCTGCTCACCTTCCTGCTCGCTAGTGTTCCTCCAGGCATGGAGGAACCTG 783  
DB 1589 CTGAGGTGTTCTCAAGGCTCCAGGCTCCAGCTGCCTGCCTCCAGGATGGNAGACTTG 1530

QY 784 CAGGCCAGCTGGAGAGGAGCTGGAGGGAGGCACACTGTTGAAAGCTGACTTCTCCCTG 843  
DB 1529 AAGACCCAGCTGGAGAAAGAACTCCAGGCTGGATCTCTGTTGAAAGTGAATTTCTCTTG 1470  
QY 844 CTGGATGGGATCAAGGCCAAACGTCATTTCTGTAGCCAGCAGCACCTGGTGCCTCTA 903  
DB 1469 CTGGATGGAGTCAAGGCTTAATGTCATCAATTTAAGCAGCAATGCGTGGCAGCCCTTG 1410  
QY 904 GTCATGCTGAATTTGAGGCTGATGGGAAACTCTTGGCCATGCTCATCAGCTTCCAGCTG 963  
DB 1409 GTCTGTCTGAAGCTTCAGGCTGATGGAGACTCTTACCCATGCTATCCAGCTCCAGCCA 1350  
QY 964 CCGCGCACAGGATCCCAACACCTCCCTTTTCTTCTGCTACGGATCCCAATGGCTGG 1023  
DB 1349 CTTGACACGGATGTCCCACTCTGCTCTTTCTGCCCTCGCATCCCCCATGGCTGG 1290  
QY 1024 CTTCTGGCCAAATGTGGTGGCGACGCTGACTTCCAGCTCCATGAGCTGCAGTCTCAT 1083  
DB 1289 CTCCTGGCCAAAGACCTGGGTCCGGAGCTCTGATTTCCAGCTGCAGCAGTTACAGTCACAT 1230  
QY 1084 CTTCTGAGGGGACACTTGATGGCTGAGGTCATTTGTGTGGCCACCATAGAGTGCCTGCCG 1143  
DB 1229 CTGCTGAGGGGACACTTGATTTGCTGAGGTTAATGCTGTGGCTACAATGAGAAGCTTGCCT 1170  
QY 1144 TCGATACATCTTATCTTCAAGCTTATATTTCCCACTGGGATTTTGCACAGATATATGACACT 1203  
DB 1169 AGCCTCCATCTTATCTACAAGCTCTGATCCCCCACTCCGCTACACCATGGCGATCAAC 1110  
QY 1204 GTCCGGGCGAGACTGGGCTGGTCTGTGACATGGGAATTTTGCACAGATATATGACACT 1263  
DB 1109 AGCTTGGCCAGAGTAGTCTTGTCTCCGNAATGGGGNAATTTTGACCTGGTGTGAGCACT 1050  
QY 1264 GGTGGGGGAGGCCACGTGCAGCTGCTCAAGCAAGCTGGAGCCTTCTAACTTACAGCTCC 1323  
DB 1049 GGTAGTGGGAAGCCACGTGGACATTTCTCAGAGAGCCATGGCTTGTGTGACCTATCATTC 990  
QY 1324 TTTCTGCTCCCTGATGATCTTGGCCGACCGGGGCTCTGGGAGTGAAGTCTTCTTCTAT 1383  
DB 989 CTCTGTCTCTGATGACCTGGCTGACCTGGGCTCTGGATGTGAAATCTTCTTTTAT 930  
QY 1384 GCCAAGATGCTGCGGCTCTGGGAAATCATC-----TATCGGTATGTGGAAGGAAT 1436  
DB 929 GGTAAAGATGCCATCAGGCTGTGGGGAATCATCAGCCGGGAATAGGTAAGTGGAGGGAT 870  
QY 1437 CGTGAGTCTCACTATAAGACAGACTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTG 1496  
DB 869 GGTGGGCTTTTCTACAAATAGTGAACAAGCCATGAAGGATGATCTAGAGCTGCAGGCTG 810  
QY 1497 GTGTGAGAGATCACTGAAATCGGGCTGCAAGGGGCGCCAGGAGGTTTCTGTCTC 1556  
DB 809 GTGCAAGAGATGACTGAGACTGGAATGCAAGGGGCGCCAAAGACCAAGGGGTTCTCATCTC 750  
QY 1557 TTTTACAGGCTCGGGACCAAGTTTGCACCTTGTCAACATGTGTATCTTCACTGCAACCGG 1616  
DB 749 CTTAGAGTCCCGGCTCAGCTCTGCACCTTGTGACCATGTGCACTTTCACATGCAAGG 690  
QY 1617 CCAACACGCTCTGTGCACCTGGGCGCAGCTGGAATGTTCTTGGGTGCTTAATGCAAC 1676  
DB 689 TCAGCATGCTTCAACACCTGGCGCAGCTGGTACTCTCTGGATCCCTTAATGGGCC 630  
QY 1677 CTGCAAGATGGGCTGCGCCCGCAACCAAGAGATGCAACGCTGGAGACAGTATGTC 1736  
DB 629 ATGCACCATGCAAGAGCCCGCCCATCTCTTAAGGATGTGACAGAGAGGATATAGTGA 570  
QY 1737 GACATGCCCCAATCTCCACAGGCTTCTCCAGATGTCATCACTTGCAGCTGGGCGAG 1796  
DB 569 CTTTACTGCCCAATCTCCACAGGACAGTATGCAAAAGACCTTCAACAAAGTTCTTGGCAG 510  
QY 1797 AGCCAGCCCGTTATGGTGGCTGTGGCGCAGCATGAGGAGGAGTATTTTTCGGGCCCTGA 1856  
DB 509 AGCCAGCCCTGTCTAT-----GCATGAGGAGAAATATTTCTCTGCTCTCTGA 465  
QY 1857 GCCTAAGGCTGTGCTGAAGAGTTTCAAGGAGAGCTGGCTGCCCTGGATAGGAAATGTA 1916

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Db      464  G C C C C A A G C T G T G C A C A T T C C A G G A G G A A C T G G C T T C C A T G G A C A A G G A G A T T G A 405
Qy      1917 G A T C C G G A A T G C A A G C T G G A C A T G C C C T A C G A G T A C C T G C G C C C C A G C G T G T G G A - A A 1975
Db      404  G G T C C G G A A T G C A G T C C T G A A C C T G C C G T G T G A G T A C C T T T G A C C C C A G C A T G T G T A G A A 345
Qy      1976 A C A G T G T G G C C A T C T A A G 1993
Db      344  A C A G C G T G A C C A T C T G A G 327
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Search completed: July 19, 2005, 13:18:37  
Job time : 922.004 secs

GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 11:52:27 ; Search time 5546.35 Seconds  
(without alignments)  
18330.926 Million cell updates/sec

Title: US-10-688-676A-1

Perfect score: 2671  
Sequence: 1 aagatgggtctctaccgcat.....aaataaaatttgcaaaag 2671

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST.\*

1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hc.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1503	56.3	1809	9 AY415836	AY415836 Homo sapi
2	986.2	36.9	1809	9 AY415838	AY415838 Mus muscu
3	955	35.8	2964	3 BC041851	BC041851 Homo sapi
4	943.4	35.3	2410	3 AK036898	AK036898 Homo sapi
5	943.4	35.3	2993	3 AK087724	AK087724 Mus muscu
6	919.4	34.4	2301	3 AK036960	AK036960 Mus muscu
7	867.8	32.5	898	5 BQ957032	BQ957032 AGENCOURT
8	815.8	30.5	997	5 BQ276406	BQ276406 AGENCOURT
9	741.4	27.8	769	6 CA311119	CA311119 UI-CF-FNO
10	728.4	27.3	781	5 BM976589	BM976589 UI-CF-EN1
11	690.4	25.8	727	6 CB305836	CB305836 UI-CF-EN1
12	632.4	23.7	682	7 CR767490	CR767490 DKF2p468J
13	619	23.2	620	5 BX644955	BX644955 DKF2p781M
14	609	22.8	622	5 BM975468	BM975468 UI-CF-EN1
15	572	21.4	701	5 BM981991	BM981991 UI-CF-EN1
16	549.6	20.6	921	2 BE538114	BE538114 Mus muscu
17	547	20.5	2216	3 AK079232	AK079232 Mus muscu
18	526	19.7	537	5 BX282722	BX282722 BX282722
19	498.8	18.7	758	7 CO575440	CO575440 AGENCOURT
20	482.8	18.1	972	4 BI661899	BI661899 603305275
21	448.4	16.8	926	5 BU935146	BU935146 AGENCOURT
22	444.2	16.6	943	5 BQ945262	BQ945262 AGENCOURT
23	410.4	15.4	423	6 CA436179	CA436179 UI-H-DT0-
24	408.2	15.3	710	4 BI080244	BI080244 602876669

25	403	15.1	705	7 CK359408	CK359408 AGENCOURT
26	398.8	14.9	920	4 BI082760	BI082760 602877796
27	391	14.6	405	5 BX113915	BX113915 BX113915
28	385.8	14.4	730	4 BI851724	BI851724 603377962
29	380.8	14.3	487	1 AI864921	AI864921 wk05a08.x
30	377.2	14.1	844	5 BX431707	BX431707 BX431707
31	377	14.1	422	7 CN258952	CN258952 170004250
32	375.6	14.1	944	5 BQ938460	BQ938460 AGENCOURT
33	371.8	13.9	780	7 CV076417	CV076417 AGENCOURT
34	361.8	13.5	855	4 BI083331	BI083331 602875604
35	356.2	13.3	851	7 CO559101	CO559101 AGENCOURT
36	349.8	13.1	688	4 BI693557	BI693557 603341938
37	348.4	13.0	940	5 BQ958508	BQ958508 AGENCOURT
38	345	12.9	1826	3 BC040450	BC040450 Homo sapi
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ACCESSION AY415836  
VERSION AY415836.1 GI:39771796  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1809)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1809)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submision  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
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Best Local Similarity 83.1%; Pred. No. 5.4e-301;  
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## RESULT 2

AY415838

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

REFERENCE

AUTHORS

AY415838 1809 bp DNA linear GSS 17-DEC-2003  
Mus musculus ALOX15 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.

AY415838  
AY415838.1 GI:39771798

GSS  
Mus musculus (house mouse)

Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1809)  
Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Perrera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.

Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios

Science 302 (5652), 1960-1963 (2003)

14671302

2 (bases 1 to 1809)

Clark, A.G., Glanowski, S., Nielsen, R., Thomas, P., Kejariwal, A.,



Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.D.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

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ACCESSION BC041851
VERSION    BC041851.1 GI:27693128
KEYWORDS   HTC.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 2964)
            Direct Submission
            Submitted (23-DEC-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgabbs@mail.nih.gov
            Tissue Procurement: Niklos Palkovits, M.D., Ph.D.
            cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www.shgc.stanford.edu
            Contact: (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
            R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
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ORGANISM	Mus musculus				
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AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
REFERENCE	2				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20493374				
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AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakauechi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wataniki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format				

JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

TITLE	JOURNAL	REFERENCE
1. The effect of the concentration of the solution on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1234
2. The effect of the temperature on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1235
3. The effect of the catalyst on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1236
4. The effect of the solvent on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1237
5. The effect of the pressure on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1238
6. The effect of the surface area on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1239
7. The effect of the concentration of the reactants on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1240
8. The effect of the concentration of the products on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1241
9. The effect of the concentration of the catalyst on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1242
10. The effect of the concentration of the solvent on the rate of the reaction.	Journal of Physical Chemistry	1950, 54, 1243

**Summary:**

**TITLE**  
**JOURNAL**

**COMMENT**

FEATURES	SOURCE
1. <b>High Accuracy:</b> The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. <b>Robustness:</b> The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. <b>Scalability:</b> The model is designed to handle large-scale data efficiently, making it suitable for big data applications.	Model Performance Metrics
4. <b>Interpretability:</b> The model's predictions are interpretable, allowing users to understand the underlying factors influencing the results.	Model Performance Metrics
5. <b>Real-time Processing:</b> The model is optimized for real-time data processing, enabling immediate insights and decision-making.	Model Performance Metrics
6. <b>Customizable:</b> The model can be tailored to specific use cases and requirements, providing flexibility in its application.	Model Performance Metrics
7. <b>Integration:</b> The model seamlessly integrates with existing systems and workflows, facilitating easy adoption.	Model Performance Metrics
8. <b>Security:</b> The model adheres to strict security protocols, ensuring that data and predictions are protected from unauthorized access.	Model Performance Metrics
9. <b>Compliance:</b> The model is designed to comply with relevant industry regulations and standards, ensuring legal and ethical use.	Model Performance Metrics
10. <b>Support:</b> Comprehensive support and documentation are provided to assist users in maximizing the model's potential.	Model Performance Metrics

**CDs**

sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861  
4  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

**The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II team.**  
**Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs**  
**Nature 420, 563-573 (2002)**

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawaji, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koyama, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sobabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akashira, S., Takada, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Murakami, M. and Hayashizaki, Y.

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail: yoshihide-gsc@riken.jp).  
URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216.

cdna library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.

URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>.

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**TITLE**

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1 Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
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AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
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AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuda, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipipillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
PUBMED 11076861  
5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
PUBMED 12029373  
6 (bases 1 to 2993)  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Hori, F., Imokani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
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DB	1331	GGTGGAGGCGGCCATGTTTCACTGTGTTACTCGGGCAGTGGCTCAGCTGACTTACCACTCC	1390
QY	1324	TTCTGTCCCTCTGATGACTTTCGCGACCGGGGCTCTCTGGGAGTGAAGTCTTCTCTCTAT	1383
DB	1391	CTCTGTCTCTCTGATGATCTGGCTTAACCGAGGCTGCTGAGAAATCCCAAGTGCTCTAT	1450
QY	1384	GCCCAAGATGGGCTCGGGCTCTGGGAATCATCTATCGGTATGTGGAAAGAAATCGTGAGT	1443

Db	1451	GCTCGGGATGCTTTACAGCTCTCGGAAGTCACTGCAGGTATGTGAAGGGATGGTCCAT	1511
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Db	1511	CTTTCTACAGAGTAGATATATGTGAGGGGAGACCCAGAGCTGCAGGCTGGTGTGCG	1570
Qy	1504	GAGATCACTGAATTCGGGTGCAAGGGGCCAGGACCGAGGGTTTCCTGTCTCTTTACAG	1563
Db	1571	GAGATCACTGAAGTGGGGCTGTGCCATGCCACGAGCAGAGGATTCCTGTGTCTCTTCCAG	1630
Qy	1564	GCTCGGGACAGGTTTGGCACAATTGTGCACCATGTGTATCTTCACTGCACCGGCGCAAC	1623
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Qy	1624	GCCTCTGTGCACCTGGGCCAGCTGGGACTGGTACTCTTTGGGTGCCTAATGCACCTGCACG	1683
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DEFINITION	Mus musculus adult female vagina cDNA, RIKEN full-length enriched library, clone:9930030L18 product:arachidonate 12-lipoxygenase, full insert sequence.		
ACCESSION	AK036960		
VERSION	AK036960.1	GI:26085524	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci, P. and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
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Konno, H., Akiyama, J., Nishi, K., Kitsuunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, S., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multipillarary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

4 The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2301)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, I., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saichou, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shingawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submision

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: <http://genome.gsc.riken.jp/>  
URL: <http://fantom.gsc.riken.jp/>

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/organism="Mus musculus"  
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Best Local Similarity 67.0%; Pred No. 5.6e-180;  
Matches 1344; Conservative 0; Mismatches 646; Indels 17; Gaps 2;

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DEFINITION 5', mRNA sequence.  
ACCESSION BQ276406  
VERSION BQ276406.1 GI:20486614  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 997)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: CGAP (Stanford)  
CDNA Library Preparation: Rubin Laboratory  
CDNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
Clone Distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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Site\_2: XhoI; CDNA made by oligo-dr priming.  
Directionally cloned into EcoRI/XhoI sites using the  
following 5' adaptor: GGCACGAG(G). Library constructed by  
Ling Hong in the laboratory of Gerald M. Rubin (University  
of California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

FEATURES  
source

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Query Match 30.5%; Score 815.8; DB 5; Length 997;  
Best Local Similarity 99.3%; Pred. No. 1.8e-158;  
Matches 839; Conservative 0; Mismatches 4; Indels 2; Gaps 2;  
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Db 181 TCCAGATGTCCATCACTTGGCAGCTGGGCAACGCGCCGTTATGCTGCTGTGGGCC 240  
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Db 241 AGCATGAGGAGAGTATTTTTCGGGCGCTGAGCCTTAAGGCTGTGCTGAAGAAGTTTCAGG 300  
QY 1886 AGGAGCTGGCTGCCCTGATTAAGGAAATTTGAGATCCGGAATGCAAGCTGGACATGCCCT 1945  
Db 301 AGGAGCTGGCTGCCCTGATTAAGGAAATTTGAGATCCGGAATGCAAGCTGGACATGCCCT 360  
QY 1946 ACGAGTACCTGCGGCCAGCGGTGTGGAACACAGTGTGGCCATCTTAAGCGTGGCACCTT 2005  
Db 361 ACGAGTACCTGCGGCCAGCGGTGTGGAACACAGTGTGGCCATCTTAAGCGTGGCACCTT 420  
QY 2006 TTGGTTATTTTCAGCCCCCATCACCAAGCCCAAGCTGACCCCTTCTGCTGTTTATAGCCCT 2065  
Db 421 TTGGTTATTTTCAGCCCCCATCACCAAGCCCAAGCTGACCCCTTCTGCTGTTTATAGCCCT 480  
QY 2066 GCCCTCCCAAGTCCCAACCTCTTCCCATGTCCCAACCTTCCCTAGAGGGGCACTTTTCAT 2125  
Db 481 GCCCTCCCAAGTCCCAACCTCTTCCCATGTCCCAACCTTCCCTAGAGGGGCACTTTTCAT 540  
QY 2126 GGTCTCTGCACCCAGTGAACATTTTACTCTAGAGGATCACTTGGGACCTTACTCTCTC 2185  
Db 541 GGTCTCTGCACCCAGTGAACATTTTACTCTAGAGGATCACTTGGGACCTTACTCTCTC 600  
QY 2186 TTTCCTTCTTCT 2245  
Db 601 TTTCCTTCTTCT 660  
QY 2246 ATCTATATGGCAATAGCCCAATTTATATAATCATTTTCAAGACTAGAAATAGGGGATAT 2305  
Db 661 ATCTATATGGCAATAGCCCAATTTATATAATCATTTTCAAGACTAGAAATAGGGGATAT 720  
QY 2306 AATACATATTACTCCACACCTTTTATGAATCAAAATATGATTTTGTGTTGTTTAAAGAC 2365  
Db 721 AATACATATTACTCCACACCTTTTATGAATCAAAATATGATTTTGTGTTGTTTAAAGAC 780  
QY 2366 AGACTCTCACTTTTGACA-CCGAGGCTGGAGTGGCCATCACCAC-GGCTCACTG 2423  
Db 781 AGACTCTCACTTTTGACA-CCGAGGCTGGAGTGGCCATCACCAC-GGCTCACTG 840  
QY 2424 CAGCC 2428  
Db 841 CAGCC 845  
RESULT 9  
CA311119/c  
LOCUS CA311119  
DEFINITION UI-CF-FNO-afc-b-13-0-UI-el UI-CF-FNO Homo sapiens cdna clone  
769 bp mRNA linear EST 04-NOV-2002  
UI-CF-FNO-afc-b-13-0-UI-3', mRNA sequence.  
ACCESSION CA311119

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VERSION CA311119.1 GI:24529217
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 769)
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
sequence: 1-39, >AT rich#Low complexity (matched complement)
123-332, >ALU 442-503, >(GGAA)n#Simple_repeat
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
source
1..769
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-FNO-afc-b-13-0-UI"
/tissue_type="Human Lung Epithelial cells"
/lab_host="PH10B (Life Technologies) (T1 phage resistant)"
/clone_lib="UI-CF-FNO"
/notes="Organ: Lung; Vector: p7T13-Pac (Pharmacia) with a
modified polylinker; Site 1: Ecor I; Site 2: Not I;
UI-CF-FNO is a subtracted cDNA library derived from two
normalized Human lung epithelial cell libraries (EN1 and
DU1) The library was subtracted according to according to
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,
1996. For additional information, contact:
bento-soares@uiowa.edu
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-FNO
TAG_SEQ=CTGCTCAGGT"

ORIGIN
Query Match 27.8%; Score 741.4; DB 6; Length 769;
Best Local Similarity 99.6%; Pred. No. 4.7e-143;
Matches 753; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1915 GAGATCCGAATGCAAAAGCTGGACATGCCCTACGAGTACTCTGGGCCGACGCTGGTGGAA 1974
DB 769 GAGATCCGAATGCAAAAGCTGGACATGCCCTACGAGTACTCTGGGCCGACGCTGGTGGAA 710
QY 1975 AACAGTGTGGCCATCTAAGCGTGCACACCTTTGGTTATTTCAGCCCCCATCACCCACGC 2034
DB 709 AACAGTGTGGCCATCTAAGCGTGCACACCTTTGG-TATTTCAGCCCCCATCACCCACGC 651
QY 2035 CACAAGCTGACCCCTTCGTGGTTATAGCCCTGCCTCCCAAGTCCACACCTCTTCCCATG 2094
DB 650 CACAAGCTGACCCCTTCGTGGTTATAGCCCTGCCTCCCAAGTCCACACCTCTTCCCATG 591
QY 2095 TCCCACCTCCCTAGAGGGGCACCTTTTCATGCTCTGACCCAGTGAACACATTTTAC 2154
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Db 590 TCCACCCCTCCCTAGAGGGGCACCTTTTCATGGTCTCTGCACCCAGTGAAACACATTTTAC 531
QY 2155 TCTAGAGGCATCACCTGGGACCTTTACTCCTCTTTTCTTCTCTCTCTCTCTCTCTCTCTCT 2214
Db 530 TCTAGAGGCATCACCTGGGACCTTTACTCCTCTTTCTTCTCTCTCTCTCTCTCTCTCTCTCT 471
QY 2215 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2274
Db 470 TTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 411
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QY 2335 TCAAAATATGATTTTTTTTTTTTGTGTAAAGACAGAGTCTCAGCTTTGACACCCAGGCTGGAG 2394
Db 350 TCAAAATATGATTTTTTTTTTTGTGTAAAGACAGAGTCTCAGCTTTGACACCCAGGCTGGAG 291
QY 2395 TGCAGTGTGTGCATCACACGGCTCAGCTGCAGGCTCAGGCTCCTGGGCTCAAATGATCCT 2454
Db 290 TGCAGTGTGTGCATCACACGGCTCAGCTGCAGGCTCAGGCTCCTGGGCTCAAATGATCCT 231
QY 2455 CCCACCTCAGCTCCTGAGTAGCTGGGACTACAGGCTCATGCGCATCATGCCAGCTAATA 2514
Db 230 CCCACCTCAGCTCCTGAGTAGCTGGGACTACAGGCTTATGCCATCATGCCAGCTAATA 171
QY 2515 TTTTTTATTTTTTCGTGGAGACGGGCGCTCAGCTATGTTGCCTAGGCTGGAATAGATTTT 2574
Db 170 TTTTTTATTTTTTCGTGGAGACGGGCGCTCAGCTATGTTGCCTAGGCTGGAATAGATTTT 111
QY 2575 GAACCCAAATTTAGTTTAAACAAATATAAAGTTGTTTTAGCTTAAGATGGAAGAAC 2634
Db 110 GAACCCAAATTTAGTTTAAACAAATATAAAGTTGTTTTAGCTTAAGATGGAAGAAC 51
QY 2635 TAGGACTCAACTATTTTAAATAAATATTTGGCAAAA 2670
Db 50 TAGGACTCAACTATTTTAAATAAATATTTGGCAAAA 15

RESULT 10
BM976589/c
LOCUS BM976589
DEFINITION UI-CF-EN1-ada-o-01-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
UI-CF-EN1-ada-o-01-0-UI 3', mRNA sequence.
ACCESSION BM976589
VERSION BM976589.1 GI:19594183
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 781)
Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.reagen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
```

sequence: 1-39, >AT\_rich#Low complexity (matched compliment)  
 123-332, >ALU 442-503, >(GGAA)n#Simple\_repeat  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

# FEATURES

source

Location/Qualifiers  
 1. .781  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-EN1-ada-o-01-0-UI"  
 /tissue\_type="Primary Lung Cystic Fibrosis Epithelial Cells"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-EN1"  
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not.I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.  
 TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h  
 TAG LIB=UI-CF-EN1  
 TAG\_SEQ=CTGCTCAGGT"

## ORIGIN

Query Match 27.3%; Score 728.4; DB 5; Length 781;  
 Best Local Similarity 98.6%; Pred. No. 2.4e-140;  
 Matches 754; Conservative 0; Mismatches 9; Indels 2; Gaps 2;  
 QY 1906 AAGGAATAGATCGGAATCGGAATCGGACATGCCCTACGAGTACTGTGGGCCACGC 1965  
 DB 777 AGGGAATAGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGGATCGG 718  
 QY 1966 GTGGTGGAAAACAGTGTGGCCATCTAAGCGTGGCCACCCCTTTGGTTATTTCAGCCCCCAT 2025  
 DB 717 GTGGT-GAAAACAGTGTGGCCATCTAAGCGTGGCCACCCCTNT-GTTATTTCAGCCCCCAT 660  
 QY 2026 CACCCAGCCACAGCTGACCCCTTCGTGGTTATAGCCCTGCCCTCCCAAGTCCACCCCT 2085  
 DB 659 CACCCAGCCACAGCTGACCCCTTCGTGGTTATAGCCCTGCCCTCCCAAGTCCACCCCT 600  
 QY 2086 CTTCCCATGTCCACCCCTCCCTAGAGGGGCACCTTTTCATGTCTCTGACCCAGTGAAC 2145  
 DB 599 CTTCCCATGTCCACCCCTCCCTAGAGGGGCACCTTTTCATGTCTCTGACCCAGTGAAC 540  
 QY 2146 ACATTTTACTCTAGAGGCATACCTGGGACCTTACTCTCTTTCTCTCTCTCTCTCTTC 2205  
 DB 539 ACATTTTACTCTAGAGGCATACCTGGGACCTTACTCTCTTTCTCTCTCTCTCTCTTC 480  
 QY 2206 CTATCTTCT 2265  
 DB 479 CTATCTTCT 420  
 QY 2266 CAATTAT 2325  
 DB 419 CAATTAT 360  
 QY 2326 TTTTATGAATCAAT 2385  
 DB 359 TTTTATGAATCAAT 300  
 QY 2386 AGGCTGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 2445

DB 299 AGGCTGGAGTGCAGTGGTGCCATCACACGGCTCACTGCAGCCTCAGCGTCTCGGGCTCA 240  
 QY 2446 AATGATCTCCACCTCAGCCTCCTGAGTAGCTGGAGTACAGGCTATGCGCATGCGC 2505  
 DB 239 AATGATCTCCACCTCAGCCTCCTGAGTAGCTGGAGTACAGGCTATGCGCATGCGC 180  
 QY 2506 CAGCTAAT 2565  
 DB 179 CAGCTAAT 120  
 QY 2566 TAGGATTTTGAACCCAAATTCAGTGTAAACAATAATAAAGTGTGTATACGCTAAAGATG 2625  
 DB 119 TAGGATTTTGAACCCAAATTCAGTGTAAACAATAATAAAGTGTGTATACGCTAAAGATG 60  
 QY 2626 GAAAGAAGTACTAGGACTGAGCTATTTTAAATAAATAATATTTGGCAAAA 2670  
 DB 59 GAAAGAAGTACTAGGACTGAGCTATTTTAAATAAATAATATTTGGCAAAA 15

## RESULT 11

CB305636/c  
 LOCUS  
 DEFINITION 727 bp mRNA linear EST 04-MAR-2003  
 UI-CF-EN1-aed-p-02-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
 CB305636  
 CB305636.1 GI:28846147  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens (human)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 COMMENT

1 (bases 1 to 727)  
 Normalization and subtraction: two approaches to facilitate gene discovery  
 Genome Res. 6 (9), 791-806 (1996)  
 97044477  
 889548  
 Contact: McCray, PB  
 McCray Lab  
 University of Iowa  
 2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
 Tel: 319 356 4866  
 Fax: 319 356 7171

Email: paul-mccray@uiowa.edu  
 Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).  
 The following repetitive elements were found in this cDNA sequence: 123-332, >ALU 442-503, >(GGAA)n#Simple\_repeat  
 Seq primer: M13 FORWARD  
 POLYA=Yes.

## FEATURES

source

Location/Qualifiers  
 1. .727  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="UI-CF-EN1-aed-p-02-0-UI"  
 /tissue\_type="Primary Lung Cystic Fibrosis Epithelial Cells"  
 /dev\_stage="Adult"  
 /lab\_host="DH10B (Life Technologies) (T1 phage resistant)"  
 /clone\_lib="UI-CF-EN1"  
 /note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; UI-CF-EN1 is a normalized cDNA library containing the following tissue(s): Primary Lung Cystic Fibrosis Epithelial Cells. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806,

1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into p773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is CTGCTCAGGT.  
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS 6hr to LPS 24h  
TAG LIB=UI-CF-EN1  
TAG\_SEQ=CTGCTCAGGT"

ORIGIN

Query Match 25.8%; Score 690.4; DB 6; Length 727;  
Best Local Similarity 99.6%; Pred. No. 1.9e-132;  
Matches 713; Conservative 0; Mismatches 1; Indels 2; Gaps 2;  
QY 1956 GCGGCCAGCGTGGTGGAAACAGTGTGGCCATCTTAAGCGTGCACACCTTTGGTTATTT 2015  
DB 727 GCGGCCAGCGTGGT-GAAAAACAGTGTGGCCATCTTAAGCGTGCACACCTTTGG-TATTT 670  
QY 2016 CAGCCCCCATCACCCAGGCACAGCTGACCCCTCGTGGTTATAGCCCTGCCCTCCCAA 2075  
DB 669 CAGCCCCCATCACCCAGGCACAGCTTACCCCTCGTGGTTATAGCCCTGCCCTCCCAA 610  
QY 2076 GTCCCAACCTCTTCCCATGTCCCAACCTCCCTAGAGGGGACCTTTTCATGTCTCTGCA 2135  
DB 609 GTCCCAACCTCTTCCCATGTCCCAACCTCCCTAGAGGGGACCTTTTCATGTCTCTGCA 550  
QY 2136 CCAGTGAACACATTTTACTCTAGAGGCATACCTGGGACCTTACTCTCTTCTTCTTCT 2195  
DB 549 CCAGTGAACACATTTTACTCTAGAGGCATACCTGGGACCTTACTCTCTTCTTCTTCT 490  
QY 2196 TCCCTCTTCTCTATCTTCT 2255  
DB 489 TCCCTCTTCTCTATCTTCT 430  
QY 2256 CAATAGCCACAAATATATAATCAATTTCAAGACTAGATAGGGGATATAATACATATT 2315  
DB 429 CAATAGCCACAAATATATAATCAATTTCAAGACTAGATAGGGGATATAATACATATT 370  
QY 2316 ACTCCACACCTTTTATGAATCAAAATAGATTTTTTTTGGTTGTTTGAAGACAGAGTCTAC 2375  
DB 369 ACTCCACACCTTTTATGAATCAAAATAGATTTTTTTTGGTTGTTTGAAGACAGAGTCTAC 310  
QY 2376 TTTGACACCCAGCTGGAGTGCAGTGGTGCATACACGGCTCACTGCAGCTCAGGCT 2435  
DB 309 TTTGACACCCAGCTGGAGTGCAGTGGTGCATACACGGCTCACTGCAGCTCAGGCT 250  
QY 2436 CTTGGGCTCAATGATCTCCCACTCAGCTCCTCAGTGTGGGACTACAGGCTCATG 2495  
DB 249 CTTGGGCTCAATGATCTCCCACTCAGCTCCTCAGTGTGGGACTACAGGCTCATG 190  
QY 2496 CCATCATGCCAGCTAATATTTTTTTTATTTTGTGGAGCGGGGCTCTCATATGTGCT 2555  
DB 189 CCATCATGCCAGCTAATATTTTTTTTATTTTGTGGAGCGGGGCTCTCATATGTGCT 130  
QY 2556 AGCTGGAATAGGATTTTGAACCCAAATGAGTTTAAACAATAAATAAGTTGTTTAC 2615  
DB 129 AGCTGGAATAGGATTTTGAACCCAAATGAGTTTAAACAATAAATAAGTTGTTTAC 70  
QY 2616 GCTAAAGATGGAAGAAGACTAGGACTGAACCTATTTTTAAATAAATAATTCGCAAAAG 2671  
DB 69 GCTAAAGATGGAAGAAGACTAGGACTGAACCTATTTTTAAATAAATAATTCGCAAAAG 14

RESULT 12

CR767490  
LOCUS  
DEFINITION  
DKFZp468J1413\_r1 468 (synonym: phrt1) Pongo pygmaeus cDNA clone  
CR767490  
ACCESSION  
DKFZp468J1413 5', mRNA sequence.

VERSION

CR767490.1 GI:52609682  
EST.  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE

1 (bases 1 to 682)

AUTHORS

Ottenwaelder,B., Obermaier,B., Deutschenbaur,S., Schaiipp,A.,  
Mewes,H.W., Weil,B., Amid,C., Osanger,A., Fobo,G., Han,M. and  
Wiemann,S.

TITLE

Pongo pygmaeus mRNA (Ottenwaelder,B., Obermaier,B.,  
Deutschenbaur,S., et al.)

JOURNAL

Unpublished (2004)

COMMENT

Contact: MIPS

MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany

This is the 5' sequence of the clone insert.

Molecular Genome Analysis, German Cancer Research Center (DKFZ);  
Email s.wiemann@dkfz-heidelberg.de; sequenced by Medigenomix  
(Martinsried/Germany) within the cDNA sequencing consortium of the  
German Genome Project. This clone (DKFZp468J1413) is available at  
the RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH in  
Berlin, Germany. Please contact RZPD for ordering.  
http://www.rzpd.de/cgi-bin/products/cl.cgi?cloneid=DKFZp468J1413  
Further information about the clone and the sequencing project is  
available at http://mips.gsf.de/projects/cdna/.

FEATURES

Location/Qualifiers

1..682

/organism="Pongo pygmaeus"

/mol\_type="mRNA"

/db\_xref="taxon:9600"

/clone="DKFZp468J1413"

/tissue type="heart"

/dev stage="adult"

/lab\_host="pH10B"

/clone\_lib="468 (synonym: phrt1)"

/note="Vector: pSpartan\_Sfi; Site\_1: SfiI; Site\_2: SfiII"

ORIGIN

Query Match 23.7%; Score 632.4; DB 7; Length 682;  
Best Local Similarity 97.6%; Pred. No. 1.9e-120;  
Matches 642; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 AAGATGGTCTCTACCGCATCGCGTGTCCACTGGGGCTCTCTCTATGCCGGTTCCAAAC 60

DB 25 AAGATGGTCTCTACCGCATCGCGTGTCCACTGGGGCTCTCTCTATGCCGGTTCCAAAC 84

QY 61 AACGAGGTGCAGCTGTGGCTTGGCCAGACACGGGAGGGCGCTCGGGAGGCGACTG 120

DB 85 AACGAGGTGCAGCTGTGGCTTGGCCAGACACGGGAGGGCGCTTGGGACGCGACTG 144

QY 121 TGGCCCGCACCGGGCAAGGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCGG 180

DB 145 TGGCCCGCACCGGGCAAGGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCGG 204

QY 181 CTGCTGTTTGTGAACACTCGCAACCGCACCTCTCTTAAAGGACGACGCTGGTTCTGCAAC 240

DB 205 CTGCTGTTTGTGAACACTCGCAACCGCACCTCTCTTACGGACGACGCTGGTTCTGCAAC 264

QY 241 TGGATCTCTGTGACGGGCCCCGGAGCCGGGACGAGGTTCAGGTTCCTTGTACCGCTGG 300

DB 265 TGGATCTCTGTGACGGGCCCCGGAGCCGGGACGAGGTTCAGGTTCCTTGTACCGCTGG 324

QY 301 GTGGAGGCAACCGGCTCTGAGCCTGCTCGAAGCCACCGCCGACCTGTGGCCGAGGAC 360

DB 325 GTGGAGGCAACCGGCTCTGAGCCTCGAAGCCACCGCCGCTACTGTGGCCGACGAC 384

QY 361 CCTCAGGGCCTGTTCCAGAAACACCGGGAAGAAGAGCTGGAGAGAGAAGAGTTGTAC 420

DB 385 CCTCAGGGCCTGTTCCAGAAACACCGGGAAGAAGAGCTGGAGAGAGAAGAGTTGTAC 444

QY 421 CGGTGGGGAACCTGGAAGGACGGGTTAATTTCTGAATATGGCTGGGGCCAAATATATGAC 480

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Db 445 CGGTGGGGAACACTGGAAGATGGGTAAATCTGTGATGTGGCTGGGCGCCAAACTATGTGAC 504
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Db 505 CTCCTGTGGATGACCGATTTCTGGAAGACAAGAGATGTGACTTTGAGGTTTCGCTGCC 564
Qy 541 AAGGGCTGGCGGACTCGCTATCAAGACNCTCTCTAAATGTTCTGACTTGTCTGGNAGGAT 600
Db 565 AAGGGCTGGCGGACTCGCTATCAAGACNCTCTCTAAATGTTCTGACTTGTCTGGNAGGAT 624
Qy 601 CTAGATGACTTCAACCGGATTTCTGGTGTGTGTGAGCAGCAAGCTGGCTGAGCGCTGC 658
Db 625 CTAGATGACTTCAACCGGATTTCTGGTGTGTGAGCAGCAAGCTGGCTGAGCGTGTGC 682

RESULT 13
BX644955 620 bp mRNA linear EST 04-SEP-2003
LOCUS DKFZp781M0636_r1.781 (synonym: h1ccc4) Homo sapiens cDNA clone
DEFINITION DKFZp781M0636_5', mRNA sequence.
ACCESSION BX644955
VERSION BX644955.1 GI:34479288
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., Oeanger,A.,
Fobo,G., Han,M. and Wiemann,S.
TITLE EST (Wambutt,R., Heubner,D., Mewes,H.W., Weil,B., Amid,C., et al.)
JOURNAL Unpublished (2003)
COMMENT Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No s1 sequence available.
This clone (DKFZp781M0636) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
1. .620
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="caxon:9606"
/clone="DKFZp781M0636"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="781 (synonym: h1ccc4)"
/note="Vector: pSpor1_Sfi; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN
Query Match 23.2%; Score 619; DB 5; Length 620;
Best Local Similarity 100.0%; Pred. No. 1.2e-117;
Matches 619; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 GCTCTATCCGGTTCCAAACACAGGTGCAGTGTGGTGTGGCCACGACGCGGAGGC 101
Db 2 GCTCTATCCGGTTCCAAACACAGGTGCAGTGTGGTGTGGCCACGACGCGGAGGC 61
Qy 102 GCGCTCGGGAAGCAGTGTGGCCGCGCAGGGGCAAGAGACAGACTCAAGGTGGAAGT 161
Db 62 GCGCTCGGGAAGCAGTGTGGCCGCGCAGGGGCAAGAGACAGACTCAAGGTGGAAGT 121
Qy 162 ACCGAGTATCTGGGGCGCTGCTCTTTGTGAACCTGCGCAACGGCACCTCTCTTAAGGA 221
Db 122 ACCGAGTATCTGGGGCGCTGCTCTTTGTGAACCTGCGCAACGGCACCTCTCTTAAGGA 181
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Qy 222 CGAGCCTGGTTCTGCAACTGGATCTCTGTGACGGGCCCCGGAGCCGGGACGAGGTGAG 281
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Qy 282 GTTCCCTTGTACCGCTGGGTGGAGGGCAACGGGCTCTGAGAGCTTCCCTGAAAGGACCCGG 341
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Qy 342 CCGCACTGTGGGCGAGACCTCAGGGCTCTTCCAGAAACACCGGGAAGAGAGCTGGA 401
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Qy 402 AGAGAGAGGAGTGTACCGGTGGGGAACCTGGAAGGACGGGTAAATCTCTGAATATGSC 461
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Qy 462 TGGGGCCAAACTATATGACCTCCCTGTGGATGAGCGATTTCTGGAAGACAAGAGATTGA 521
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Qy 522 CTTTGAGGTTTCGCTGGCCAAAGGGCTGGCCGACCTCGCTATCAAAAGACTCTCTAAATGT 581
Db 482 CTTTGAGGTTTCGCTGGCCAAAGGGCTGGCCGACCTCGCTATCAAAAGACTCTCTAAATGT 541
Qy 582 TCTGACTTGTGGAGGATCTAGATGACTTCAACCGGATTTCTGCTGTGTCGAGACAA 641
Db 542 TCTGACTTGTGGAGGATCTAGATGACTTCAACCGGATTTCTGCTGTGTCGAGACAA 601
Qy 642 GCTGGCTGAGCGCTGCGG 660
Db 602 GCTGGCTGAGCGCTGCGG 620

RESULT 14
BM975468/c 622 bp mRNA linear EST 21-FEB-2003
LOCUS UI-CF-EN1-acv-i-02-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
DEFINITION UI-CF-EN1-acv-i-02-0-UI 3', mRNA sequence.
ACCESSION BM975468
VERSION BM975468.1 GI:19593059
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@uiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com) or from Open Biosystems
(www.openbiosystems.com).
The following repetitive elements were found in this cDNA
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POLYA=Yes.
Location/Qualifiers
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/organism="Homo sapiens"
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/clone_lib="UI-CF-EN1"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site_1: EcoR I; Site_2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dT primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGGT.
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGGT"

ORIGIN
Query Match 22.8%; Score 609; DB 5; Length 622;
Best Local Similarity 100.0%; Pred. No. 1.4e-115;
Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2123 CATGGTCTCTGCACCCAGTGAACACATTTTACTCTAGAGGCATCATCTGGGACCTTACTC 2182
DB 562 CATGGTCTCTGCACCCAGTGAACACATTTTACTCTAGAGGCATCATCTGGGACCTTACTC 503
QY 2183 CTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2242
DB 502 CTCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 443
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DB 442 CAGATCTATATGCAATAGCCACCAATATATAAATCATTTCAAGACTAGATAGGGGA 383
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DB 382 TATAATACATATTACTCCACACCTTTTATGAATCAATATGATTTTTTTTGTGTTAA 323
QY 2363 GACAGATCTCATTTTGACACCCAGGCTGGAGTGCAGTGGTGCAATCATCACGGCTCACT 2422
DB 322 GACAGATCTCATTTTGACACCCAGGCTGGAGTGCAGTGGTGCAATCATCACGGCTCACT 263
QY 2423 GCAGCTCAGCTCCCTGGGCTCAAAATGATCCCTCCACCTCAGCTCCTCAGTAGCTGGGA 2482
DB 262 GCAGCTCAGCTCCCTGGGCTCAAAATGATCCCTCCACCTCAGCTCCTCAGTAGCTGGGA 203
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DB 202 CTACAGGCTCATGCCATCATGCCAGCTAATATTTTTTTTATTTTCTGGAGACGGGCTC 143
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QY 2603 AAGTTGTTTTTACCTAAGATGGAAGAAAGAACTAGGACTGAATCTATTTTAAATAAATAT 2662
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QY 2663 TGGCAAAAG 2671
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Db 22 TGGCAAAAG 14

RESULT 15  
BM981991/c  
LOCUS  
DEFINITION  
UI-CF-EN1-adg-b-14-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone  
UI-CF-EN1-adg-b-14-0-UI 3', mRNA sequence.  
ACCESSION  
BM981991  
VERSION  
BM981991.1 GI:19605029  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
1 (bases 1 to 701)  
AUTHORS  
Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE  
Normalization and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL  
Genome Res. 6 (9), 791-806 (1996)  
MEDLINE  
97044477  
PUBMED  
889548  
COMMENT  
Contact: McCray, PB  
McCray Lab  
University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171  
Email: paul-mccray@uiowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.resgen.com) or from Open Biosystems  
(www.openbiosystems.com).  
The following repetitive elements were found in this cDNA  
sequence: 123-173, >ALU 272-333, >(GGAA)n#simple\_repeat  
Seq primer: M13 FORWARD  
POLYA=Yes.

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Cells"  
/dev\_stage="Adult"  
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a  
modified polylinker; Site\_1: EcoR I; Site\_2: Not I;  
UI-CF-EN1 is a normalized cDNA library containing the  
following tissue(s): Primary Lung Cystic Fibrosis  
Epithelial Cells. The library was constructed according to  
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,  
1996. First strand cDNA synthesis was primed with an  
oligo-dT primer containing a Not I site. Double stranded  
cDNA was ligated to an EcoR I adaptor, digested with Not  
I, and cloned directionally into pT7T3-Pac vector. The  
oligonucleotide used to prime the synthesis of  
first-strand cDNA contains a library tag sequence that is  
located between the Not I site and the (dT)18 tail. The  
sequence tag for this library is CTGCTCAGGT.  
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS  
6hr to LPS 24h  
TAG LIB=UI-CF-EN1  
TAG\_SEQ=CTGCTCAGGT"

ORIGIN  
Query Match 21.4%; Score 572; DB 5; Length 701;

Best Local Similarity 99.1%; Pred. No. 6.4e-108;			
Matches 575; Conservative 0; Mismatches 5; Indels 0; Gaps 0;			
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Db	701	TGGCTGTGGCCAGCATGAGGAGAGTATTTTTCGGGCCCTGAGCCTAAGGCTGTGCTGA	642
QY	1874	AGAACTTCAGGAGAGAGCTGGCTGGATAGGAAATTGAGATCCGGAATGCAAAAGC	1933
Db	641	AGAACTTCAGGAGAGAGCTGGCTGGATAGGAAATTGAGATCCGGAATGCAAAAGC	582
QY	1934	TGGACATGCCCTACGAGTACCTGGCGCCAGCGTGTGGAACACAGTGTGGCCATCTAAG	1993
Db	581	TGGACATGCCCTACGAGTACCTGGCGCCAGCGTGTGGAACACAGTGTGGCCATCTAAG	522
QY	1994	CCTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCACCCCAAGCCACAAAGCTGACCCCTTCGT	2053
Db	521	CCTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCACCCCAAGCCACAAAGCTGACCCCTTCGT	462
QY	2054	GGTTATAGCCCTGCCCTCCCAAGTCCACCCCTTTCCCAATGTCACCCCTCCCTAGAGGG	2113
Db	461	GGTTATAGCCCTGCCCTCCCAAGTCCACCCCTTTCCCAATGTCACCCCTCCCTAGAGGG	402
QY	2114	GCACCTTTTCATGGTCTCTGACCCAGTGACACATTTTACTCTAGAGGCATCACCTGGG	2173
Db	401	GCACCTTTTCATGGTCTCTGACCCAGTGACACATTTTACTCTAGAGGCATCACCTGGG	342
QY	2174	ACCTTACTCCTCTTTCCCTTCCTTCCTATCTTCCCTCTCTCTCTCTCTCTCTCTCT	2233
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QY	2234	TTCCTCATTCAGATCTATATGGCAAAATAGCCCAATATATAAATCATTTCAAGACTAGA	2293
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QY	2294	ATAGGGGATATATACATATTTACTCCACACCTTTTATGAATCAATATGATTTTTTGT	2353
Db	221	ATAGGGGATATATACATATTTACTCCACACCTTTTATGAATCAATATGATTTTTTGT	162
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Db	161	TGTTGTTAAGACAGAGTCTCCTATGTTGCCCTAGGCTGA	122

Search completed: July 19, 2005, 21:20:53  
Job time : 5557.35 secs

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3	2671	100.0	2671	11	G28561	G28561 SHGC-35280
4	2669.4	99.9	2707	9	BC029032	BC029032 Homo sapi
5	2644.2	99.0	2844	6	AX535974	AX535974 Sequence
6	1640.4	61.4	2881	4	PTGLGX12A	M31417 Pig atrachid
7	1583.6	59.3	2884	4	BOV12LIP	M81320 Bos taurus
8	1583.6	59.3	2884	4	BOV12LPOX	M62516 Bovine 12-1
9	1511.6	56.6	2897	4	S96247	S96247 12-lipoxylge
10	1480.6	55.4	2777	4	OC12LIP	Z97654 Oryctolagus
11	1465.8	54.9	3614	4	RABCS15L	M27214 Oryctolagus
12	1316.6	49.3	2216	10	S69383	S69383 12-lipoxylge
13	1306	48.9	2048	10	RATL1POX	L06040 Rattus norv
14	1299.8	48.7	2482	10	BC081546	BC081546 Mus muscu
15	1299.8	48.7	2485	10	BC056625	BC056625 Mus muscu
16	1275.2	47.7	2413	10	MUS12L1POX	L34570 Mouse 12-li
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19	1058.2	39.6	2237	10	MWU39200	MWU39200 Mus musculu





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QY	2581	AAATTTGAGTTTAACTAATAAAGAGTTGTTTACGCTAAGATGGAAGAACTAGGAC	2640
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Db	2641	TGAATCTATTTTAAATAATATTTGCAAAAG	2671
RESULT 2			
LOCUS	HUMLOX15A	2671 bp mRNA linear	PRI 11-JUN-1993
DEFINITION	Human 15-lipoxygenase mRNA, complete cds.		
ACCESSION	M23892		
VERSION	1		
KEYWORDS	15-lipoxygenase.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Sigal, E., Craik, C.S., Highland, E., Grunberger, D., Costello, L.L., Dixon, R.A., and Nadel, J.A.		
TITLE	Molecular cloning and primary structure of human 15-lipoxygenase		
JOURNAL	Biochem. Biophys. Res. Commun. 157 (2), 457-464 (1988)		
MEDLINE	89076270		
PUBMED	3202857		
COMMENT	Original source text: Human reticulocyte, cdna to mRNA, clone 15LOX.		
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Query Match	100.0%; Score 2671; DB 9; Length 2671;		
Best Local Similarity	100.0%; Pred. No. 0;		
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Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from M23892  
-- Washington University/Merck EST sequence.  
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QY 61 AACCAAGTGCAGCTGTGGCTGTGGCCAGCAGCGGGAGGCGCGCTCGGGAGCGACTG 120  
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QY 181 CTGCTGTTTGTGAACCTGCGGAAACGGCACTCTTTAAGGACGACCGCTGGTTCGCAAC 240  
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QY 241 TGGATCTGTGACGGGCCCCGGGCGGGGAGGAGTCAAGTCCCTGTTTACCGCTGG 300  
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QY 301 GTGGAGGGCAACGGGCTCTGAGCCTGCTGAAGCAGCGCGCGCACTGTGGCGGAGGAC 360  
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QY 361 CCTCAGGGCTGTTCCAGAAACACCGGGAAAGAGCTGGAAAGAGAGAGAGAGAGAGAG 420  
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QY 421 CGGTGGGAACTGGNAGACGGGTAAATCTGAATATGGCTGGGGCCAACTATATGAC 480  
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QY 721 GTGCTGAGCGCTCTGCTCACTCTTCTGCTCGCTAGTGTTCCTCCAGGCATCGAGGAA 780  
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QY 1681 ACGATGGGCTGCCCGCCCAACCAAGATGCAACGCTGGAGACAGTATGCGGACA 1740  
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VERSION BC029032.1 GI:20809660
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2707)
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## AUTHORS

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheet, T.E., Brownstein, M.J., Udín, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodrigues, S., Sanchez, A., Whitting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalusz, D.E., Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932

2 (bases 1 to 2707)

Strausberg, R.

Direct Submission

Submitted (01-MAY-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgi.nci.nih.gov>

Contact: MGC help desk

Email: [cgapbs@mail.nih.gov](mailto:cgapbs@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

Sequencing Center

Sequenced by: Baylor College of Medicine Human Genome Center

Center code: BCM-HGSC

Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>

Contact: [amg@bcm.tmc.edu](mailto:amg@bcm.tmc.edu)

Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louleaged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAK Plate: 50 Row: a Column: 3

This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4502054.

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## ORIGIN

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Matches 2670; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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AUTHORS Harland,L., Arvizu,C., Das,D., Griffin,J.A., Baughn,M.R., Ding,L.,  
Walia,N.K., Yao,M.G., Lu,X., Elliott,V.S., Thangavelu,K.,  
Ramkumar,J., Lal,P.G. and Tribouley,C.M.  
TITLE Lipid metabolism enzymes  
JOURNAL Patent: WO 0229036-A 13 11-APR-2002;  
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ORIGIN

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RESULT 6  
PIGLOX12A

LOCUS PIGLOX12A 2881 bp mRNA linear MAM 27-APR-1993  
DEFINITION Pig arachidonate 12-lipoxygenase mRNA, complete cds.

ACCESSION M31417  
VERSION M31417.1 GI:164536  
KEYWORDS arachidonate 12-lipoxygenase; lipoxygenase.  
SOURCE Sus scrofa (pig)

## ORGANISM

Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
1 (bases 1 to 2881)  
Yoshimoto, T., Suzuki, H., Yamamoto, S., Takai, T., Yokoyama, C. and  
Tanabe, T.

## REFERENCE

AUTHORS Cloning and sequence analysis of the cDNA for arachidonate  
12-lipoxygenase of porcine leukocytes  
Proc. Natl. Acad. Sci. U.S.A. 87 (6), 2142-2146 (1990)  
MEDLINE 90192763  
PUBMED 2315307

## COMMENT

Original source text: Porcine leukocyte, cDNA to mRNA.  
Draft entry and computer-readable sequence for [1] kindly submitted  
by S.Yamamoto, 17-JAN-1990.

## FEATURES

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## ORIGIN

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Matches 1861; Conservative 0; Mismatches 346; Indels 3; Gaps 1;
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RESULT 7

BOV12LIP

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

BOV12LIP

2884 bp

mRNA

linear

MAM 26-APR-1993

complete cds.

De Marzo,N., Sloan,D.L., Dicharry,S., Highland,E. and Sigal,E.

Cloning and expression of a new isoform of 12-lipoxygenase: Evidence that the enzyme from bovine tracheal epithelium is the homologue of the human 15-lipoxygenase

Unpublished (1991)

Original source text: Bos taurus trachea cDNA to mRNA.

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QY 1803 CGCCAGCCCATCATGTGGTGTGGGTGAGCATGAGAGAGTACTTCTCAGGGCCCTGAG 1862
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QY 1858 CCTAAGGCTGTGTGAAGATTTCAGGAGAGGCTGCTGCCCTTGGATTAAGGAATTTGAG 1917
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LOCUS
DEFINITION
Bovine 12-lipoxygenase gene, complete cds.
ACCESSION
M62516.1 GI:162589
VERSION
12-lipoxygenase.
KEYWORDS
Bos taurus (cow)
SOURCE
ORGANISM
Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Rutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
REFERENCE
1 (bases 1 to 2884)
De Marzo,N., Sloane,D.L., Dicharry,S., Highland,E. and Sigal,E.
Cloning and expression of an airway epithelial 12-lipoxygenase
JOURNAL
Am. J. Physiol. 263 (1 Pt 1), 1 (1992)
MEDLINE
92343798
PUBMED
1636733
COMMENT
Original source text: Bos taurus tracheal cDNA to mRNA.
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DEFINITION 12-lipoxigenase [cattle, tracheal epithelium, mRNA, 2897 nt].  
TITLE  
ACCESSION S96247  
VERSION S96247.1 GI:246172  
KEYWORDS  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
Bovinae; Bos  
REFERENCE 1 (bases 1 to 2897)  
AUTHORS De Marzo,N., Sloane,D.L., Dicharry,S., Highland,E. and Sigal,E.  
TITLE Cloning and expression of an airway epithelial 12-lipoxigenase  
JOURNAL Am. J. Physiol. 262 (2 Pt 1), L198-L207 (1992)  
MEDLINE 92170942  
PUBMED 1539676  
REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 96247] from the original journal article.  
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DEFINITION Oryctolagus cuniculus mRNA for 12-lipoxygenase.
ACCESSION 297654
VERSION 297654.1 GI:2266737
KEYWORDS 12-lipoxygenase.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1
AUTHORS Berger M., Schwarz K., Thiele H., Reimann I., Huth A.,
Borgraber S., Kuhn H. and Thiele B.J.
TITLE Simultaneous expression of leukocyte-type 12-lipoxygenase and
reticulocyte-type 15-lipoxygenase in rabbits
J. Mol. Biol. 278 (5), 935-948 (1998)
MEDLINE 98263260
PUBMED 9600854
REFERENCE 2 (bases 1 to 2777)
AUTHORS Thiele B.J.
TITLE Direct Submission
SUBMITTED (14-JUN-1997) Institute of Biochemistry, University
Clinics Charite, Humboldt-University, Hessische Str 3-4, Berlin
D-10115, Germany
COMMENT Related sequence: Cell 89:597-606 (1997).
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Qy 1918 ATCCGGAATGCAAGCTGGACATGCCCTTACGAGTACTTGGGCGCCAGGCTGGTGAAGAAC 1977  
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## RESULT 12

S69383  
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DEFINITION 12-lipoxygenase [rats, pineal glands, mRNA, 2216 nt].  
ACCESSION S69383  
VERSION S69383.1 GI:545793  
KEYWORDS  
SOURCE Rattus sp.  
ORGANISM Rattus sp.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 2216)  
Hada, T., Hagiya, H., Suzuki, H., Arakawa, T., Nakamura, M., Matsumura, S.,  
Yoshimoto, T., Yamamoto, S., Azekawa, T., Morita, Y. et al.



QY 1618 CAACAGCCCTCTGTGACCTGGCCAGCTGGACTGGTACTCTTGGTGCTTAATGACCC 1677  
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 Db 2103 CAAAGCCCCACCC 2115

RESULT 13  
 RATLIPOX 2048 bp mRNA linear ROD 27-APR-1993  
 LOCUS Rattus norvegicus 12-lipoxygenase mRNA, complete cds.  
 DEFINITION L06040  
 ACCESSION L06040  
 VERSION L06040.1 GI:205212  
 KEYWORDS lipoxygenase.  
 SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 2048)  
 AUTHORS Watanabe,T., Medina,J.F., Haeggstrom,J.Z., Radmark,O. and Samuelsson,B.  
 TITLE Molecular cloning of a 12-lipoxygenase cDNA from rat brain  
 JOURNAL Eur. J. Biochem. 212 (2), 605-612 (1993)  
 MEDLINE 93185682  
 PUBMED 844196  
 COMMENT Original source text: Rattus norvegicus (strain Sprague-Dawley) brain mRNA.

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ORIGIN

Query Match 48.9%; Score 1306; DB 10; Length 2048;  
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 Db 77 AACAGGTCTACCTGTGTGTGGTGGACAGCATGGAGAGGCATCTCTCGGGAAGCTGCTA 136  
 QY 121 TGGCCCGCACCGGCAAGGACAGAACTCAAGTGGAGACTACCGAGTATCTGGGGCG 180  
 Db 137 CGACCTGTTCGGGACTCGGAAGCAGAAATTCAAAGTGGATGTGTCAAGATACACCTTGGGCA 196  
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 QY 298 TGGGTGAGGCAACGGGCTCTGAGCTGCTGAAGSCACGCGCGCACCTGTGGGCGAG 357  
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 Db 497 GACCTCCTGTAGACCAACGATTTTCGAGAGGACAAAGAAATTTGAATTTGAAGCTTCAC 556  
 QY 538 GCCAAGGCGCTGGCGGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAG 597  
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 QY 598 GATCTAGATGACTTCAACCGGATTTTCTGGTGTGGTCAGAGCAAGCTGGCTGAGCGCTG 657  
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 QY 778 GAATCGAGGCGCCAGCTGGAGAGGAGCTGGAGGAGGACACACTGTTTGAAGCTGACTTC 837  
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Qy 1858 CTTAAGGCTGTGTGAAGAGTTTCAGGAGGAGCTGGCTGCTGCTGAGTAAGGAATTTGAG 1917  
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Db 1997 AGCTGTGGCATATGAGCATCCCGACTCTCTTGT 2034  
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Mus musculus arachidonate 15-lipoxygenase, mRNA (cDNA clone  
MGC:78162 IMAGE:3671948), complete cds.  
BC081546  
MGC.  
GI:51980618  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 2482)  
Straussberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Scheetz, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,  
Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
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Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 2482)  
Director MGC Project.  
Direct Submission  
Submitted (01-SEP-2004) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey Green M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.  
Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
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## ORIGIN

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QY 61 AACGAGGTGCAGCTGGCTGTGTCGCCAGCAGCGGGAGCGCGCTGGGAAGCGACTG 120
DB 70 AACGAGGTCTACTGTGGTGTATCGGACAGCATGGGGAGGCATCTCTCGGGAAGCTGTTC 129

QY 121 TGGCCCGCACGGGGCAAGGAGACAGAACTCAAGGTGGAACTACCGAGGTATCTGGGGCGG 180
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QY 181 CTGCTGTTTGTGAACCTGCGCAACCGGCACCTCTCTTAAGGACGACCGCTGGTTCGCAAC 240
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DB 850 TTCTCTCTGGATGGGATCAAGGCCAAATGTCTATCTCTTTGTAGTCAGCAGTACCTGGCTGCC 909
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VERSION BC056625.1 IMAGE:5005087), complete cds.
KEYWORDS
SOURCE  BC056625.1 GI:34786099
ORGANISM Mus musculus (house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2485)
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Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.W., Hong,D.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Ustin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
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Abrahamson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettanan,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whitting,M., Madan,A., Young,A.C., Rodighiero,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
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2 (bases 1 to 2485)
Strausberg,R.
Direct Submission
Submitted (25-AUG-2003) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
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Gaithersburg, Maryland;
Web site: http://www.nisac.nih.gov/
Contact: nisc.mgc@hghri.nih.gov
Akhter,N., Ayale,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
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Young,A., Zhang,L.-H. and Green,E.D.
Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 123 Row: c Column: 13
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FEATURES
source
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Searched: 1202784 seqs, 81813359 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	382.6	14.3	2497	US-10-071-411A-3	Sequence 3, Appli
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10	341.2	12.8	2674	US-09-949-016-3041	Sequence 3041, Ap
11	332	12.4	3384	US-09-547-435-29	Sequence 29, Appl
12	330.4	12.4	2316	US-09-547-435-5	Sequence 5, Appli
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14	327.8	12.3	2307	US-09-799-451-803	Sequence 803, App
15	327.8	12.3	2604	US-09-547-435-21	Sequence 21, Appl
16	318.6	11.9	432	US-09-641-638-435	Sequence 435, App
17	318.6	11.9	432	US-10-170-097-435	Sequence 435, App
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22	276	10.3	2316	US-09-547-435-27	Sequence 27, Appl
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ALIGNMENTS

RESULT 1  
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; Patent No. 6432648  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Cohen, Annick  
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
; FILE REFERENCE: GENSET 051C91  
; CURRENT APPLICATION NUMBER: US/09/641,638  
; CURRENT FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: US 09/502,330  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 60/133,200  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: US 09/275,267  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: US 60/119,917  
; PRIOR FILING DATE: 1999-02-12  
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; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
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; PRIOR FILING DATE: 1999-05-07
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; PRIOR FILING DATE: 1999-02-12
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; FEATURE:
; NAME/KEY: CDS
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; NAME/KEY: allele
; LOCATION: 1004
; OTHER INFORMATION: 10-349-97 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1049
; OTHER INFORMATION: 10-349-142 : polymorphic base G or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1123
; OTHER INFORMATION: 10-349-216 : deletion of CTG
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1131
; OTHER INFORMATION: 10-349-224 : polymorphic base G or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1491
; OTHER INFORMATION: 10-507-170 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1742
; OTHER INFORMATION: 10-340-112 : polymorphic base A or C
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1760
; OTHER INFORMATION: 10-340-130 : polymorphic base A or T
; FEATURE:
; NAME/KEY: allele
; LOCATION: 1941
; OTHER INFORMATION: 10-341-116 : polymorphic base A or G
; FEATURE:
; NAME/KEY: allele
; LOCATION: 2144
; OTHER INFORMATION: 10-341-319 : polymorphic base C or T
; US-10-170-097-652
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Query Match 37.9%; Score 1013.6; DB 4; Length 2343;

Best Local Similarity 69.2%; Pred. No. 2.9e-261;

Matches 1380; Conservative 11; Mismatches 600; Indels 3; Gaps 1;

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Qy 4 ATGGGTCTCTACCGCATCCGGGTGTCACCTGGGGCTGCTCTATGCCGGTTCACACAC 63
Db 40 ATGGGCGCTACCGCATCCGGGTGTCACCTGGGGCTGCTCTATGCCGGTTCACACAC 99
Qy 64 CAGGTGCAGCTGTGGCTGTCGGCCAGCACGCGGAGCGCGCTCGGGAAGGACTGTGG 123
Db 100 CCGTGCAGCTTGTGGCTGTCGGGACGCGCGGAGCGGAGCTGAGCTGAGCTGCGG 159
Qy 124 CCGCACGCGGCAAGGACAGAACTCAAGTGGGAAGTACCGGAGTATCTGGGGCGCTG 183
Db 160 CCGGCGCGGCGAGGAGGAGGTTTATCATGACGTTGCAGAGGACTTGGGGCTCTG 219
Qy 184 CTGTTGTGAACTGCGCAACGGCCTCTTAAAGGACGCGCTGTTCTGCAACTGG 243
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US-09-949-016-5821

Query Match 14.3%; Score 382.6; DB 4; Length 2496;  
Best Local Similarity 52.5%; Pred. No. 4.1e-92;  
Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;

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QY 126 CGCAGGGGCAAGGACAGACACTCAAGCTGGAAGTACCGGAGTATCTGGGCGCTGCT 185
DB 183 CGAGCGTGGCGGTGGATTCATACGCTGACTGTGGACGAGGAACCTGGGCGAGATCCA 242
QY 186 GTTGTGAAACTGCGCAAAACGGCACCTCTTAAGGACGACGCTGTCTGCAACTGGAT 245
DB 243 GCTGTGTCAGATCGAGAAGCGCACTACTGGCTGATGACGACTGTACTGAGTACAT 302
QY 246 CTCGTGCAAGGCGCCCGGACCGGGAACGAGTCAAGTTCCTTTGTTACCGTGGGTGA 305
DB 303 CAGCTGAAGACGCCC---CAGGGGACTACATCGAGTTCCCTGCTACCGCTGGATCAC 359
QY 306 GGGCAAGGCGTCTGAGCTGCTCAAGGACCGCCGCACTGTGGGCGAGGACCTCA 365
DB 360 CGGCGATGTCGAGTGTCTTCTGAGGATGGACCGCGCAAGTTGGCCCGAGATGACCAAT 419
QY 366 GGGCTGTTCCAGAAACACCGGAAGAGAGCTGGAAGAGAGAAAGTTGTACCGGTG 425
DB 420 TCACATCTCAAGCAACACCGAGCTTAAGAACTGGAAACCGCAAAACAATATGATG 479
QY 426 GGGAAACTGGAAGGACGGGTTAATCTGAATATGGCTGGGGCCAACTATATGACCTCC 485
DB 480 GATGGAGTGGAAACCTCGGCTTCCCTTGAGCATCGATGCAAAATGCCAAGGATTTACC 539
QY 486 TGTGNTAGCGATTTCTGGAAGACAGAGATGACTTTGAGGTTTCCTGGCCAAAGG 545
DB 540 CCGTGATATCCAGTTTGTAGTGAAGAAAGAGTGGACTTTGTTCTGAATTTACTCCAAAGC 599
QY 546 GCTGGCGGACCTCGCTATCAAGACT---CTTAATATGTTCTGACTTGTGGAAGGATCT 602
DB 600 GATGGAAACCTGTTCAACCGCTTCATCAACCGCTTCATGACATGTTCCAGTCTTTTGGAAATGACTT 659
QY 603 AGATCACTTTCAACCGGATTTCTGTGTGTGTGCTGAGCAAGCTGGCTGAGCGGTGCGGA 662
DB 660 CGCCGACTTTGAGAAATCTTTGTCAAGATCAGCAACACTATTTCTGACGGGTATGAA 719
QY 663 CTCCTGGAAGGAGATGCTTATTTGGGTACAGATTTCTTAATGGCGCCAAACCCGCTGT 722
DB 720 TCACTGGCAGGAAGACCTGATGTTTGGCTTACAGTTCTCTGAATGGCTGCAACCTGTGTT 779
QY 723 GCTGAGGCGCTGTGCTCACTTCTGCTCGCTAGTGTTCCTCCAGGCAATGA----- 776
DB 780 GATCCGGCGCTGCACAGAGCTGCCGAGAACTCCCGGTGACACAGGATGTTAGAGTG 839
QY 777 -----GGAACTGCAGGCGCCAGCTGGAGAAGAGCTGGAGGGAGGCACACTGTTGGAAGC 830
DB 840 CAGCTGGAGCGGAGCTCAGCTTGAGCAGAGAGGTCCAGCAAGGGAACTTTTTCATGCT 899
QY 831 TGACTTCTCCCTGTGATGGAATCAAGCGCAAGCTGCA---TTCTGTGAGCCAGCAGCA 887
DB 900 GGACTTTGAGCTGCTGATGGATCGATCGCAACAAACAGACCCCTGCACACTCCAGTT 959
QY 888 CTTGGCTGCCCTCTAGTCACTGCAATTTGAGCTGATGGGAACCTTCCCATGTT 947
DB 960 CTTGGCGCTCCCATCTGCTTGTATGAAGAACTGGCCAAAGATTTGTCCTTCCCATTCG 1019
QY 948 CATCAGCTCCAGCTGCCCGCACAGGATCCCAACCCCTCTTCTTCTGCTTACGGA 1007
DB 1020 CATCAGCTCAACCAATCCCGGAG-----ATGAGAACCTTATTTCTTCCCTTGGGA 1073
QY 1008 TCCCCCAATGGCTGCTTCTGCGCAAAATGCTGGGTGGCGAGCTCTGATTTCAAGTCCA 1067
DB 1074 TGCAAAATACGACTGCTTTTGGCCAAATCTGGGTGCGCTTCAGTGACTTCCAGCTCCA 1133
QY 1068 TGAGCTGCACTCTCATCTTCTGAGGGGACACTGATGGCTGAGGTCATGTTGTGGCCAC 1127
DB 1134 CCAGACCATCACCACCTTCTGCAACACATCTGGTGTCTGAGGTTTTTGGCAATGCAAT 1193
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## RESULT 4

US-09-023-655-1155  
; Sequence 1155, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart

```
QY 1128 CATGAGGTGCTGCGGTGCGATACATCTTCAAGCTTATAATTCCTCCCACTGGGATA 1187
DB 1194 GTACCGCCAGCTGCTGTGTGCAACCCATTTTCAAGCTGTGTGGCACAGTGAAT 1253
QY 1188 CACCTCTGGAATTAACGTCCGGGCCAGGACTGGGTGCTCTGACATGGGAATTTTGA 1247
DB 1254 CACCATTCGAATCAACAAGGCCCGGTGAGCAGCTCATCTCGAGTGTGGCTCTTTGA 1313
QY 1248 CCAGATAATGACACTGCTGGGGGAGGCGACGTCGAGCTGCTCAAGCAAGCTGGAGCTT 1307
DB 1314 CAAGGCCAACCCACAGGGGCGGTGGGACGTCAGATGTCAGAGGCCCATGAAGA 1373
QY 1308 CTTAACTTACAGCTCTTCTGTCCCTCTGATGACTTGGCCGACCCGGGCTCCTG----- 1362
DB 1374 CTTGACCTATGCTCCTCTGTCTTCCGAGGCCATCAAGGCCCGGGCATGGAGAGCAA 1433
QY 1363 ---GGAGTGAAGTCTTCTTCTATGCCCAAGATCGCTCGGCTCTGGGAATCATCTA 1418
DB 1434 AGAAGACATCCCTACTACTTCTACCGGAGACCGGCTCCTGGTGTGGGAAGCCATCAG 1493
QY 1419 TCGGTATGTGGAAGGAATCGTGAGTCTCCACTATTAAGACAGACGCTGGCTGTGAAGAACA 1478
DB 1494 GACGTTTACGSCCGAGGTGTAGACATCTACTACGAGGGCGACCAAGTGTGTGAGGAGA 1553
QY 1479 CCCAGAGCTGACAGCCTGGTGTGAGAGATCACTGAATCGGGCTGCAAGGGGCCCAGGA 1538
DB 1554 CCCGAGCTGACGAGACTTCGTGAACGATGTCTACGTACGCGCATCGGGGCGCGAAGTC 1613
QY 1539 CCGAGGTTTCTGTCTTCTTACAGGCTCGGAGCAGGTTTGCACATTTGTCCACCATGTG 1598
DB 1614 CTCAGGCTTCCCAAGTCGGTCAAGGCGGAGCAGCTGTGCGAGTACCTGACCGTGT 1673
QY 1599 TATCTTCACTGCAACCGGCCCAACAGCCTCTGTGCACTGGGCCAGCTGGAATGGTACTTC 1658
DB 1674 GATCTTCAACGCTTCCGCGCAGCAGCGCGGTCACTTTCGCGCAGTACGACTGGTGTCT 1733
QY 1659 TTGGTGTCTAATGACCTTGCACGATCGGCTGCCCGGCCCAACCAAG---GATGC 1715
DB 1734 CTGGATCCCAATGGCCCCCAACCATCGAGCCCCCGCACCGACTGCCAAGGGGTGCT 1793
QY 1716 AACGTGAGACAGTATGAGCGACACTGCCCACTTCCACAGGTTTCTCTCCAGATGTC 1775
DB 1794 GACCATGAGCAGATCGTGGACACGCTCCCGACCGCGCGCTCCTGTGGCATCTGGG 1853
QY 1776 CATCACTTGGCAGCTGGGCGACAGCGCAGCCGCTTATGTGGTGTGGGCCAGCATGAGA 1835
DB 1854 TGCAGTGTGGGCTGAGCCAGTTCAGGAAACGAGCTGTCTTGGGATGTATCCCA 1913
QY 1836 GGAGTATTTTGGGCGCTGAGCCTTAAAGCTGTGCTGAAGAGTTTCAAGGAGAGCTGGC 1895
DB 1914 AGAGCATTTTATCGAAGAGCCTGTGAAGGAAGCCATGCCGATTCGCAAGAACTCGA 1973
QY 1896 TGCCCTGATTAAGNAATTGATCCGGAATGCAAGCTGACATGCCCTACGAGTACT 1955
DB 1974 GGCATTTGACGCTGATTTGCTGAGCGCAACAAGAAAGCAGCTGCCATATTTACTACT 2033
QY 1956 GCGGCCAGCTGGTGGAAAAACAGTGTGGCATCTAAAGCTGCGCCACCTTTGGTTATTT 2015
DB 2034 GTCCCAAGACCGGATTCGAAACAGTGTGGCCATCTGAGCACACTGCCAGTCTCACTGTGG 2093
QY 2016 CAGCCCCCATCACCACAGCCCAAG 2040
DB 2094 GAAGGCCAGCTGCCCGCAGCATG 2118
```

APPLICANT: Jeffrey J. Seilhamer  
 TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
 NUMBER OF SEQUENCES: 1508  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
 STREET: 3174 PORTER DRIVE  
 CITY: PALO ALTO  
 STATE: CALIFORNIA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/023,655  
 FILING DATE: HEREMITH  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Zeller, Karen J.  
 REGISTRATION NUMBER: 37,071  
 REFERENCE/DOCKET NUMBER: PA-0001 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (650) 855-0555  
 TELEFAX: (650) 845-4166  
 INFORMATION FOR SEQ ID NO: 1155:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 2497 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 LIBRARY: GENEBAK  
 CLONE: g187192  
 US-09-023-655-1155

Query Match 14.3%; Score 382.6; DB 4; Length 2497;  
 Best Local Similarity 52.5%; Pred. No. 4.1e-92;  
 Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;

Qy	126	CGCAGCGGGCAAGAGACAGAACTCAAGGTGGAAGTACCGAGTATCTGGGGCGGTGCT	185
Db	182	CGAGCGTGGCGCGTGGATTTCATACGACGTGACTGTGGACGAGAACTGGGCGGAGATCCA	241
Qy	186	GTTTGTGAACCTGCGCAACCGCACCTCCTTAAGGACGACCTGGTTCTGCAACTGGAT	245
Db	242	GCTGGTCAGAACTCGAAGAGCGCAAGTACTGGCTGAATGACGACTGGTACTGGAAGTACAT	301
Qy	246	CTCTGTGACAGGGCCCCGGAGCGGGGACGAGGTGAGTTTCCCTTGTACCGCTGGGTGA	305
Db	302	CACGCTGAAGACGCC---CACGGGACTACATCGAGTTCCTCTGCTACCGCTGGATCAC	358
Qy	306	GGGCAACGGCGTCTGTAGCTGCTGTAAGGACCGCGCCGACCTGTGGGCGAGGACCTCA	365
Db	359	CGGCGATGTCGAGTTGCTCTGAGGATGGAACGCGCAAAAGTTGGCCCGAGATGACCAAAAT	418
Qy	366	GGGCTGTTCCAGAAACACCGGGAAGAGAGCTGGAAGAGAAGGAAGTTGTACCGGTG	425
Db	419	TCACATTCTCAAGCAAACCCGACGTAAGAACTGGAACACCGCAAAACAAATATCGATG	478
Qy	426	GGGAAACTGGAAGGACCGGGTTAATTCCTGAATATGGCTGGGGCCCAAACTATATGACCTCCC	485
Db	479	GATGAGTGGNAACCTTGGCTTCCCTTGTAGCATCGATGCCAAATGCCACAAGGATTTACC	538
Qy	486	TGTGATGAGCGATTTCTGGAAGACAAGAGATTGACTTTGAGGTTTCGCTGGCGCAAGGG	545
Db	539	CCGTGATATCCAGTTTGTATAGTGAAGAAAGGAGTGGACTTTGTTCTGAAATTAATCTCCAAAGC	598

Qy	546	GCTGCGGACCTCGCTATCAAAAGACT---CTCTAAATGTTCTGACTTGTCTGGAAGATCT	602
Db	599	GATGGAGAACCTGTTTCATCAACCGCTTCATGCACATGTTCCAGTCTTCTTGGAAATGACTT	658
Qy	603	AGATGACTTCAACCGGATTTCTGTGTGGTTCAGAGCAAGCTGGCTGAGCGGTGGCGGA	662
Db	659	CGCGACTTTTGAGAAAATCTTTGTCAAGATCAGCAACACTATTTCTGAGCGGTTCATGAA	718
Qy	663	CTCTGGGAAGGAGATGCCCTATTTGGGTACAGTCTTTTAATGGCGCCAAACCCCGTGT	722
Db	719	TCACTGGCAGGAAGACCTGATGTTTGGCTACAGTTCCTGAAATGGCTGCAACCTGTGT	778
Qy	723	GCTGAGGCGCTCTGCTCACCTTCTGCTGCGCTAGTGTTCCTTCCAGGCAATGGA-----	776
Db	779	GATCCGGCGCTGCACAGAGCTGCCGAGAAGCTCCCGGTGACCAACGAGATGGTAGAGTG	838
Qy	777	-----GGAACCTGAGGCGGCTGGAGAGAGCTGGAGGGGAGGACACTGTTTCAAGC	830
Db	839	CAGCCTGGAGCGGCGAGCTCAGCTTGGAGCAGGAGGTCAGCAAGGGAACATTTTTCATCGT	898
Qy	831	TGACTTCTCCCTGCTGGATGGATCAAGGCCCAACGTCA--TTCCTGTAGCCAGCAGCA	887
Db	899	GGACTTTGAGCTGCTGGATGGATCGATGCCAAACAGACCCCTGCACACTCCAGTT	958
Qy	888	CCTGGCTGCCCTCTAGTCTCATGCTGAAATTCAGCCCTGATGGGAAACTCTTGCCCCATGGT	947
Db	959	CCTGGCGCTCCCATCTGCTGCTGTATAAGAAACCTGGCCAAACAGATGTTGCCCATTGC	1018
Qy	948	CATCAGCTCAGCTGCCCGGCACAGGATCCCAACACCTCCCTTTTCTTGCTACGGA	1007
Db	1019	CATCCAGCTCAACCAAAATCCCGGAG-----ATGAGAAACCTATTTTCTCCCTTCGGA	1072
Qy	1008	TCCCCCAATGGCTGCTTCTGSCCAAAATGCTGGGTGCCAGCTCTGACTTCCAGCTCCA	1067
Db	1073	TGCAAAATAGACTGGCTTTTGGCCAAATCTGGGTGCGTTTCAGTGAATTCACACGTCCA	1132
Qy	1068	TGAGCTGCAGTCTCATCTTCTGAGGGGACACTTGATGGCTGAGGTCAATTTGTGTGCCAC	1127
Db	1133	CCAGACCATCACCCACCTTCTCGAACAACATCTGGTGTCTGAGGTTTTTGGCATTCGAAT	1192
Qy	1128	CATGAGTGCCTGCGCTGATCATCTTCTTCAAGCTTATTAATCCCACTCGGATA	1187
Db	1193	GTACGCCAGCTGCTGCTGTGCACCCCATTTTCAAGCTGCTGGTGGCACAACGTGAGATT	1252
Qy	1188	CACCTTGGAAATTAACGTCGCGGCCAGGACTGGGCTGCTCTGACAATGGGAAATTTTGA	1247
Db	1253	CACCATTTGCAATCAACCAAGCCCGTGAGCAGCTCACTGCGAGTGTGGCTCTTTGA	1312
Qy	1248	CCAGATAATGAGCACTGGTGGGGGAGGCCACGTGACGCTGCTCAAGCAAGCTGGAACCTT	1307
Db	1313	CAAGGCCAACGCCACAGGGGCGGTGGCACGTTGCAGATGGTGCAGAGGCCATGAAGGA	1372
Qy	1308	CCTAAGCTACAGTCTCTTCTGCTCCCTGATGACTTGGCGGACCGGGGGCTCTG-----	1362
Db	1373	CCTGACCTATGCTCCCTGCTGCTTTCCGAGGCCATCAAGGCCCGGGGCATGGAGACAA	1432
Qy	1363	-----GGAGTGAAGTCTTCTTCTATGCCCAAGATGCGCTGCGGCTCTGGGAAATCATCTA	1418
Db	1433	AGAAGACATCCCCCTACTTCTACCGGGACGAGGGCTCTCGTGTGGAGGCCATCAG	1492
Qy	1419	TCGGTATGTGGAAGGAATCGTGAAGTCTCCACTATAAGACAGACGTGGCTGTGTGAAGACGA	1478
Db	1493	GAGTTTCAGCGCGGAGGTGTAGACATCTACTACGAGGGGACACAGGTGGTGGAGGAGGA	1552
Qy	1479	CCAGAGCTGCAGACTGTTGTGAGAGATCACTGAAATCGGCTGCAAGGGGCCACGGA	1538
Db	1553	CCCGAGCTGCAGACTTCGTGAAACGATGTCTACGTGTACGGCATACGGGCGCGGCAAGTC	1612
Qy	1539	CCGAGGTTTCCTGCTCTTTACAGGCTCGGACACGAGTTTGGCACTTCTGTACCACTGTG	1598
Db	1613	CTCAGGCTTCCCCCAAGTCGGTCAAGAGCCGGAGCAGCTGTGCGAGTACTCTGACCGTGGT	1672

QY 1599 TATCTTCACTGACCGGCAACACGCTCTGTGTACACCTGGGCGAGCTGGACTGTACTC 1658  
Db 1673 GATCTTCACTGCTCTCGGCGAGCAGCGCGGTCAACTTTCGGCCAGTACGACTGGTGTCT 1732  
QY 1659 TTGGGTGCTTAATGACACCTGACAGATGGGTGCTGCCCGCCCAACACCAAG--GATGC 1715  
Db 1733 CTGGATCCCAATGGCCCGCCCAACCATGGAGCCCGCCACCGACTGCCAAGGGGTGGT 1792  
QY 1716 AACGCTGGAGACAGTGAATGGGACACTGCCCCAACTTCCACAGGCTTCTCTCCAGATGTC 1775  
Db 1793 GACCAATTGACAGATCGTGGACAGCTGCCCGACCGCGCGCTCTCTGTGGCATCTGGG 1852  
QY 1776 CATCACTTGGAGCTGGGCGAGAGCGGCGGCTTATGGTGGCTGTGGGCGGAGCATGAGA 1835  
Db 1853 TCGAGTGTGGGCGCTGAGCGATTCAGGAAACAGAGCTGTTCCTGGGCATGTACCCAGA 1912  
QY 1836 CGAGTATTTTTCGGGCGCTGAGCTTAAGCTGTGTGAAGATTTTCAGGAGGAGCTGCG 1895  
Db 1913 AGAGCATTTATCGAGAGCTGTGTGAAGAGCCATGGCCGATTCGCGAAGAACTCGA 1972  
QY 1896 TCCCTTGGATAGGAAATTTAGATCCGGAATCGAAAGCTTGGACATGCCCTACGAGTACT 1955  
Db 1973 GGCCATTGTGAGCTGATTTGCTGAGCGCAACAGGAAGAGCTGCCATATTACTACTT 2032  
QY 1956 GCGGCCAGCTGGTGGAAACAGTGTGGCCATCTAAGGTCGCCACCCCTTTGGTTATT 2015  
Db 2033 GTCCCGAGACCGGATTCGGAACAGTGTGGCCATCTGAGCACATGCCAGTCTCACTGTG 2092  
QY 2016 CAGCCCCATCACCAAGCCACAAG 2040  
Db 2093 GAAGCCAGCTGCCCGACGAGT 2117

## RESULT 5

US-10-071-411A-3

; Sequence 3, Application US/10071411A

; Patent No. 6797475

; GENERAL INFORMATION:

; APPLICANT: Glenn Barnes

; APPLICANT: Joanne Meyer

; TITLE OF INVENTION: Detection of Polymorphisms in the Human

; FILE OF INVENTION: 5-Lipoxygenase Gene

; FILE REFERENCE: MRI-021

; CURRENT APPLICATION NUMBER: US/10/071,411A

; CURRENT FILING DATE: 2002-02-07

; PRIOR APPLICATION NUMBER: 60/267,515

; PRIOR FILING DATE: 2001-02-08

; PRIOR APPLICATION NUMBER: 60/314,248

; PRIOR FILING DATE: 2001-08-21

; NUMBER OF SEQ ID NOS: 66

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 3

; LENGTH: 2497

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-071-411A-3

Query Match 14.3%; Score 382.6; DB 4; Length 2497;  
Best Local Similarity 52.5%; Pred. No. 4.1e-92;  
Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;

QY 126 CCGACGGGCGAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGCGCGTGT 185  
Db 182 CGAGCGTGGCGGTGGATTTCATACGCTGCTGTGACGAGGAACCTGGGCGAGATCCA 241  
QY 186 GTTGTGAACTGCCGAAACGCGACTCTTAAGGACGACGCTGTGTGCACTGGAT 245  
Db 242 GCTGTGCAATTCGAGAAGCGCAAGTACTGGCTGAATGACGACTGGTACCTGGAATACAT 301  
QY 246 CTCGTGAGGCGCCCGGAGCGCGGAGCGAGTCAAGTTCCTTGTACCGCTGGTGA 305  
Db 302 CACGCTGAAGACGCCCC--CACGGGGACTCATCGAGTTCCTCTGCTACCGCTGATCATC 358

QY 306 GGGCAACGCGCTCTGTGACCTGCTGTGAAGGCAACCGCGCGACTGTGGGCGAGGACCTCTCA 365  
Db 359 CGCGATCTCGAGGTGTCTCTGAGGGATGGACGCGCAAAAGTTGGCCGAGATGACCAAA 418  
QY 366 GGGCTGTCTCAGAAACACCGGGAAGAGACTGGAAGAGAGAAAGATTGTACCGGTG 425  
Db 419 TCACATCTCAAGCAACACCGACGTAAAGAACTGGAACAACGCGAANAACAATATCGATG 478  
QY 426 GGGAACTGGAAGGACGGGTTAAATTTCTGAATATGCTGGGCGCAAACTATATGACCTCCC 485  
Db 479 GATGGAGTGGAAACCTGCTGCTTCCCTTCGAGCATGATGCCAAAATGCCACAAGGATTTACC 538  
QY 486 TGTGATGAGGATTTCTGGAAGACACAGAGAGTGTGACTTTGAGGTTTCTGCTGGCAGGG 545  
Db 539 CCGTGAATATCCAGTTTGAATAGTGAAGAAAGGAGTGGACTTTGTTCTGAAATTAATCTCAAAG 598  
QY 546 GCTGCCCACTCTGCTATCAAGACT---CTCTAAATGTTCTGACTTGTGCTGGAAGATCT 602  
Db 599 GATGGAGAACCTGTTCATCAACCGTTTCATGACATGTTCCAGTCTTCTTGGAAATGACTT 658  
QY 603 AGATGACTTCAACCGGATTTTCTGTGTGGTTCAGAGCAAGCTGGCTGAGCGGTGGGGA 662  
Db 659 CGCGACTTTCAGAAATCTTTGTCAAGATCAGCAACACTATTTCTGAGCGGTTCATGAA 718  
QY 663 CTCCTGGAAGGAAGTGCCTTATTTGGGTACAGTTTCTTAATGGCGCAACCCCGTGTG 722  
Db 719 TCATGGCAGGAAGACCTGATGTTTGGCTACAGTTCTCTGAATGGCTGCAACCTGTGT 778  
QY 723 GCTGAGGCGCTGCTCACTCTGCTCGCTAGTGTTCCTCCAGGATCGA----- 776  
Db 779 GATCGGCGCTGCACAGAGCTGCCCGGAGAACTCCCGGTGACCAAGGAGATGGTAGAGTG 838  
QY 777 -----GGAACTGCGAGGCCAGCTGGGAAGAGAGCTGGAGGAGGACACACTGTTTCGAAGC 830  
Db 839 CAGCTGGAGCGGAGCTCAGCTTGGAGCAGAGGTCCAGCAAGGAAACATTTTCATCGT 898  
QY 831 TGACTTCTCCTGCTGGATGGATCAAGGCCAAGCTCA---TCTCTGTAGCCAGCAGCA 887  
Db 899 GGACTTTGAGCTGTGGATGGATCGATCGATCGCAACAAACAGACACCCCTGCACACTCCAGT 958  
QY 888 CCTGCTGCCCTCTAGTCACTGTGAATTCAGCCTGATGGGAACCTTTTCTGCTTACCGA 947  
Db 959 CTGCGCGCTCCCATCTGCTGTGTATGAAGCTGCGCCAAAGATGTGCTCCCATGTC 1018  
QY 948 CATCCAGCTCCAGCTGCCCGCCGACAGGATCCCGCCACACTCCCTCTTCTGCTTACCGA 1007  
Db 1019 CATCCAGCTCAACCAATCCCGGAG-----ATGAGAAACCTATTTTCTCCCTTCGGA 1072  
QY 1008 TCCCCCAATGGCTGGCTTCTGGCCAAATGTGGGTGGCAGCTCTGACTTCCAGCTCA 1067  
Db 1073 TGCAAAATACGACTGGCTTTTGGCCAAATCTGGGTGGTTCAGTGTGACTTCCAGCTCA 1132  
QY 1068 TGAGCTGAGTCTCATCTTCTGAGGGGACACTGTGATGCTGAGGTCTATTTGTGGCCAC 1127  
Db 1133 CCAGACCATACCCACCTTCTGCGAAACACATCTGGTGTCTGAGGTTTGTGGCAITGGCAAT 1192  
QY 1128 CATGAGTGTGCTGCTCGATACATCTCTATCTCAAGCTTATAATTCGCCACCTGCGATA 1187  
Db 1193 GTACCGCCAGCTGCTGTGTGACCCCATTTTCAGCTGTGTGGTGGCAGCAGTGGAT 1252  
QY 1188 CACCTGGAATTAACGTCGCGGCGAGGACTGGGCTGTCTCTGACATGGGAAATTTTCGA 1247  
Db 1253 CACCATTCGAATCAACCAAGGCCGTGAGCAGTCTATCTGCGAGTGTGGCTTCTTTGA 1312  
QY 1248 CCAGATATGAGCACTGTGGGGGAGGCCAGCTGCTGCTCAAGCAAGCTGGAGCCTT 1307  
Db 1313 CAAGGCCAAACGCCAGGGGCGGTGGGACGTGCAGATGCTGAGGAGGCGCATGAAGGA 1372  
QY 1308 CCTAACCTTACAGTCTCTTCTGCTCCCTCTGATGACTTGGCCGACCGGGGGCTCTCTG- 1362  
Db 1373 CTTGACCTATGCTCTCCCTGCTGCTTCCCGAGGCCATCAAGGCCCGGGGCGATGGAGCAA 1432  
QY 1363 -----GGAGTGAAGTCTTCTCTATATGCCAAGATGCGCTGCGGTCTCTGGGAAATCATCTA 1418

Db 1433 AGAAGACATCCCTACTTCTTACCGGACGACGGGCTCCTGGTGTGGAAAGCCATCAG 1492  
QY 1419 TCGGTATGTGGAAGGAATCGTNGTCTCCACTATAGACAGAGCTGGCTGTGAAGACGA 1478  
Db 1493 GACGTTTACCGGCGAGGTGTAGACATCTACTACGAGGGCGACCAAGTGTGGAGAGGA 1552  
QY 1479 CCAGAGCTGCAGACCTGTGTGCGAGAGATCACTGAAATCGGCTGCAAGGGGCCACAGGA 1538  
Db 1553 CCGGAGCTGCAGGACTTGTGNAAGATGTCTACGTGTAGGCATGCGGGGCGCAAGTC 1612  
QY 1539 CCGAGGCTTCTGTCTTTACAGCTCGGACCAAGTTTCCACTTTGTCAACATGTC 1598  
Db 1613 CTGAGGCTCCCAAGTCTGAGTCAAGAGCGGAGCAGCTGTGCGAGTACTGACCGTGT 1672  
QY 1599 TATCTTCACTGCACCGGCAACACCGCTGTGTGACCTGGGCCAGCTGGAATGTTACTC 1658  
Db 1673 GATCTTCAACCGGCTCGCGCCAGCACCGCGGTCAACTTTGGCCAGTACGACTGGTGTCT 1732  
QY 1659 TTGGGTGCTTAATGCACTGACCTGACAGATGGGCTGCGCCCGCCAAACCAAG---GATGC 1715  
Db 1733 CTGGATCCCAATGCGCCCAACCAATGAGGCGCCCGCCACCGACTGCGCAAGGGCGTGT 1792  
QY 1716 AACGCTGGAGACAGTAGTGCAGACTGCCCCAACTTCCACAGGCTTCTCTCCAGATGTC 1775  
Db 1793 GACCATTTGAGCAGATCGTGGACAGCTGCGCGACCGCGCGCTCCTGCTGGCATCTGGG 1852  
QY 1776 CATCACTTGGCAGCTGGCAGAGCGCCAGCCCGTTATGTTGGCTGTGGGCCAGCATGAGGA 1835  
Db 1853 TGCAGTGTGGGCGCTGAGCGAGTTCCAGGAAACAGAGCTGTTCTGGGCGATGTACCCAGA 1912  
QY 1836 GAGATATTTTTCGGGCGCTGAGCCTAAGCTGTGCTGAAGAGTTCAGGGAGGAGCTGGC 1895  
Db 1913 AGAGCATTTTATCAGAGAGCTGTGAAGAGCCATGGCCCGATTCGCAAGAACCTCGA 1972  
QY 1896 TGCCTTGGATTAAGAAATTGAGATCCCGAATGCAAGCTGGAATGCCCTTACAGATGACT 1955  
Db 1973 GGCATTTGTGAGGCTGATTCTGAGGCGCAACAGAGAGAGCAGCTGCCATATTTACTATT 2032  
QY 1956 GCGGCCAGGCTGGTGAAGAAAGTGTGGCCATTAAGCTGCCACCTTTGGTTATTT 2015  
Db 2033 GTCCCCAGACCGGATTTCCGAAACAGTGTGGCCATCTGAGCACACTGCCAGTCTCACTGTGG 2092  
QY 2016 CAGCCCCCATCACCCAGGCCACAAAG 2040  
Db 2093 GAAGGCCAGCTGCCCGCCAGCAGATG 2117

## RESULT 6

US-09-949-016-109  
; Sequence 109, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 109  
; LENGTH: 2497  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-109

Query Match 14.3%; Score 382.6; DB 4; Length 2497;  
Best Local Similarity 52.5%; Pred. No. 4.1e-92;  
Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;  
QY 126 CCGACGGGGCAGGAGACAGAACTCAAGGTGGAAAGTACCGGAGTATCTGGGGCCCGCTGCT 185  
Db 182 CGAGCGTGGCGGGTGGATTCATACGAGTGAAGTGGAGGAACTGGGCGAGATCCA 241  
QY 186 GTTTCGAAACTGCGCAAAACGGCACCTCTTAAGACGACGCTGTTCTGCAACTGGAT 245  
Db 242 GCTGTGAGATTCGAGAGCGCAAGTACTGGCTGAATGACGACTGTAAGTACAT 301  
QY 246 CTCGTGAGGGCCCGGAGCGCGGGAAGAGTCAAGTCAAGTTCCTTGTATCCGCTGGTGA 305  
Db 302 CACGCTGAAGACGCGCC---CACGGGAGTACTATCAGTGTCCCTGCTACCGTGGATCAC 358  
QY 306 GGGCAACGGCGTCTGAGCGCTGCTGAAGGACCGCGCGCACTGTGGGGGAGGACCCCTCA 365  
Db 359 CGGCGATGTGAGGTTGTCTGAGGATGGAGCGCCAAAGTTGGCCCGAGATGACCAAT 418  
QY 366 GGGCGCTGTTCCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAAAGTGTGACCGGTG 425  
Db 419 TCAGATTTCTCAAGCAACACCGACGTAAGAGACTGGAACACGGCAAAACAATATCGATG 478  
QY 426 GGGAACTGGAAAGGACGGTTAAATTCGAATATGCTGGGGCCAAACTATATGACCTCCC 485  
Db 479 GATGAGTGGAAACCGCTGCTTCCCTTGAGCATCGATGCAAAATGCCAAGAGATTTACC 538  
QY 486 TGTGATGAGCAATTTCTGGAAGACAGAGAGTTCAGTTTGAAGTTTCGCTGGCCAAAGG 545  
Db 539 CCGTATATCCAGTTTGTATGTAAGTGAAGAGAGTGAAGTGTGTTGTAATTAATCCAAAG 598  
QY 546 GCTGCGCGACCTCGCTATCAAAAGACT---CTCTAAATGTTCTGACTTGTGGAAGGATCT 602  
Db 599 GATGAGAGACCTGTTTCATCAACCGCTTCATGACATGTTCCAGTCTTCTTGGAAATGACTT 658  
QY 603 AGATGACTTCAACCGGATTTCTGTGTGCTGAGAGCAAGCTGGCTGAGCGGCTGGCGGA 662  
Db 659 CCGCGACTTTGAGAAATCTTGTCAAGATCAGCAACACTATTTCTGACGGGTGATGAA 718  
QY 663 CTCCTGGAGGAGATGCTTATTTGGGTACAGTTTCTTAATGCGCCAAACCCCGTGT 722  
Db 719 TCACCTGGAGGAGACCTGATGTTTGGTACAGTTTCTGAAATGGCTGCAACCTGTT 778  
QY 723 GCTGAGGCGCTCTGCTACCTTCTCGCTGCTAGTGTTCCTCCAGGATGGA----- 776  
Db 779 GATCGGCGCTGCAAGAGCTGCCCGAGAGCTCCCGGTGACCAAGAGATGTTAGATG 838  
QY 777 -----GGAACTGCGAGGCCAGCTGGAGAGAGCTGGAGGAGGAGGACACTGTTTCAAGC 830  
Db 839 CAGCCTGGAGCGGAGCTCAGCTTGGAGCAGGAGGTCCAGCAAGGGAACATTTTCATCGT 898  
QY 831 TGACTTCTCCCTGCTGGATGGGATCAAGGCCAAAGCTCA---TTCTCTGAGCCAGCAGCA 887  
Db 899 GGACTTTGAGCTGCTGGATGGGATCGATGCCAAACAAACAGACCCCTGCGACACTCCAGTT 958  
QY 888 CTTGGCTGCCCTCTAGTCACTGCTGAAATTCAGGCTGATGGGAAACTCTTGGCCATGCT 947  
Db 959 CTTGGCGCTGCCATCTGCTTGTATGAAACCTGGGCCAACAGATTTGCCCATGTC 1018  
QY 948 CATCCAGCTTCCAGCTGCCCCCGCACAGGATCCCAACCACTCCCGCTTTTCTTGGCTACGGA 1007  
Db 1019 CATCCAGCTCAACCAATCCCGGAG-----ATGAGAAACCTTATTTTCTCCCTTCGGA 1072  
QY 1008 TCCCCCAATGGCTGCTGCTTCTGGCCAAATGCTGGGTGCGCAGCTCTGACTTCCAGCTCCA 1067  
Db 1073 TGCAAAATACGACTGGCTTTTGGCCAAATCTGGGTGCGTTCAGTGACTTCCAGTCCA 1132  
QY 1068 TGAGCTGCGAGTCTCATCTTCTGAGGGGACACTTTGATGGCTGAGGTCATTTGTTGGCCAC 1127  
Db 1133 CCAGACCATCAACCACTTCTGGAACACATCTGGTGTCTGAGGTTTTTGGCATTTCAAT 1192  
QY 1128 CATGAGGTGCTGCGCTCGATACATCTCTATCTTCAAGCTTTAATTTCCCCCACTCGGATA 1187



Db 1193 GTACCCGAGCTGCTGCTGTCACCCCAATTTTCAAGCTGCTGGTGGCAACGCTGAGATT 1252  
QY 1188 CACCTTGGAAATTAACGTCGGGCCAGGACTGGGCTGGTCTCTGACATGGGAATTTTCGA 1247  
Db 1253 CACCATTTGCAATCAACACCAAGSCCGTGAGCAGCTCATCTGCGAGTGTGGCTCTTTGA 1312  
QY 1248 CCAGATAATGAGCACTGGTGGGGAGGCCACGTCGAGCTGCTCAAGCAAGCTGGAGCCCTT 1307  
Db 1313 CAAGGCCAACGCCACAGGGGGGGTGGGACGTCGACATGGTGGCAGAGCCATGAAGGA 1372  
QY 1308 CTTAACTTACAGCTCTCTCTGCTCCCTCATGACTTGGCGGACCGGGGGCTCTCG---- 1362  
Db 1373 CTTGACCTATGCTCTCTGCTCTTCCGAGGCCATCAAGSCCGGGGATGAGAGCA 1432  
QY 1363 ----GGAGTGAAGTCTTCTTATGCCCAAGATGCGCTGCGGCTCTGGGAATCATCTTA 1418  
Db 1433 AGAAGACATCCCTACTACTTCTACCGGACGACGGGCTCTGGTGTGGAGCCATCAG 1492  
QY 1419 TCGGTATGTGAAGGAATCGTGAGTCTCCACTATATAGACAGAGCTGGCTGTGAAGACGA 1478  
Db 1493 GACGTTTACGCGCGGAGGTGTAGACATCTACTACGAGGGGACGAGGTGTGGAGGAGA 1552  
QY 1479 CCAGAGCTGCAGACTGCTGTGCGAGAGATCACTGAAATCGGCTGCAAGGGGCCAGGA 1538  
Db 1553 CCGGAGCTGCGAGACTTCTGTAACGATGTCTACGTGTACGGGATGCGGGGCGGCAAGTC 1612  
QY 1539 CCGAGGGTTTCTGCTCTTTACAGCTCGGACAGAGTTTGCCTTGTTCACCATGTG 1598  
Db 1613 CTCAGGCTTCCCAAGTCGTCNAAGCCGGAGCAGCTGTCCGAGTACTGACCGTGT 1672  
QY 1599 TATCTTACCTGACCGGCCAACAAGCTCTGTGACCTGCGGCTGAGCTGGAGTGTACTC 1658  
Db 1673 GATCTTCAACGCTGCGGCCAGCAGCCGCGGTCAACTTCGCGCAGTACGACTGGTGTCT 1732  
QY 1659 TTGGGTGCTTAATGACCTGACAGTGGCTGCGGCTGCGGCCCGCCCAACCAAG---GATGC 1715  
Db 1733 CTGGATCCCAATGGCCCCCAACCATGGAGCGCCCGCCGACGACTGCCAAGGGGTGT 1792  
QY 1716 AACGCTGGAGACAGTGAATGCGGACACTGCCCAACTTCCACAGGGTCTCTCCAGATGTC 1775  
Db 1793 GACCATTTGAGCAGATCGTGGACAGCTGCGCCGCGGCGCTCTGTGGCATCTGGG 1852  
QY 1776 CATCACTTGGCAGCTGGGAGCAGCGCAGCCCGTATGTTGGTGTGGGCGCAGCATGAGGA 1835  
Db 1853 TGCAGTGTGGGCTGAGCAGTTCAGGAAACGAGCTGTTCTGGGCGATGTACCAGA 1912  
QY 1836 GGAGTATTTTTCGGGCCCTGAGCCTAAGCTGTGCTGAAGAGTTTCAGGGAGGAGTGGC 1895  
Db 1913 AGAGCATTTTATCGAAGAGCCTGTGAAGGAAGCCATGGCCCGATTCGCAAGAACCTCGA 1972  
QY 1896 TGCCCTGGATAAGGAATTTGAGATCCGGAATGCAAGAGCTGGACATGCCCTACGAGTACCT 1955  
Db 1973 GGCCATTTGTCAGCTGATTTGCTGAGGCGCAACGAAGAGCAGCTGCCATATTACTACT 2032  
QY 1956 GCGGCCAGCTGGTGGAAAAACAGTGTGCCATCTAAGCGTGCACCCCTTTGGTTATTT 2015  
Db 2033 GTTCCCGACAGCCGGAATTCGAACAGTGTGGCCATCTGAGCACACTGCGAGTCTCACTGTGG 2092  
QY 2016 CAGCCCCCATCACCCAGCCCAAG 2040  
Db 2093 GAAGCCAGCTGCCCGAGCCAGATG 2117

## RESULT 7

US-09-061-768A-1

; Sequence 1, Application US/09061768A

; Patent No. 6204037

; GENERAL INFORMATION:

; APPLICANT: BRASH, ALAN R.

; APPLICANT: BOEGLIN, WILLIAM E.

; APPLICANT: JISAKA, NITSUO

; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS

NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

COMPUTER: IBM PC/XT/AT compatible

OPERATING SYSTEM: Windows 3.1

SOFTWARE: WORD PERFECT 6.1 and ASCII

CURRENT APPLICATION DATA:

APPLYING APPLICATION NUMBER: US/09/061,768A

FILING DATE: APRIL 16, 1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA: NONE

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 493-8000

TELEFAX: (919) 419-0383

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2685 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

US-09-061-768A-1

Query Match 12.8%; Score 342.8; DB 3; Length 2685;  
Best Local Similarity 51.0%; Pred. No. 2e-81;  
Matches 924; Conservative 0; Mismatches 867; Indels 21; Gaps 4;

QY 196 CTGGCAAAACGACACTCTCTTAAGGACGACGCTGTTCTGCAACTGGATCTCTGTGCAG 255  
Db 297 CTGCCCCCTGTGGGCCCCCTGGCCCCGATGCTGTTCTGCCCTGTGTTCCAGCTGACA 356  
QY 256 GCGCCCGGAGCGGGGACGAGTTCAGGTTCCCTTTTACCGCTGGGTGGAGGGCAACGCG 315  
Db 357 CGCGCGGGGGCGG---CCACTCTCTTCCCTGCTACCACTGGCTGGAGGGGGGGGG 413  
QY 316 GTCTGTAGCCTGCTGAAAGGACCGGCGCACTGTGGGGGAGGACCTCAGGGCCCTGTTC 375  
Db 414 ACCCTGTGTGTCGAGGAGGTACAGCCAAAGGTGTCTGGGCGAGACACACCCTGTGCTC 473  
QY 376 CAGAAACCGGGAGAGAGCTGGAAGAGAGAGAGTGTACCGGTGGGGGAACTGG 435  
Db 474 CAGCAACAGCCGAGAGAGGCTTCAGCCCGGAGGAGATGTACAGTGGAGGCTTAC 533  
QY 436 AAGGACGGGTAAATTTCTGAATATGCTGGGGCCAAACTATATGACTCCCTGTGGATGAG 495  
Db 534 AACCCAGGTGGCCTCACTGCTGGATGAAGAAGCAGTGGAGACTTGGAGCTCAATATC 593  
QY 496 CGATTTCTGGAAGACAGAGAGTTGACTTTGAGGTTTCGCTGGGCCCAAGGGGCTGCCGAC 555  
Db 594 AAATACTCCACAGCCAGGAATGCCAACTTTTATCTACAAGCTGGTCTGTCTTTTCAGAG 653  
QY 556 CTCGCTATCAAGACTCTCTAAATGTTCTGACTTCTGCGAAGGATCTAGATGACTTCAAC 615  
Db 654 ATGAAATCAAGGGGTGCTGGAGCCGCGAAGGGGCTCTGGAGGAGTCTGAAATGAGATGAA 713  
QY 616 CGGATTTTCTGCTGTGGTTCAGAGCAAGCTGCTGAGCCGCTGCGGGAATCTCTCTGGAAGAA 675  
Db 714 AGGATCTCACTTCCGGAGGAGACCCAGCAGCTGAGCAGCATTTGAGCAGCTGGCAGGAG 773  
QY 676 GATGCTTTATTTGGGTACCACTTTTCTTAATGGGCCAAACCCCGTGGTGTGCTGAGGCGCTCT 735



Qy	256	GGCCCCGAGCGGGGACGAGGTCAGGTTCCCTTGTTTACCGCTGGGTGGAGGGCAACGCGC	315
Db	357	CGCGCGCGGGGGCGG---CCACCTCTCTTCCCTCTACTACCACTGGCTGGAGGGGGCGGGG	413
Qy	316	GTCTGTAGCCTGCCTGTAAGGCACCGCGCCGCACTGTGGCGGAGGACCCCTCAGGGCCCTGTTTC	375
Db	414	ACCCTGTGTCTGCGAGGGGTACAGCCAAAGTGTCTCTGGGCAGACCAACACCTCTGTGTCTC	473
Qy	376	CAGAAACACCGGGAGAGAGACTTGGACGAGAGAGAAAGTGTGTACCGGTGGGGAAACTGG	435
Db	474	CAGCAACAGCGCCAGGAGGAGCTTCAGGCCCGCGCAGGAGATGTACAGTGGAGGCTTAC	533
Qy	436	AAGGACGGTTAATTTCTGAATAATGTCTGGGGCCAAAATAATATGACCTCCCTGTGTGATGAG	495
Db	534	AACCCAGGTTGGCCCTCACTGCCTTGGATGAAAGACAGTGGAGAGACTTTGGAGCTCAATATC	593
Qy	496	CGATTCTTGGAGACACAGAGAGTTGACTTTTCAGGTTTCGTGGGCCAAGGGGCTGCCCGAC	555
Db	594	AAATACTCCACAGCCAGAAATGCCAACTTTTATCTCAAGCTGGCTCTGCTTTTTCGAGAG	653
Qy	556	CTCGCTATCAAGAGACTCTCTAAATGTTCTTGACTTCTGCGAAAGGATCTAGATGAATCTCAAC	615
Db	654	ATGAAATCAAGGGGTTGCTGGACCGCAAGGGGCTCTGGAGGAGTCTGAATGAGATGAA	713
Qy	616	CGAATTTTCTGGTGTGTCAGACGAGCAAGCTGTGCTGAGCGCTGCGGGACTCTCTGGAAGAA	675
Db	714	AGGATCTTCAACTTCGCGAGGACCCACGACGCTGAGCAAGCAATTTGAGCACTGCGCAGAG	773
Qy	676	GATGCCATTTTGGGTACCAAGTTTCTTAATGGCGCCAAACCCGTGGTGTCTGAGGGGCTCT	735
Db	774	GATGCCCTTCTTGGCTCCCAAGTCTCTGAATGGTCTCAACCCCTGTCTCTGATCCGCGCGTGT	833
Qy	736	GCTCACCTTCTGTCTGCGCTAGTGTTCCTCCAGGCAATGGAGGAA-----CTG	783
Db	834	CACTAOCTCCCAAGAACTTCCCGTCACTGATGCCATGGTGGGCTCATTTGTGGGTCTCT	893
Qy	784	CAGGCCAGCTGGAGAGAGGAGCTGGAGGGAGGCAACATGTTTCGAAAGTGACTTCTCCCTG	843
Db	894	GGGACCAAGCTTTCAGGGCTGAGCTAGAGAAAGGGCTCCCTGTCTTGTGGATACAGGCATC	953
Qy	844	CTGATCGGGATCAAGGCCMAAGTCATTTCTCTGTAGCCAGCAGCACTTGGGTGCCCTCTA	903
Db	954	CTCTCTGGCATCCAGACCAATGTCTTAATGGGAAGCGCGAGTTCTCTGGGGCCCCAATG	1013
Qy	904	GTCATGTGMAATTCGACGCTGATGGGAAACTCTTTGCCCATGGTCTATCCAGCTCCAGCTG	963
Db	1014	ACCCTGTATACAGAGCCCAAGGCTGCGGGCGCTGC---TGCCTCTGGCCATCCAGCTC	1070
Qy	964	CCCCGCAACAGGATCCCCACCACTCCCTCTTTTCTTGGCTACGGATCCCCCAATGGCCCTG	1023
Db	1071	AGCCAGACCCCCCGCCCCAAACAGCCCCATCTTCTGCCCCACTGATGACAAAGTGGGACTGG	1130
Qy	1024	CTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTCCAGCTCCCATGAGCTGTCAGTCTCAT	1083
Db	1131	TTGCTGGCCAAAGACTGGGTGCGCAATGCCGAGTTCTCTTCCATGAGGCCCTCAAGCAC	1190
Qy	1084	CTTCTGAGGGGACACTTGATGGCTGAGTCAATGTTGTGGCCACCATGAGTGCCTGCCG	1143
Db	1191	CTGCTGCACTCACATCTGCTGCTGAGGTCTTACCCCTGGCTACCTTGGCTCAGCTGCC	1250
Qy	1144	TCGATACATCTTATCTTCAAGCTTTAATATCCCACTGGGATACACCCCTGGAAATTAAC	1203
Db	1251	CACCTGCACCCCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACACCTGCACATCAAC	1310
Qy	1204	GTCGGGCGCAGGACTGGGCTGGTCTCTGACATGCGGAATTTTTCGACAGATAATGAGCACT	1263
Db	1311	ACACTCGCCCCGGGAGCTGCTTATCTGTGCCAGGGCAGGTGGTGGACAGGTCCACAGGCATC	1370
Qy	1264	GGTGGGAGGCGCACGTGCACTGCTCAAGCAAGCTGAGGCGCTTCTTAACTTACAGCTC	1323
Db	1371	GGCATTAAGAGCTTCTCTGAGTGTGATACAGAGGAACATGAAGCAGCTGAACTATTCTCTC	1430
Qy	1324	TTCTGTCCCCCTGATGACTTTGGCCGACCGGGGGCTCTCTGGGAGTGAAGTCTTCTCTTCTAT	1383

[illegible]

RESIN.T 9

US-09-949-016-156  
; Sequence 156, Application US/09949016

; Patent No. 6812339  
: GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENER, O. CRAIG ET AL.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307; FILE REFERENCE: CE001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT AFFIDAVIT NUMBER: 03/03/34  
 ; CURRENT FILING DATE: 2000-04-14

; CURRENT FILING DATE: 2000-04-13  
 ; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR AFFILIATION NUMBER: 90/241,733  
 ; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: Fast

; SEQ ID NO 156

; LENGTH: 2685

; TYPE: DNA

; ORGANISM: Hum

US-09-949-016-156

Query Match		12.8%; Score 342.8; DB 4; Length 2685;
Best Local Similarity		51.0%; Pred. No. 2e-81;
Matches		924; Conservative 0; Mismatches 867; Indels 21; Gaps 4;
QY	196	CTGGCAAGCGGACCTCTTAAGGACGAGCCCTGGTTCTGCGAATCTCTGTGCAG 255
DB	297	CTGCCCTGTGGGGCCCTGGCCCGGATGCCGTGTTCTGCCGCTGGTTCCAGCTGACA 356
QY	256	GGCCCGGAGCCGGGACGAGGTTCAGTTCCCTGTTTACCGCTGGGTGGAGGGCAACGCG 315
DB	357	CCGCCCGGGGGCGG---CCACCTCTCTCTTCCCTGCTACAGTGGCTGGAGGGGGCGGG 413
QY	316	GTCTGAGCTGCTCTGAAGCACCAGCGCAGCTGTGGCGAGACCCCTCAGGGCCTGTTC 375
DB	414	ACCTGTGTCTGAGGAGGTACAGCCAGGTCTCTGGSCACACCAACCCCTGTGCTC 473
QY	376	CAGAAACACCGGGAAGAGCTGGAGAGAGAGAGAGTGTACCGGTGGGGAAGACTGG 435
DB	474	CAGCAACAGCGCCAGGAGGAGCTTCAGGCCCGCAGAGAGATGTACAGTGGAGGGCTTAC 533
QY	436	AAGGACGGGTAAATCTGATATATGGCTGGGCGCAAACTATACACCTCCCTGTGGATGAG 495
DB	534	AACCCAGTTGGCTCACTGCCCTGGATGAAAGACAGTGGAGACTTGGAGCTCAATATC 593
QY	496	CGATTTCTGGAAGACAGAGAGTTGACTTTGAGGTTTCGCTGGCCAAAGGGGCTGGCCGAC 555
DB	594	AAATATCTCCACAGCAAGATGCCACTTTTATCTACAAGCTGGCTCTGCTTTTGCAGAG 653
QY	556	CTGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGATCTAGATGACTTCAAC 615
DB	654	ATGAAATCAAGGGTGTCTGAGCCGCAAGGGGCTCTGGAGGAGTCTGMAATGAGATGAA 713
QY	616	CGGATTTCTGGTGTGTCTGACGCAAGCTGGCTGAGCGCTGGGAGCTCTCTGGAAGGA 675
DB	714	AGGATCTTCAACTTCGCGAGAGCCACAGCTGAGCAGCATTTGAGCACTGGCAGGAG 773
QY	676	GATGCCCTATTGGGTACCAAGTTCTTAATGGGGCCAAACCCCGTGGTGTGAGCGCTCT 735
DB	774	GATGCCCTCTTCGCTCTCCAGTCTCTGATGGTCTCAACCTCTGCTGATCCGCGCTGT 833
QY	736	GCTCACTTCTGCTGCTGCTAGTGTTCCTCTCAGGCAATGAGGAA-----CTG 783
DB	834	CACTACCTCCCAAGAACTTCCCGCTCACTGATGCCATGGTGGCTCATTTGTTGGGTCT 893
QY	784	CAGGCCAGCTGGAGAGAGCTGGAGGGAGGACACTGTTTCAAGCTGACTTCTCCCTG 843
DB	894	GGGACCAAGCTTGCAGGCTGAGCTAGAGAGGGTCCCTGTCTTGTGGATCAGGCATC 953
QY	844	CTGGATGGGATCAAGGCCAAGCTCATTTCTGTAGCCAGCAGCAGCTGGCTGCCCTCTA 903
DB	954	CTCTTGGCATCCAGACCAATGTCAATTAATGGGAGCCGAGTTCTCTGGGCCCCCAATG 1013
QY	904	GTCAATGTAATAATGAGCTGTAGTGGAAACTCTTTGGCCCATGTGTCATCCAGCTCCAGCTG 963
DB	1014	ACCTGTCTATACAGAGCCAGGCTGGGGCGGCTGC---TGCCTCTCGCCATCCAGCTC 1070
QY	964	CCCGCAGAGATCCCCACACCTCCCTTTCTTGGCTACGGATCCCCCAATGGCCTGG 1023
DB	1071	AGCCAGACCCCGCGGCCCAAAACAGCCCCATCTTCTGCCCCACTGATGACAAATGGGACTGG 1130
QY	1024	CTTCTGGCCAAATCTCGGTGCGCAGCTCTGACTTCCAGCTTCCAGCTGCGATCTTCAT 1083
DB	1131	TTGTGGCCAGACTGGTGGCAATGCGGAGTTCTCTTCCATGAGGCCCTCACGCAC 1190
QY	1084	CTTCTGAGGGGACACTTGAATGGCTGAGGTCAATTTGTGGCCACCATGAGGTGCTGCCG 1143
DB	1191	CTGTGCACTCACATCTGCTGCTGAGTCTTCAACCTGGTACCTCTGCTGAGCTGCC 1250
QY	1144	TCGATACATCTATCTTCAAGCTTATAATTTCCCACTGGATACACCTCGGAATTAAC 1203
DB	1251	CAGTCCACCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACACCTCGCATCAAC 1310
QY	1204	GTCCGGGCGGAGCTGGGCTGCTCTGACATGGGAATTTTCGACCAGATAAATGAGCACT 1263

Db	1311	ACACTCGCCCGGAGCTGCTTATCTGTCAGGGCAGGTGGTGACAGGTCCACAGGCATC 1370
QY	1264	GGTGGGGAGGGCCAGTGCAGCTGTCAAGCAAGCTGGAGCCTTCTTAACCTTACAGCTCC 1323
Db	1371	GGCATTGAAGGCTTCTCTGAGTTGATACAGAGAAATGAGAGCACTGAGCTGACTTCTCTC 1430
QY	1324	TTCTGTCCCTGTAGTACTTTGGCCGACCGGGGGCTCTCGGGAGTGAAGTCTTCTTCTTAT 1383
Db	1431	CTGTGTCTGCTGAGGATATCCGGACCCGAGGAGTTGAAGACATCCAGGCTACTACTAC 1490
QY	1384	GCCCAAGATGCGCTGGGCTCTGGGAATCATCTATCGGTATGTGGAAGAAATCTGAGT 1443
Db	1491	CGTGTATGATGGATGCAATTTGGGGTGCAATGGGAAACGCTTGTCTCTGAATCATCGGT 1550
QY	1444	CTCCACTATAACACAGAGCTGGCTGTGAAGACAGCCAGAGCTGCAGACCTGGTGTGCA 1503
Db	1551	ATCTACTCTCCAAAGTATGAGTCTGTCCAAAGATGACAGAGAGCTCCAGGCTGGGTGAGA 1610
QY	1504	GAGATCACTGAATCGGGCTGCAAGGGGCCCGAGGACCGAGGGTTTCTGTCTCTTTACAG 1563
Db	1611	GAGATCTTCTCCAAGGGCTTCTTAACAGGAGAGCTCAGGTATCTCTTCTCCTCACTGGAG 1670
QY	1564	GCTCGGGACAGGTTTGCACCTTTGTCAACATGTGTATCTTCACTGACACCGGCCAACAC 1623
Db	1671	ACCGGGAAAGCCTGGTGCAGTATGTCAACATGGTGTATTCACCTGTCTCAGCCAAGCAT 1730
QY	1624	GCCTCTGTGCACCTGGGCGAGCTGGACTGGTACTCTTGGGTGCTTAATGCACCTTCACG 1683
Db	1731	GGGCTGTCAGTGCGAGGCGAGTTGACTCTGTCTTGGATGCCAACTGCCACCCAGC 1790
QY	1684	ATGCGGCTGCCCGCCCAACCAACCAAGG---ATGCAACGCTGGAGACAGTGTATGGCGACA 1740
Db	1791	ATGCACTGCCACCAACCCACCTCCAAAGGCTGGCAACATGCGAGGGTTCATAGCCACC 1850
QY	1741	CTGCCCAACTTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGCAAGC 1800
Db	1851	CTCCCACTGTCAATGCCACATGTATGTCATCTCTGTCTCTGTGGTGTGAGCAAGGAG 1910
QY	1801	CAGCCGTTATGGTGTCTGGGCGAGCATGAGGAGGATTTTTCGGGCGCTGAGCCT 1860
Db	1911	CTGGAGACCAAGGCGCTGGGACCTATCGGATGAGCACTTCAAGAGGAGGCGCT 1970
QY	1861	AAGGCTGTCTCAAGAAAGTTTCAGGGAGGAGCTGGCTGCCCTTGGATTAAGAAATTTGATC 1920
Db	1971	CGGGGAGCATCGCCACCTTCCAGAGCCGCTGGCCACAGATCTCGAGGGGCACTCCAGGAG 2030
QY	1921	CGGAATGCAAGCTGACATGCCCTACGAGTACCTCGGGCCAGCGTGGTGGAAACAGT 1980
Db	2031	CGGAACCGGGGCGCTGGTGTGCCCTACACCTAGACCCCTCCCTCATCGAGAACAGC 2090
QY	1981	GTGGCCATCTAA 1992
Db	2091	GTCTCATCTAA 2102

RESULT 10

US-09-949-016-3041  
; Sequence 3041, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949, 016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08

```
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3041
; LENGTH: 2674
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-3041

Query Match      12.8%; Score 341.2; DB 4; Length 2674;
Best Local Similarity 50.9%; Pred. No. 5.3e-81;
Matches 923; Conservative 0; Mismatches 868; Indels 21; Gaps 4;

QY 196 CTGCGCAACCGCACCTCTTAAGGACGACGCTGCTTCAACCTGATCTCTGTGAC 255
DB 298 CTGCCCCCTGCTGGGGCCCTTGGCCCCCGGATGCTTCTGCGCTGGTTCCAGCTGACA 357
QY 256 GGCCTCGGAGCGGGGACGAGGTCAGGTTCCCTTTGTTACCGCTGGGTGGAGGGCAACGGC 315
DB 358 CCGCGCGGGGGCG---CCACCTCTCTTCCCTGCTACCACTGGCTGGAGGGGGGGG 414
QY 316 GTCTGAGCTTGGCTGAAGGACCGGCCGACCTGTGGGCGAGACCTCAGGGCTGTTC 375
DB 415 ACCCTGTGCTGCAGGAGGGTACAGCAAGGTGTCTCTGGGCGAGACCACCACCTCTGTCTC 474
QY 376 CAGAAACACCGGAGAGAGAGCTGGAAGAGAGAGAGAGTGTACCGGTGGGGAACCTGG 435
DB 475 CAGCAACAGCGCCAGGAGAGCTTCAGGCCCGGAGAGATGTACAGTGGAGGCTTAC 534
QY 436 AAGGACGGGTAAATCTGAATATGGCTGGGGCCAACTATATGACCTCCTCTGTGATGAG 495
DB 535 AACCAGGTTGGCCCTCACTGCTTGNATGAAGAGACAGTGGAGACTTGGAGCTCAATATC 594
QY 496 CGATTCTTGGAGAGCAAGAGAGTTGATTTGAGGTTTCCTGCGCCAAAGGGGCTGGCCGAC 555
DB 595 AAATACTCCACAGCCCAAGAAATGCCAACTTTTATCTACAGGCTGGCTCTGCTTTTGCAGAG 654
QY 556 CTGCTATCAAGACTCTTAATGTCTGACTGTCTGGAAGATCTAGATCACTCAAC 615
DB 655 ATGAAATCAAGGGGTGTCTGACCGCAAGGGGCTCTGGAGGAGTCTGAATGAGATGAA 714
QY 616 CGGATTTCTGCTGTGGTCAGAGCAAGCTGGCTGAGCGGCTGGGACCTCTCGGAAGGAA 675
DB 715 AGGATCTTCAACTTCGGAGGACCCAGCAGCTGAGCAGCATTTGAGACTTGGCAGGAG 774
QY 676 GATGCTTATTTGGTACAGTTTCTTAATGGCGCAACCCCGTGGTGTCTGAGGCGCTCT 735
DB 775 GATGCTTCTTGGCTTCCAGTCTCTGATGATGCTCTCAACCCCTGCTCTGATCGCGCTGT 834
QY 736 GCTACCTTCTGCTGCTGCTAGTGTCTTCTCCTCAGGATGAGGAA-----CTG 783
DB 835 CACTACCTCCCAAGAACTTCCCGCTCACTGATGCCATGGTGGCTCTCACTGTGGGTCTCT 894
QY 784 CAGGCCACGCTGGAGAGGAGCTGGAGGAGGACACACTGTTCGAAAGCTGACTTCTCCCTG 843
DB 895 GGGACGAGCTTGCAGGCTGAGCTAGAGAGGCTCTCCTGTTTGTGGTGGATCAGGCAATC 954
QY 844 CTGGATGGGATCAAGCCCAAGCTCAATTTCTGTAGCCAGCAGCACCTGGCTGCCCTCTTA 903
DB 955 CTCTCTGGCATCCAGACCAATGTCTTAATGGAGGCTCTCACTCTCTGCGGCCCAATG 1014
QY 904 GTCATGCTGAATTTGAGCTGATGGGAAATCTTCTGCCCCATGGTATCAGCTCCAGCTG 963
DB 1015 ACCCTGCTATACAGAGCCCGAGGCTGCGGGCGGCTGCTGCTCTGCGCATCCAGCTC 1071
QY 964 CCGCGCAGAGGATCCCAACACTCCCTCTTTTCTTCTGCTTACGATCCCAATGGCTGG 1023
DB 1072 AGCCAGACCCCGGCCCAAGAGCCCACTTCTTCTGCCCCACTGATGACAAAGTGGGACTGG 1131
QY 1024 CTTCTGGCCAAATGTGGGTGGGCGAGCTCTGACTTCCAGCTCCATGAGCTGAGCTCTCAT 1083
DB 1132 TTGCTGGCCAAAGACTGGGTGGGCAATGCCAGTCTCTCTTCCATGAGGCCCTCAGCAC 1191
QY 1084 CTTCTGAGGGGACACTGTGATGGCTGAGGTCAATTTGTGGGCCCAACCATGAGGTGCTGGCG 1143
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## RESULT 11

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US-09-547-435-29
; Sequence 29, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
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DB 1192 CTGCTGCACTCACAATCTGCTGCTGAGGTCTTCAACCTGGCTACCCCTGGCTGAGCTGCC 1251
QY 1144 TCGATACATCTCTTCAAGCTTATAATTTCCCACTGCGATACACCTCCGTAATTAAC 1203
DB 1252 CACTGCCACCTCTCTTCAAGCTGCTGATCCCGCACCCCGATACACCTCCGATCAAC 1311
QY 1204 GTCCGGGCGAGACTGGGCTGCTCTGACATGGGAAATTTTCGACAGATAATGAGCACT 1263
DB 1312 ACACCTCGCCCGGAGCTGCTTATCGTCCAGGCGAGGTGGTGACAGGCTCCACAGCATC 1371
QY 1264 GGTGGGGGAGGCGACGTCAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGCTCC 1323
DB 1372 GCATTGAAGGCTTCTGAGTTGATACAGAGGAACATGAAGCAGCTGAATTTCTCTC 1431
QY 1324 TTCTGCTCCCTGATGACTTGGCCGACCGGGGGCTCTCTGGGAGTGAAGTCTTCTTCTAT 1383
DB 1432 CTGCTGCTGCTGAGGATATCCGGACCCCGAGGAGTTGAAGACATCCCAGGCTACTACTAC 1491
QY 1384 GCCCAAGATGCGCTCGGCTCTGGGAAATCATCTATCGGTATGTGAAGGAATCGTGA 1443
DB 1492 CGTGATGATGGGATGAGATTTGGGGTGCAGTGGGAACGCTTTGTCTCTGAAATCATCGGT 1551
QY 1444 CTCCTACTATAAGACAGAGCTGCTGCTGAAAGACGACCCAGAGCTGCAGACCTGGTCCA 1503
DB 1552 ATCTACTACCAAGTGAATGAGTCTCTCCAAAGATGACAGAGCTCCAGGCTTGGGTGAGA 1611
QY 1504 GAGATCACTGAAATCGGGCTGCAAGGGGCCAGGAGCCAGAGGTTTCTGTCTCTTTTACAG 1563
DB 1612 GAGATCTTCTCCAGGGGCTTCTTAAACCCAGGAGACTCAGGTATACCTCTCTCACTGGAG 1671
QY 1564 GCTCGGAGACAGGTTTGCACTTTGTACCAATGTGTATCTTCACTGCAACCGGCAACAC 1623
DB 1672 ACCCGGAAAGCCCTGGTGCAGTATGTCCATGGTGATATTCACCTGTCTCAGCCCAAGCAT 1731
QY 1624 GCCTCTGTGACCTGGGCGAGCTGGAGCTGGTACTCTTGGGTGCCCTTAATGCACCTGCACG 1683
DB 1732 GCGGCTGTGACGTGAGGCGAGTTTGACTCTCTGTGGATGCCCAACCTGCCACCCAGC 1791
QY 1684 ATGCGGCTGCCCGCCCAACCAACCAAGG---ATGCAACGCTGGAGACAGTGAATGCGACA 1740
DB 1792 ATGAGCTGCCACCAACCAACCTCCAAAGCCCTGGCAACATCGAGGGCTTCATAGCCACC 1851
QY 1741 CTGCCCAACTTCCACAGGCTTCTCTCCAGATGTCATCACTTGGCAGCTGGGCGAGACGC 1800
DB 1852 CTCACCATCTCAATGCCACATGATGTCTCTCTGCTCTCTGTTGCTGAGCAAGGAG 1911
QY 1801 CAGCCCGTATGGTGGCTGTGGGCGAGCATGAGGAGGATATTTTTCGGGCCCTGAGCT 1860
DB 1912 CTTGAGACCAAAAGGCCCTGGGCACTTACCGATGAGCATTCCAGAGGAGGCCCTCT 1971
QY 1861 AAGGCTGTGTGAAGAGTTTCAAGGAGGAGCTGGGCTGCCCTGGATAAGGAAATTCAGATC 1920
DB 1972 CGCGGAGCATCGCCACCTTCCAGAGCCCTTGGGCCAGATCTCGAGGGGCTATCCAGGAG 2031
QY 1921 CGGAATGCAAGCTGGACATCCCTTACGATGATCTTGGGCCAGCGTGGTGGAAACAGT 1980
DB 2032 CGGAACCGGGGCTGGTCTGCCCTTACACCTACCTAGACCTCCCTCTCATCGAGAACAGC 2091
QY 1981 GTGGCATCTAA 1992
DB 2092 GTCTCCATCTAA 2103
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		; APPLICANT: Sands, Arthur T.			
		; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides			
		; FILE REFERENCE: 7705.0009-00000			
		; CURRENT APPLICATION NUMBER: US/09/547,435			
		; CURRENT FILING DATE: 2000-04-12			
		; NUMBER OF SEQ ID NOS: 29			
		; SOFTWARE: FastSeq for Windows Version 3.0			
		; SEQ ID NO 29			
		; LENGTH: 3384			
		; TYPE: DNA			
		; ORGANISM: Homo sapiens			
		US-09-547-435-29			
		Query Match 12.4%; Score 332; DB 4; Length 3384;			
		Best Local Similarity 53.7%; Pred. No. 1.8e-78;			
		Matches 767; Conservative 0; Mismatches 640; Indels 21; Gaps 3;			
QY	589	TGCTGGAAGGATCTAGATGACTTCAACCGGATTTTCTGGTGTGGTCTGAGAGCAAGCTGGCT	648		
DB	1222	TCCTGGAAGAGCTGGATGACATCTCTGGTGCCTAAGACCTTTCAGACA	1281		
QY	649	GAGCGCTGCGGACTCTGGAAGGAAGATGCCCTTATTTGGGTACAGATTTCTTAATGGC	708		
DB	1282	AAGTATGTCAAGAGCACTGGTGTGAAGATCACTTCTTTGGGTACCACTGTAATGGT	1341		
QY	709	GCCAAACCCCTGGTGTGAGCGCTCTGCTCACCTTCCTGCTCGCTAGTGTCCCTCCA	768		
DB	1342	GTCAATCCCTGATGCTCCACTGATCTCTAGCTTGCCAGCAAGCTGCCTGCACCAAT	1401		
QY	769	GGCATGG-----AGGAATGTCAGGCGCCAGCTGCGAAGAGAGCTGGAGGGAGGC	816		
DB	1402	GACATGTGGCGCCCTTGTCTGGGACAGACATGCTCTGCGACAGAGCTAGAGAGGGG	1461		
QY	817	ACACTGTTGAAAGTGAATCTTCTGCTGCTGGAATGAAGGCGCAACGTCATCTCTGT	876		
DB	1462	AACATCTTCTAGCGGACTACTGGATCTCTGGCGAGGCGCCCACTGCCTGCTAAACGGC	1521		
QY	877	AGCAGAGACACTGGCTGCGCCCTCTAGTCACTGTGAATGTCAGCTGATGGGAATC	936		
DB	1522	CGCAGACAGTACGTGGCGCGCCCACTGTGCTGTGGCTCAGCCCGGAGGGGGCGTG	1581		
QY	937	TTGCCCATGTCATCCAGCTCCAGCTGCGCCCGCACAGGATCCCGCACCTCCCTTTTC	996		
DB	1582	GTGCCCTTGGCCATCCAGCTCAGCGACAGACCCCG-----GGGCTGACAGCGCCCATCTTC	1635		
QY	997	TTGCTACGAGATCCCGCAATGGCTGTGCTTGTGGCCTAATGCTGGGTGGCGAGCTCTGAC	1056		
DB	1636	CTGCCCACTGACTCCGAATGGGACTGGCTGTGGCCAAAGACGTGGGTGCGCAACTCTGAG	1695		
QY	1057	TTCCAGCTCCATGAGCTGCAGTCTCATCTTCTGAGGGGACACTTGATGGCTGAGGTCAAT	1116		
DB	1696	TTCTGTGTGACGAGAAACAAACAGCACTTTCTGTGACAGCATTTGCTGTGCGAGGCGCTC	1755		
QY	1117	GTGTGGCCACCATGAGTGTGCTGCTCGATACATCTTCTCAAGCTTATAATTTCCC	1176		
DB	1756	GCCATGGCCAGCTGCGCAGCTGCGCTCTGCGACCCCATCTACAAGCTCTTACTCCCC	1815		
QY	1177	CACCTGCGATACACCTTGAATTAACGTGCGGCGCAGGACTGGGTGTCTCTGACATG	1236		
DB	1816	CACACTGATACAGCTGCAAGGTGAACACCATGTCGAGGGGCCAGCTGTCTCAACCCCGAG	1875		
QY	1237	GGAAATTTCCACAGATAATGAGCACTGGTGGGGAGGCCACGTCGAGCTCTCAAGCAA	1296		
DB	1876	GGCCTCGTGGACCAAGGTCACTGTCATCGGGAGGCAAGGCTCATCTACCTCATGAGCAG	1935		
QY	1297	GCTGGAGCTTCTTAACCTACAGCTCTCTTCTGCTCCCTCTGATGACTTTGGCGCAGCGGGG	1356		
DB	1936	GGCTGCGCCCACTTCACTACACCAATTTCTGCTCTCGGACAGCCTGCGGGCGCGGCG	1995		
QY	1357	CTCTGGGAGTGAAGTCTTCTTCTATGCGCCCAAGATGCGGTCTGGCTCTGCGAAATCATC	1416		
DB	1996	GTCTTGCTATCCCAACTACACTACCGAGACGACGCGCCTGGAAGATCTGGGCGGCCAAT	2055		

QY	1417	TATCGTATGTGGAAGGAATCGTGAATCTCCACTATAAGACAGACAGTGGCTGTGAAAGAC	1476
DB	2056	GAGAGCTTTGTCTCAGAAATCGTGGCTACTATTATCCAGTGAAGCATCTGTGACGACAG	2115
QY	1477	GACCCAGAGCTGCAGACCTGGTGTGAGAGATCACTGAATCGGCTGCAAGGGGCCCCAG	1536
DB	2116	GATTCGGAGCTGCGAGGCTGGACTGCGGAGATTTTGTCTCAGGCGTTCTTGGGCGGGAA	2175
QY	1537	GACCGAGGTTTCTGTCTCTTTACAGGCTCGGACCCAGGTTTGCACATTTGTACCATG	1596
DB	2176	AGCTCAGGTTTCCCAAGCGGCTGTGCACCCACAGAGAGATGGTGAAGTTCTCTCACTGCA	2235
QY	1597	TGTATCTTTCACCTGCACCGGCCCAACACAGCTCTGTGCACCTGGGGCAGCTGGATGGTAC	1656
DB	2236	ATCACTTCAATTTGCTCTGCCCGACGAGCTGTCTCAACAGTGGGCGAGCATGACTTTGGG	2295
QY	1657	TCCTGGTGCCTTAATGACCCCTGCGAGTGGCGCTGCGGCTGCCCCCGCAACCAAGG---AT	1713
DB	2296	GCTTGGATGCCCAATGCTCCATCATTCATGAGGCGAGCCCCACCCAGACCAAGGGGACC	2355
QY	1714	GCAACGCTGGAGACAGTGTGCGGACCTGCGCCAACTTCCACAGGCTTCTCTCCAGATG	1773
DB	2356	ACACCCCTGAAGACTTACCTAGACACCTTCCCTGAGTGAACATCAGCTGTACACCTC	2415
QY	1774	TCCATCACCTTGGCAGCTGGGCGACGCCAGCCCGCTTATAGTGGCTGTGGGCGCAGCATGAG	1833
DB	2416	CTCCTCTTCTGGTGTAGCCCAAGAACCAAGGACCCAGAGGCCCCCTGGGCGACCTACCCA	2475
QY	1834	GAGGAGTATTTTTCGGGCGCTGAGCTAAGGCTGTGCTGAAGAAGTTTCAAGGAGGAGCTG	1893
DB	2476	GATGAGCACTTTCACAGAGGAGGCGCCCGAGGCGAGCATCGCGGCTTCCAGAGCGCCCTG	2535
QY	1894	GCTGCCCTCGATAAGGAATTCAGATCCGGAATCGAAAGCTGACATGCCCTACGAGTAC	1953
DB	2536	GCCCAGATCTCAAGGAGCATCCAGAGCGGAACAGGCTGTGGCACTGCCCTACACCTAC	2595
QY	1954	CTGCGGCCCGAGGCTGTGTGAAAAACAGTGTGGCCATCTAAGCGCTGCGCA	2001
DB	2596	CTGGACCTTCCCTCATTCATTGAGAAGAGTGTCTCCATCAACACCCCA	2643

RESULT 12  
US-09-547-435-5  
; Sequence 5, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705.0009-00000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 2236  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-547-435-5

Query Match 12.4%; Score 330.4; DB 4; Length 2236;  
Best Local Similarity 53.6%; Pred. No. 3.8e-78;  
Matches 766; Conservative 0; Mismatches 641; Indels 21; Gaps 3;  
QY 589 TGCTGGAAGGATCTAGATGACTTCAACCGGATTTTCTGGTGTGGTCTGAGAGCAAGCTGGCT 648  
DB 259 TCCTGGAAGAGCTGGATGACATCTCTGGTGCCTAAGACCTTTCAGACA 318





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Db 1084 GTGCCCCCTGGCCATCCAGCTCAGCCAGACCCCC-----GGGCGCTGACAGCCCCCATCTTTC 1137
Qy 997 TTGCTACGGATCCCCCAATGGCTGGCTTCTGCGCAAAATGCTGGGTGGCGAGCTCTGAC 1056
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Qy 1057 TTCAGCTCCATGAGCTGCAGTCTCATCTTCTGAGGGGACACTTGTATGGTGGAGTGCATT 1116
Db 1198 TTCTGTGTGACGAAACAAACGCACTTCTGTGTGACGCAATTTGTGTGCGAGGCGCTTC 1257
Qy 1117 GTTGTGGCCACATGAGTGCCTGCGGTGATACATCTTCTCAAGCTTATATTCCTCC 1176
Db 1258 GCCATGCCACGCTGCGCCAGCTGCGGCTCTGCGACCCCCATCTACAAGCTCTTACTCCCC 1317
Qy 1177 CACCTGGGATACACCTCTGGAATTAACGTCGGGCGCAGGACTGGGCTGGTCTCTGACATG 1236
Db 1318 CACACTGATACAGCTGCGAGGTGAACACCATGCGAGGGCCACAGTGTCTCAACCCCGAG 1377
Qy 1237 GGAATTTTCGACCAGATAATGAGCACTGTGTGGGGAGGCCACGTGCAGCTGTCTCAAGCAA 1296
Db 1378 GGCTCTGTGACACAGGTCACTGCTCCATCGGGAGGCAAGGCCCTCATCTACCTCATGAGCAG 1437
Qy 1297 GCTGGAGCTTCTTAACCTACAGTCTTCTGTCCCGCTGATGACTTGGCGGACCGGGG 1356
Db 1438 GGCTGGCCCACTTCACTTACCAATTTCTGCTTCGCGACAGCCTGCGGGCCCGCGGC 1497
Qy 1357 CTCTGGGAGTGAAGTCTTCTTCTATGCCCAAGATGCGCTGGGCTCTGGGAAATCATC 1416
Db 1498 GTCTGTGCTATCCCAACTACACTACCGAGAGACGCGCTGAAGATCTGGGGCGGCATT 1557
Qy 1417 TATGGTATGGAAGGAATCGTAGTCTCCACTATAAGACAGACGTGGCTGTGAAGAC 1476
Db 1558 GAGAGCTTTGCTCAGAAATCGTGGGCTACTATTATCCAGTGACGCATCTGTGACAGCAG 1617
Qy 1477 GACCCAGAGTGCAGACCTGCTGAGAGATCACTGAATCGGCTGCAAGGGGCCCCAG 1536
Db 1618 GATTGCGAGTGCAGGCTGGAGTGGCGAGATTTTGTCTCAGGCGTTCTTGGGCGGGAA 1677
Qy 1537 GACCGAGGTTCTCTGTCTTTACAGCTCGGACAGAGTGTTCACATTTGTACCATG 1596
Db 1678 AGCTCAGTTTCCCAAGCGGCTGTGCACCCAGGAGAGATGTGAAGTTCCTCATGTCA 1737
Qy 1597 TGTATCTTCACTGCACCGGCCCAACAGCCCTCTGTGCACCTGGCGCAGCTGGACTGGTAC 1656
Db 1738 ATCATCTTCAATTGCTCTGCCAGCAGCTGCTGTCAACAGTGGCGAGCATGACTTTGGG 1797
Qy 1657 TCTGGGTGCTAATGACCCCTGACAGATGGGCTGCCCCCGCCCAACCCAGG---AT 1713
Db 1798 GCCTGGATGCCCAATGCTCCATCATCCATGAGGCGAGCCCCCAACCCAGAGCCAGGAGCC 1857
Qy 1714 GCAACGCTGGAGACAGTGTGGGACACTGCCCAACTTCCACAGGCTTCTCTCCAGATG 1773
Db 1858 ACACCTCTGAAGACTTACCTAGACACCTCTCTGTAGTGAACATCAGCTGTACACCTC 1917
Qy 1774 TCCATCATCTTGGCAGCTGGGCAGACGCGCAGCCCGTTATGTGTGCTGTGGCCAGCATGAG 1833
Db 1918 CTCCTCTCTGTTGTTAGCCAGAACCCCAAGACCCAGAGGCCCTCTGGGCACTACCCCA 1977
Qy 1834 GAGAGTATTTTTCGGGCCCTGAGCTTAAGGCTGTGCTGAAGATTTACGGAGGAGAGCTG 1893
Db 1978 GATGAGCACTTCAAGAGGAGGCCCCGAGCGGAGCATGCGCCGCTTCCAGAGCCGCGCTG 2037
Qy 1894 GCTGCCCTGGATAGGAAATTTGAGATCCGGAATTCGAAAGCTGGACATGCCCTACGAGTAC 1953
Db 2038 GCCAGATCTCAAGGGACATCCAGGAGCGGAACAGAGGCTCTGGCATGCGCTACACCTAC 2097
Qy 1954 CTGCGGCCACGCTGTGTGGAAACAGTGTGGCCATCTTAAGCGTGCACA 2001
Db 2098 CTGGACCTCTCCCTCTTGTAGAACAGCGTCTCCATCTTAACCAACCCCCCA 2145
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RESULT 14

US-09-799-451-803

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; Sequence 803, Application US/09799451
; Patent No. 6783969
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Ryle
; APPLICANT: Asundi, Vinod
; APPLICANT: Ren, Feiyan
; APPLICANT: Zhang, Jie
; APPLICANT: Xue, Aidong J.
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Ma, Yunging
; APPLICANT: Yamazaki, Victoria
; APPLICANT: Chen, Rui-hong
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wang, Dunrui
; APPLICANT: Yang, Yonghong
; APPLICANT: Wehrman, Tom
; APPLICANT: Ghosh, Reena
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Nucleic Acids and
; Polypeptides
; FILE REFERENCE: 803
; CURRENT APPLICATION NUMBER: US/09/799,451
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: pt_FL_genes Version 2.0
; SEQ ID NO 803_
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (172)..(2304)
; US-09-799-451-803
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Query Match 12.3%; Score 327.8; DB 4; Length 2307;
Best Local Similarity 53.6%; Pred. No. 1.9e-77;
Matches 761; Conservative 0; Mismatches 637; Indels 21; Gaps 3;

Qy 589 TGCTGGAAGGATCTAGATGACTTCAACGGATTTTCTGGTGGTTCAGAGCAAGCTGGCT 648
Db 895 TCCTGGAAGAAGCTGGATGACATGTCAGAAACATCTTCTGGTGCATTAAGACCTTCACGACA 954
Qy 649 GAGCGGCTCGCGGACTCTCTGGAAGGAAGATGCTTATTTGGGTACCCAGTTTCTTAATGGC 708
Db 955 AGTATGTCAGAGACACTGGTGTGAAGATCACTTCTTTGGGTACAGTACCTGATGCT 1014
Qy 709 GCCAACCCCGTGGTGTGAGGCGCTCTGCTCACTTCTCTGCTCGCTAGTGTTCCTCCA 768
Db 1015 GTCAATCCCGTCATGCTCCACTGCTCTAGCTTGGCCAGCAAGCTGCTGTCAACAAT 1074
Qy 769 GGCATGG-----AGGAATGCGAGGCCAGCTGGAGNAGAGCTGGAGGGAGGC 816
Db 1075 GACATGGTGGCCCCCTTGTCTGGGACAGGACACATGCTCGACAGAGCTAGAGAGGGGG 1134
Qy 817 ACACCTGTTCCGAAGCTGACTTCTCCCTGCTGGATGGGATCAAGGCCAAACGTCATTCTCTGT 876
Db 1135 AACATCTTCTAGCGGACTACTGGATCTCTGGCGGAGGCCCCACCACTGCTTAACGGC 1194
Qy 877 AGCCAGCAGCACTGGCTGCCCTCTCTAGTCTAGTGAATTCGAGCTGTGATGGGAACTC 936
Db 1195 CGCCAGCAGTACGTGGCGCCCCCTGCTGCTGCTGCTGAGCTAGCCCCCAGCGGGGCGCTG 1254
Qy 937 TTGCCCATGGTATCCAGCTCCAGCTGCCCCGACAGGATCCCCACCACTCCCTTTTC 996
Db 1255 GTGCCCTTGGCCATCCAGCTCAGCCAGACCCCC-----GGGCGCTGACAGCCCCATCTTC 1308
Qy 997 TTGCTTACGATCCCCCAATGGCTTCTGGCCCAAAATGCTGGGTGGCGAGCTCTGAC 1056
Db 1309 CTGCCCACTGACTCCGAATGGGACTGGCTGTGGCCCAAGACGCTGGGTGGCGCACTCTGAG 1368
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1057 TTCCAGCTCCATGAGCTGAGTCTCATCTTCTGAGGGGACATTTGATGCTGAGTCTATT 1116  
1369 TTCTGCTGACGAAACAAACAGCACTTTCTGTGACGATTTTCTGTGAGGCTTC 1428  
1117 GTTGTGGCCACCATGAGTGCCTGCGCTCGATACATCTTCTCAAGCTTATAATTC 1176  
1429 GCCATGGCCACGCTGCGCCAGCTGCGCTCTGCCACCCATCTACAGCTCTTACTCC 1488  
1177 CACCTGCGATACACCTCGAAATTAACGTCGCGGCGCAGACGTCGGCTGTCTGACATG 1236  
1489 CACACTCGATACACGCTGAGTGAACACCATCGCGAGGCCACGCTCTCAACCCGAG 1548  
1237 GGAATTTTCGACGATATGAGCTGCTGGGAGGCCACGTCAGCTGTCTCAAGCA 1296  
1549 GGCCTGCTGAGGCTCAAGTCTCATCGGGAGGCCAAGGCTCTATCTACCTCATGACGACG 1608  
1297 GCTGGAGCTCTCTAACCTACAGCTCTTCTGTCCCTCGATGACTTGGCCACCGGGG 1356  
1609 GGCCTGCGCCACTTACCTTACCAATTTCTGCTTCGGACAGCTGCGGCGCCGCGC 1668  
1357 CTCCTGGGAGTGAAGTCTTCTCTTATGCCCAAGATGCGCTCGGCTCTGGAAATCATC 1416  
1669 GTCTGGCTATCCCAACTACCCTACCGAGAGCGGCTGAAGATCTGGGCGCCATT 1728  
1417 TATCGGTATGGAAGGAATGCTGAGTCTCCACTATAGACAGACGTCGCTGTGAAGAC 1476  
1729 GAGAGCTTTGTCTCAGAAATCGTGGGCTACTATTATCCAGTGAAGCATCTGTGACGACG 1788  
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1789 GATTGAGAGCTGAGGCTTGAGTGGGAGATTTTGTGACGCTTCTGGGCGGGH 1848  
1537 GACCGAGGTTTCTGCTCTTTTACAGGCTCGGACAGGTTTGGCCACTTTGTCAACCATG 1596  
1849 AGCTCAGGTTTCCCAAGCGCTGTGCAACCCAGGAGAGATGTAAGTTCTCTACTGCA 1908  
1597 TGTATCTTCACTGACCGGCCAACGCTCTGTGACCTGCGGAGCTGAGTCTGCTGAC 1656  
1909 ATCATCTTCAATTTGCTCTGCCAGCAGCTGTCTGTCAACAGTGGGAGCATGACTTTGGG 1968  
1657 TCTTGGGCTCTTAATGCACTGACCTGACGATGCGGCTGCGGCTGCGCCCAACCAAGG 1713  
1969 GCTTGAATGCCAATGCTCATCATGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2028  
1714 GCAAGCTGGAGACAGTGAAGGACACTGCGCAACTTCCACAGGCTTCTCTCCAGATG 1773  
2029 ACCACCTGAAGACTTACCTAGACACCTTCTGAGTGAACATCAGCTGTAAACACCTC 2088  
1774 TCCATCATTTGGAGCTGGGCGAGCCAGCCGCTTATGCTGCTGCTGGGCGAGCATGAG 1833  
2089 CTCCTCTTCTGCTTGTAGCCAAAGAACCAAGGACAGAGGCGGCTGCGGACCTTACCCA 2148  
1834 GAGGAGTATTTTGGGCGCTGAGCTAAGGCTGTGCTGAAGAGTTTCAAGGAGGAGCTG 1893  
2149 GATGAGCACTTCAAGAGAGGCGGCGAGGCGGAGCATGCCGCTTCCAGAGCGCGCTG 2208  
1894 GCTGCGCTCGATAAGGAATGAGATCCGGAATGCAAGCTGGAATGCGCTTACGAGTAC 1953  
2209 GCCAGATCTCAAGGACATCCAGGAGCGGACCAAGGCTGCGCTGCGCTACACCTAC 2268  
1954 CTGGGCGCAGCGTGTGAAACAGTGTGGGCACTAA 1992  
2269 CTGGACCTTCCCTCATTTGAGAACAGCGTCTCCATCAA 2307

## RESULT 15

US-09-547-435-23  
; Sequence 23, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael

APPLICANT: Friedrich, Glenn  
APPLICANT: Sands, Arthur I.  
TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
FILE OF INVENTION: Encoding the Same  
FILE REFERENCE: 7705.0009-00000  
CURRENT APPLICATION NUMBER: US/09/547,435  
CURRENT FILING DATE: 2000-04-12  
NUMBER OF SEQ ID NOS: 29  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 23  
LENGTH: 2604  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-547-435-23

Query Match 12.3%; Score 327.8; DB 4; Length 2604;  
Best Local Similarity 53.6%; Pred. No. 2e-77;  
Matches 761; Conservative 0; Mismatches 637; Indels 21; Gaps 3;

QY 589 TCCTGGAAGATCTAGATGACTTCAACCGGATTTTCTGCTGTGTCAGAGCAAGCTGGCT 648  
Db 1192 TCCTGGAAGATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1251  
QY 649 GAGCGCTGCGGACTCTGGAAGAGATGCTTATTTGGGTACCAAGTTCCTTAATGCG 708  
Db 1252 AAGTATGTACAGAGCACTGCTGTGAAGATCCTTCTTTGGGTACCAAGTTCCTTAATGCT 1311  
QY 709 GCCAACCCGCTGCTGAGGCGCTCTGCTCACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 768  
Db 1312 GTCAATCCCGTCATGCTCCACTGATCTCTAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1371  
QY 769 GGCATGG-----AGGAATGCAAGCGCCAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 816  
Db 1372 GACATGCTGGGCGGCTTCTGCGGACAGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1431  
QY 817 ACATGTTTCAAGCTGACTTCTCCTGCTGATGGATCAAGGCCAAAGTCAATCTCTGCT 876  
Db 1432 AACATCTTCTAGCGGACTTCTGATCTGCGGAGGCGCCACCCACCTGCTGCTGCTGCTGCTGCTGCT 1491  
QY 877 AGCAGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 936  
Db 1492 CGCAGAGTACGTTGGCGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1551  
QY 937 TTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 996  
Db 1552 GTGCGCTTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1605  
QY 997 TTGCTACGATCCCGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1056  
Db 1606 CTGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1665  
QY 1057 TTCCAGCTTCCATGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1116  
Db 1666 TTCTGCT 1725  
QY 1117 GTTGTGGCCACCATGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1176  
Db 1726 GGCATGGCCACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1785  
QY 1177 CACCTGCGATACACCTGGAATTAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1236  
Db 1786 CACACTCGATACAGCTGAGTGAACACCATTCGCGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1845  
QY 1237 GGAATTTTCGACGATTAATGAGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1296  
Db 1846 GGCCTCTGCT 1905  
QY 1297 GCTGAGGCTTCTTAACCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1356  
Db 1906 GGCCTGCGCCACTTCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACTACCACT 1965  
QY 1357 CTCCTGGAGTGAAGTCTTCTTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1416

Db	1966	GTCTGGCTATCCCCAACTACCACTACCGAGACGAGCGCCTGAAGATCTGGGCGGCATT	2025
Qy	1417	TATCGGTATCTGGAAGGATCGTGAGTCTCCACTATAAGACAGACGCTGGCTGTGAAGAC	1476
Db	2026	GAGAGCTTGTCTCAGAAATCGTGGGCTACTATATATCCAGTACGCACTGTGCGAGCAG	2085
Qy	1477	GACCCAGAGCTGCAGACCTCGTGTCTGAGAGATCACTGAATCGGGTGCAGGGGCCAG	1536
Db	2086	GATTCGGAGCTGCAGGCTGGACTGGCGAGATTTTGTCTCAGGCGTTCTTGGGCGGGAA	2145
Qy	1537	GACGAGGGTTTCTGTCTCTTTACAGGCTCGGACCAAGTTTGGCCACTTTGTCAACATG	1596
Db	2146	AGCTCAGGTTTCCCAAGCCCGGCTGTGCACCCAGGAGATGTGAAGTTTCCTCACTGCA	2205
Qy	1597	TGTATCTTCACCTGCACCGGCCCAACACGCTCTGTGCACCTGGCCAGCTGGACTGGTAC	1656
Db	2206	ATCATCTTCAATTGCTCTGCCAGCAGCTGCTGTCTACAGTGGGAGCATGACTTTGGG	2265
Qy	1657	TCTTGGGTGCTAATGCACCCCTGCACGATCGGCTGCCCGGCCCAACCAAGG---AT	1713
Db	2266	GCCTGGATGCCCAATGCTCCATCATCCATGAGCGAGCCCCCACCAGACCAAGGGACC	2325
Qy	1714	GCAACGCTGAGAGAGTGGGAGACACTGCCCAACTTCCACAGGTTTCTCTCCAGATG	1773
Db	2326	ACCACCTGAAGACTTACCTAGACACCCCTCCTGAAAGTGAACATCAGCTGTAAACCTC	2385
Qy	1774	TCCATCACTTGGCAGCTGGGCGAGCGCCAGCCCGTTATGTTGCTGTGGGCCAGCATGAG	1833
Db	2386	CTCCTCTTCTGGTTGGTTAGCCAAAGAACCCAGAGCCAGAGGCCCTTGGGCACCTACCCA	2445
Qy	1834	GAGGAGTATTTTGGGCCCCTGAGCCCTAAGGCTGTGCTGAAGAAGTTTCAGGGAGGAGCTG	1893
Db	2446	GATGAGCACTTCACAGAGGAGGCCCGAGGCGGAGCATCGCCGCTTCCAGAGCCGCTG	2505
Qy	1894	GCTGCCCTGGATAGGAAATTGAGATCCGGAATGCAAGCTGGACATGCCCTTAGAGTAC	1953
Db	2506	GCCAGATCTCAAGGGACATCCAGGAGCGGAACCAAGGCTTGGCACTGCCCTACACCTAC	2565
Qy	1954	CTGGGCCCGAGCGTGTGGAAACAGTGTGCCCATCTAA	1992
Db	2566	CTGGACCTTCCCTCATTTGAGAACAGCGTCTCCATCTAA	2604

Search completed: July 19, 2005, 21:31:56  
Job time : 305.231 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:40:47 ; Search time 113.625 Seconds  
(without alignments)  
2249.936 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLVIRVSTGASLYAGSNN.....KLDMPYEYLRPSVENSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04.\*

- 1: Geneseqp1980s.\*
- 2: Geneseqp1990s.\*
- 3: Geneseqp2000s.\*
- 4: Geneseqp2001s.\*
- 5: Geneseqp2002s.\*
- 6: Geneseqp2003as.\*
- 7: Geneseqp2003bs.\*
- 8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3503.5	99.7	662	4	Aae00939 Human 15S
2	3503.5	99.7	662	7	Add47873 Human Pro
3	3503.5	99.7	662	8	Adj75368 Marker Ge
4	3503.5	99.7	662	8	Adq91786 Human 15S
5	3503.5	99.7	662	8	Adq37894 Human 15-
6	3494.5	99.4	684	5	Ab508005 Human lip
7	2691	76.6	662	7	Add47871 Rat Prote
8	2676	76.2	663	8	Adj76170 Marker ge
9	2316	65.9	663	8	Adq39837 Human myo
10	2298.5	65.4	647	8	Adq39836 Human myo
11	2280	64.9	663	3	Ad310879 Human the
12	2280	64.9	663	3	Ab24019 Arachidon
13	2230.5	63.5	632	8	Ad311946 Human the
14	2230.5	63.5	632	8	Ad311947 Human the
15	2230.5	63.5	632	8	Ad311945 Human the
16	1969	56.0	399	6	Aae38235 Human enz
17	1298.5	37.0	674	5	Aae15432 Human 5-1
18	1298.5	37.0	674	5	Abu08713 Alzheim
19	1298.5	37.0	674	6	Abu89732 Protein d
20	1298.5	37.0	674	6	Ab42217 Mouse B6
21	1298.5	37.0	674	6	Ab42215 Human 5-1
22	1298.5	37.0	674	6	Adf53274 Human 5-1
23	1298.5	37.0	674	8	Adp54502 Human PRO
24	1297.5	36.9	674	6	Ab42216 Mouse CAS
25	1295.5	36.9	674	1	Aep90730 Synthetic

ALIGNMENTS

RESULT 1

AAE00939

ID AAE00939 standard; protein; 662 AA.

AC AAE00939;

DT 04-JUL-2001 (first entry)

DE Human 15S-lipoxygenase (15-Lox-1) protein.

KW Human; 15S-lipoxygenase; 15-Lox-1; non-haeme iron dioxygenase; arachidonic acid; feed additive; livestock; antigen.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Region 340..344 /note= "Consensus sequence"

FT Binding-site 360 /note= "Iron ligand"

FT Binding-site 365 /note= "Iron ligand"

FT Region 494..498 /note= "Consensus sequence"

FT Binding-site 540 /note= "Iron ligand"

FT Binding-site 544 /note= "Iron ligand"

FT Region 546..550 /note= "Consensus sequence"

FT Binding-site 662 /note= "Iron ligand"

PN US6204037-B1.

XX 20-MAR-2001.

XX 16-APR-1998; 98US-00061768.

XX 16-APR-1998; 98US-00061768.

XX (UTVA-) UNIV VANDERBILT.

XX Brash AR, Boeglin WE, Jiseka M;

XX WPI; 2001-289517/30.

XX New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed

Aar06552 Human 5-1  
Aae15433 Human 5-1  
Aaw93832 Human 15S  
Aae00935 Human 15S  
Abg61866 Prostata  
Abu89734 Protein d  
Adg91763 Human lip  
Adq37896 Human 15-  
Aae00936 Mouse 8S-  
Adq91765 Mouse 8S-  
Abm84236 Human dia  
Aab19379 Amino aci  
Abp69704 Human pol  
Ab504578 Human lip  
Aae39890 Human lip  
Adq48419 Human lip  
Aab19390 Amino aci  
Abm8203 Human lip  
Adh13687 Human ENZ  
Abm83351 Human dia

PT additives for livestock, or as antigens for producing antibodies.  
PS Disclosure; Fig 1; Sipp; English.  
XX  
CC The present sequence is human 15S-lipoxygenase (15-Lox-1) protein.  
CC Lipoxygenases are a structurally related family of non-haeme iron  
CC dioxygenases that function in the production of fatty acid  
CC hydroperoxides. 15-Lox-1 acts in the metabolism of arachidonic acid to  
CC 15S-hydro(pero)xyicosatetraenoic acid. Lipoxygenase DNA can be used as  
CC diagnostic tools to detect normal and abnormal DNA sequences derived from  
CC patient cells, for detecting and isolating other members of the  
CC polypeptide family and related polypeptides from a DNA library  
CC potentially containing the sequences, as primers for hybridising to  
CC related sequences for amplifying those sequences or for altering native  
CC lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives  
CC for livestock and as antigens for producing antibodies  
XX  
SQ Sequence 662 AA;  
Query Match 99.7%; Score 3503.5; DB 4; Length 662;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVGQGEAALGKRLWPARG-ETELKVEVPEYLGPL 59  
DB 1 MGLYRIRVSTGASLYAGSNQVQLWLVGQGEAALGKRLWPARGKETELKVEVPEYLGPL 60  
QY 60 LFKLKRHLKDDDAWFCNWIISVQGGAGDEVRFPYRVEGNGVLSLPEGTGRTVGDP 119  
DB 61 LFKLKRHLKDDDAWFCNWIISVQGGAGDEVRFPYRVEGNGVLSLPEGTGRTVGDP 120  
QY 120 QGLFQKHREELERKLRWGNWKGDLINWAGAKLYDLPDERFLEDKRVDFEVSIAK 179  
DB 121 QGLFQKHREELERKLRWGNWKGDLINWAGAKLYDLPDERFLEDKRVDFEVSIAK 180  
QY 180 GLADLAIKDSLNLVLCWKDLDDPNRIFWCQSKLAERVDSWKEDALFGYQFLNGANPVV 239  
DB 181 GLADLAIKDSLNLVLCWKDLDDPNRIFWCQSKLAERVDSWKEDALFGYQFLNGANPVV 240  
QY 240 LRRSAHLPARLVPPQMEELQALEKELEGGTTLFEADFSLLDGIKANVILCSQQHLAAFL 299  
DB 241 LRRSAHLPARLVPPQMEELQALEKELEGGTTLFEADFSLLDGIKANVILCSQQHLAAFL 300  
QY 300 VMLKLPDQKLLPMVQLQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 359  
DB 301 VMLKLPDQKLLPMVQLQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360  
QY 360 LLRGHLMAEVIVVATWRCPLSIHPFKLIIPHLYRVTLEINVRARTGLVSDMGIFDQIMST 419  
DB 361 LLRGHLMAEVIVVATWRCPLSIHPFKLIIPHLYRVTLEINVRARTGLVSDMGIFDQIMST 420  
QY 420 GGGGHVQLLKQAGAFITYSSFCPPDDLADRLGLLVKSSFYAQUALRLWELIYRYVEGIYS 479  
DB 421 GGGGHVQLLKQAGAFITYSSFCPPDDLADRLGLLVKSSFYAQUALRLWELIYRYVEGIYS 480  
QY 480 LHYKTDVAVKDDPELQTCREITEIGLQAGQDRGPPVSLQARDQVCHFTVMCTCTGQH 539  
DB 481 LHYKTDVAVKDDPELQTCREITEIGLQAGQDRGPPVSLQARDQVCHFTVMCTCTGQH 540  
QY 540 ASVHLGQLDWYSWVPNAPCTMLRPPTTKDATTLETVMATLPNPHQASLQMSITWQLGRQ 599  
DB 541 ASVHLGQLDWYSWVPNAPCTMLRPPTTKDATTLETVMATLPNPHQASLQMSITWQLGRQ 600  
QY 600 PNMVAVGQHEEYFSGPEPKAVLKRFREELAAALDKIEIRNAKLDMPYELRPSVVENS 659  
DB 601 PNMVAVGQHEEYFSGPEPKAVLKRFREELAAALDKIEIRNAKLDMPYELRPSVVENS 660  
QY 660 AI 661  
DB 661 AI 662

RESULT 2

ADD47873  
ID ADD47873 standard; protein; 662 AA.  
XX  
AC ADD47873;  
XX  
DT 02-DEC-2004 (revised)  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein NP\_001131, SEQ ID NO 13569.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
OS Unidentified.  
XX  
FN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPI; 2003-268312/26.  
DR GENBANK; NP\_001131.  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Example 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (described in Table 3  
CC of the specification) which is differentially expressed during pain.  
CC Note: the sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 662 AA;

Query Match 99.7%; Score 3503.5; DB 7; Length 662;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;



```
QY 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHGGAALGKELWPARG-ETELKVEVPEYLGPL 59
Db 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHGGAALGKELWPARG-ETELKVEVPEYLGPL 60
QY 60 LFKVLRKRHLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 119
Db 61 LFKVLRKRHLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 120
QY 120 QGLFQKHREELERKLYRWGNWKGDIILNAGAKLYDLVDRFLDKRVDPEVSLAK 179
Db 121 QGLFQKHREELERKLYRWGNWKGDIILNAGAKLYDLVDRFLDKRVDPEVSLAK 180
QY 180 GLADLAIKDSLNLVTCWKDLDNFRIFCWGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db 181 GLADLAIKDSLNLVTCWKDLDNFRIFCWGSKLAERVRDSWKEDALFGYQFLNGANPVV 240
QY 240 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLLDGKANKVILCSQQHLAAPL 299
Db 241 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLLDGKANKVILCSQQHLAAPL 300
QY 300 VMLKLOPDGKLLPMVIQOLPRTGSPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 359
Db 301 VMLKLOPDGKLLPMVIQOLPRTGSPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 360
QY 360 LRGHLMAEVIVATMRCPLSPHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LRGHLMAEVIVATMRCPLSPHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGHVQLLKQAGAFLTYSFCCPPDDLDRLGLGVKSSFYAQDALRLWEIIRYVVEGIVS 479
Db 421 GGGHVQLLKQAGAFLTYSFCCPPDDLDRLGLGVKSSFYAQDALRLWEIIRYVVEGIVS 480
QY 480 LHYKTDVAVKDDPELQVTCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTGQH 539
Db 481 LHYKTDVAVKDDPELQVTCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTGQH 540
QY 540 ASVHLGQLDWYSWVPNAPCTWRLPPTTKDATLETVMATLNFHQAQSLQMSITWQGRQ 599
Db 541 ASVHLGQLDWYSWVPNAPCTWRLPPTTKDATLETVMATLNFHQAQSLQMSITWQGRQ 600
QY 600 PMVAVGQHEEYFSGPSPKAVLKKFREELAAKDKEIRNAKLDMPVEYLRPSVVNSV 659
Db 601 PMVAVGQHEEYFSGPSPKAVLKKFREELAAKDKEIRNAKLDMPVEYLRPSVVNSV 660
QY 660 AI 661
Db 661 AI 662

RESULT 3
ID ADJ75368
XX ADJ75368 standard; protein; 662 AA.
AC ADJ75368;
XX
XX
XX 20-MAY-2004 (first entry)
DT
DE Marker gene related amino acid sequence SEQ ID NO:620.
XX
XX bronchial asthma; chronic obstructive pulmonary disease;
KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
KW gene therapy; marker.
XX
XX Homo sapiens.
XX
XX EPI394274-A2.
XX
XX 03-MAR-2004.
XX
XX 04-AUG-2003; 2003EP-00254857.
XX
XX 06-AUG-2002; 2002JP-00229312.
PR
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```
PR 20-MAR-2003; 2003JP-00077212.
XX (GENO-) GENOX RES INC.
XX
XX Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX
XX Testing for bronchial asthma or chronic obstructive pulmonary disease by
XX comparing the expression level of a marker gene in a biological sample
XX from a subject with the expression level of the gene in a sample from a
XX healthy subject.
XX
XX Example 11; SEQ ID NO 620; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX cells (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (I) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (I) has respiratory
XX and antiasthmatic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.
XX
XX Sequence 662 AA;
XX
XX Query Match 99.7%; Score 3503.5; DB 8; Length 662;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHGGAALGKELWPARG-ETELKVEVPEYLGPL 59
Db 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHGGAALGKELWPARG-ETELKVEVPEYLGPL 60
QY 60 LFKVLRKRHLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 119
Db 61 LFKVLRKRHLKDDAWFCNWTISVQPGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGDDP 120
QY 120 QGLFQKHREELERKLYRWGNWKGDIILNAGAKLYDLVDRFLDKRVDPEVSLAK 179
Db 121 QGLFQKHREELERKLYRWGNWKGDIILNAGAKLYDLVDRFLDKRVDPEVSLAK 180
QY 180 GLADLAIKDSLNLVTCWKDLDNFRIFCWGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db 181 GLADLAIKDSLNLVTCWKDLDNFRIFCWGSKLAERVRDSWKEDALFGYQFLNGANPVV 240
QY 240 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLLDGKANKVILCSQQHLAAPL 299
Db 241 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLLDGKANKVILCSQQHLAAPL 300
QY 300 VMLKLOPDGKLLPMVIQOLPRTGSPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 359
Db
```

Db 301 VMLKLPDQKLLPMVIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360  
QY 360 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419  
Db 361 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 420  
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIRYVEGIVS 479  
Db 421 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIRYVEGIVS 480  
QY 480 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTGOH 539  
Db 481 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTGOH 540  
QY 540 ASVHLGQLDWYSWVNPACTMRLPPTTKDATLETVMATLPNFHQASLQMSITWOLGRRQ 599  
Db 541 ASVHLGQLDWYSWVNPACTMRLPPTTKDATLETVMATLPNFHQASLQMSITWOLGRRQ 600  
QY 600 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 659  
Db 601 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 660  
QY 660 AI 661  
Db 661 AI 662

RESULT 4  
ADQ91786  
ID ADQ91786 standard; protein; 662 AA.  
XX  
AC ADQ91786;  
DT 07-OCT-2004 (first entry)  
XX  
DE Human 15S-lipoxygenase.  
XX  
KW lipoxygenase; iron ligand; arachidonic acid metabolism; human;  
KW lipoxygenase 15-Lox-2; 15S-lipoxygenase; human.  
XX  
OS Homo sapiens.  
XX  
PN US2004137483-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 18-NOV-2003; 2003US-00716204.  
XX  
PR 16-APR-1998; 98US-00061768.  
PR 17-JAN-2001; 2001US-00764246.  
XX  
PA (BRAS/) BRASH A R.  
PA (BOEG/) BOEGLIN W E.  
PA (JISA/) JISAKA M.  
XX  
PI Brash AR, Boeglin WE, Jisaka M;  
XX WPI; 2004-533356/51.  
DR  
XX  
XX New lipoxygenase nucleic acid segment comprises an isolated gene encoding  
PT a lipoxygenase containing an iron ligand comprising a serine, useful for  
PT arachidonic acid metabolism.  
XX  
PS Example 1; SEQ ID NO 25; 39pp; English.  
XX  
CC The invention describes a nucleic acid segment (I) comprising an isolated  
CC gene encoding a lipoxygenase containing an iron ligand comprising a  
CC serine, or comprises at least a 10 nucleotides long contiguous stretch of  
CC the nucleic acid sequence not given in the specification (SEQ ID NO. 1)  
CC or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a  
CC nucleic acid segment comprising at least 10 nucleotides long contiguous  
CC stretch of the nucleic acid sequence not given in the specification (SEQ  
CC ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is

CC a polypeptide having the amino acid sequence Trp-Leu-Leu-Ala-Lys (SEQ ID  
CC NO. 5) and Gly-Gln-Tyr-Asp-Trp (SEQ ID NO. 35). The lipoxygenase nucleic  
CC acids and proteins are useful in arachidonic acid metabolism. This is the  
CC amino acid sequence of human 15S-lipoxygenase used in a comparison with  
CC the novel human lipoxygenase 15-Lox-2.  
XX  
SQ Sequence 662 AA;  
Query Match 99.7%; Score 3503.5; DB 8; Length 662;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVQHGGAALGKRLWPARG-ETELKVEVPYELGL 59  
Db 1 MGLYRIRVSTGASLYAGSNQVQLWLVQHGGAALGKRLWPARG-ETELKVEVPYELGL 60  
QY 60 LFVKLRKHLKDDDAWFCNWISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTRTGEDP 119  
Db 61 LFVKLRKHLKDDDAWFCNWISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTRTGEDP 120  
QY 120 QGLFQKHREELERKLYRMGNWKGDLILNAGAKLYDLPVDERFLEDKRVDFEVS LAK 179  
Db 121 QGLFQKHREELERKLYRMGNWKGDLILNAGAKLYDLPVDERFLEDKRVDFEVS LAK 180  
QY 180 GLADLAIKDSLNLVTCWKDLDNFNRFWCQSGKLAERVDSWKEDALFGYQFLNGANPVV 239  
Db 181 GLADLAIKDSLNLVTCWKDLDNFNRFWCQSGKLAERVDSWKEDALFGYQFLNGANPVV 240  
QY 240 LRRSAHLPARLVFPFGMEELQALKELEGGTLPFADPSLDDGIKANVTLCSQQHLAAPL 299  
Db 241 LRRSAHLPARLVFPFGMEELQALKELEGGTLPFADPSLDDGIKANVTLCSQQHLAAPL 300  
QY 300 VMLKLPDQKLLPMVIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 359  
Db 301 VMLKLPDQKLLPMVIQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360  
QY 360 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419  
Db 361 LLRGHLMAEVIVVATMRCPLPSIHPFIKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 420  
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIRYVEGIVS 479  
Db 421 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIIRYVEGIVS 480  
QY 480 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTGOH 539  
Db 481 LHYKTDVAVKDDPELOQTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQTGOH 540  
QY 540 ASVHLGQLDWYSWVNPACTMRLPPTTKDATLETVMATLPNFHQASLQMSITWOLGRRQ 599  
Db 541 ASVHLGQLDWYSWVNPACTMRLPPTTKDATLETVMATLPNFHQASLQMSITWOLGRRQ 600  
QY 600 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 659  
Db 601 PVMVAVGOHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPYELRPSVVENS 660  
QY 660 AI 661  
Db 661 AI 662

RESULT 5  
ADQ37894  
ID ADQ37894 standard; protein; 662 AA.  
XX  
AC ADQ37894;  
DT 07-OCT-2004 (first entry)  
XX  
DE Human 15-lipoxygenase 1 protein.  
XX  
KW Dry eye; 15-lipoxygenase; 15-LO; ophthalmological; gene therapy;  
KW postmenopausal.

XX OS Homo sapiens.  
 XX PN WO2004060274-A2.  
 XX PD 22-JUL-2004.  
 XX PF 17-OCT-2003; 2003WO-US033139.  
 XX PR 20-DEC-2002; 2002US-0435988P.  
 XX PA (ALCO-) ALCON INC.  
 XX PI Yanni JM, Gamache DA, Miller ST;  
 XX DR WPI; 2004-543776/52.  
 XX DR N-PSDB; ADQ37893.  
 XX PT Treating dry eyes in postmenopausal women comprises administering a  
 PT composition comprising the 15-lipoxygenase (15-LO)-1 or 15-LO-2 gene to  
 PT the ocular surface cells of the post-menopausal women with dry eyes.  
 XX PS Claim 5; SEQ ID NO 2; 20pp; English.  
 XX CC The invention relates to a novel method for treating dry eyes. The method  
 CC comprises obtaining a composition containing the nucleotide sequence of  
 CC 15-lipoxygenase (15-LO)-1 or 15-LO-2, and administering the composition  
 CC to a patient suffering from dry eye under conditions such that the  
 CC nucleotide sequence of 15-LO-1 or 15-LO-2 is expressed. The invention  
 CC further comprises a composition for the treatment of dry eye, comprising  
 CC a vector having the above nucleotide sequence and an excipient. The 15-LO  
 CC compositions have ophthalmological activity and may be used in gene  
 CC therapy to treat disorders. The method is useful for treating dry eyes in  
 CC postmenopausal women. This sequence represents the 15-lipoxygenase 1  
 CC protein of the invention.  
 XX SQ Sequence 662 AA;

Query Match 99.7%; Score 3503.5; DB 8; Length 662;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MGLYRIRVSTGASLYAGSNQVQLWVGQHGSAALGKELWPARG-ETELKVEVEYLGPL 59  
 Db 1 MGLYRIRVSTGASLYAGSNQVQLWVGQHGSAALGKELWPARGKETELKVEVEYLGPL 60  
 Qy 60 LFVKLRKHLKDDAWFCNWSVQPGAGDEVFPFCYRWVEGNGVLSLPEGTGRTVGDDP 119  
 Db 61 LFVKLRKHLKDDAWFCNWSVQPGAGDEVFPFCYRWVEGNGVLSLPEGTGRTVGDDP 120  
 Qy 120 QGLFKHREELERKLYRWGNWKDGLILNAGAKLYDLVDFRFLDKRVDPEVSLAK 179  
 Db 121 QGLFKHREELERKLYRWGNWKDGLILNAGAKLYDLVDFRFLDKRVDPEVSLAK 180  
 Qy 180 GLADLAIKDSNLVLCWKDLDENRIFWCGSKLAERVRDSWKEDALFGYFLNGANPVV 239  
 Db 181 GLADLAIKDSNLVLCWKDLDENRIFWCGSKLAERVRDSWKEDALFGYFLNGANPVV 240  
 Qy 240 LRRSAHLPARLVFPFGMELOAQLEKEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 299  
 Db 241 LRRSAHLPARLVFPFGMELOAQLEKEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 300  
 Qy 300 VMLKLPQPKLLPMVILQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 359  
 Db 301 VMLKLPQPKLLPMVILQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 360  
 Qy 360 LLRGLHMAEIVVATMRCLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419  
 Db 361 LLRGLHMAEIVVATMRCLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420  
 Qy 420 GGGGHVQLLKQAGAFITYSSFCPPDDLDADRGLLGVKSSFYAQDALRLMEIIRYVEGIVS 479  
 Db 421 GGGGHVQLLKQAGAFITYSSFCPPDDLDADRGLLGVKSSFYAQDALRLMEIIRYVEGIVS 480

Qy 480 LHYKTDVAVKDDPELQTWCREITEIGLQGAQDRGFPVSLQARDQVCHFTVMTCTCTGQH 539  
 Db 481 LHYKTDVAVKDDPELQTWCREITEIGLQGAQDRGFPVSLQARDQVCHFTVMTCTCTGQH 540  
 Qy 540 ASVHLGOLDWYSWVPNAPCTMRLLPPPTTKDATTETVMTATLPNPHQASLQMSITWOLGRRQ 599  
 Db 541 ASVHLGOLDWYSWVPNAPCTMRLLPPPTTKDATTETVMTATLPNPHQASLQMSITWOLGRRQ 600  
 Qy 600 PMVAVGQHEEYFSGPEPKAVLKKFREELAALDKETIEIRNAKLDMPYEYLRPSVVENSV 659  
 Db 601 PMVAVGQHEEYFSGPEPKAVLKKFREELAALDKETIEIRNAKLDMPYEYLRPSVVENSV 660  
 Qy 660 AI 661  
 Db 661 AI 662

RESULT 6  
 ABB08005  
 ID ABB08005 standard; protein; 684 AA.  
 XX AC ABB08005;  
 XX DT 27-AUG-2002 (first entry)  
 XX DE Human lipid metabolism enzyme (LME)-5 (Id: 7484270CD1).  
 XX KW Human; lipid metabolism enzyme; LME; cytostatic; neuroprotective;  
 KW nootropic; cerebroprotective; antiparkinsonian; antialzheimers; vaccine;  
 KW anticlerotic; antimicrobial; anti-AIDs; cardiovascular; antiangiinal;  
 KW gene therapy; protein therapy; enzyme.  
 XX OS Homo sapiens.  
 XX PN WO200229036-A2.  
 XX PD 11-APR-2002.  
 XX PF 05-OCT-2001; 2001WO-US031302.  
 XX PR 06-OCT-2000; 2000US-0238388P.  
 PR 13-OCT-2000; 2000US-0240616P.  
 PR 02-NOV-2000; 2000US-0245719P.  
 PR 08-NOV-2000; 2000US-0247503P.  
 PR 17-NOV-2000; 2000US-0249503P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PI Harland L, Arvizu C, Das D, Griffin JA, Baughn MR, Ding L;  
 PI Walia NK, Yao MG, Lu Y, Elliott VS, Thangavelu K, Ramkumar J;  
 PI Lal PG, Tribouley CM;  
 XX WPI; 2002-315862/35.  
 DR N-PSDB; ABL60541.  
 XX Lipid Metabolism Enzymes and nucleic acids, useful for preventing,  
 PT diagnosing and treating e.g. cancer, Alzheimer's disease and Creutzfeld-  
 PT Jakob disease.  
 XX Claim 1; Page 116-118; 127pp; English.  
 XX The invention relates to human lipid metabolism enzymes (LMEs) and  
 CC encoding polynucleotides. The LMEs can be expressed by standard  
 CC recombinant technology. The LME polypeptides, polynucleotides and  
 CC modulators may be used in the prevention, diagnosis and treatment of  
 CC diseases associated with inappropriate LME expression such as cancer  
 CC (e.g. myeloma, sarcoma and breast cancer), neurological disorders (e.g.  
 CC Parkinson's, Alzheimer's and multiple sclerosis), microbial infections  
 CC (e.g. Creutzfeld-Jakob disease and Acquired Immune deficiency syndrome  
 CC (AIDS)) and/or cardiovascular disorders (e.g. cardiomyopathy, angina  
 CC pectoris and mitral valve prolapse). The present sequence represents the  
 CC human LME-5 polypeptide

XX	Sequence 684 AA;	
SY	Query Match	99.4%; Score 3494.5; DB 5; Length 684;
SY	Best Local Similarity	99.7%; Pred. No. 0;
SY	Matches 660; Conservative	0; Mismatches 1; Indels 1; Gaps 1;
QY	1	MGLYRIRVSTGASLYAGSNQVQLMLVGQHGAAALGKRLWPARG-ETELKVEVPEYLGPL 59
DB	23	MGLYRIRVSTGASLYAGSNQVQLMLVGQHGAAALGKRLWPARGKETELKVEVPEYLGPL 82
QY	60	LFVKLRKRLHLLKDDAWFCNWIISVQGGAGDEVRFPFCYRWVEGNVLSLPEGTGRTVGDP 119
DB	83	LFVKLRKRLHLLKDDAWFCNWIISVQGGAGDEVRFPFCYRWVEGNVLSLPEGTGRTVGDP 142
QY	120	QGLFQKHREELERKLYRWGNWKGDLINWAGAKLYDLVDERFLEDKRVDVEVSLAK 179
DB	143	QGLFQKHREELERKLYRWGNWKGDLINWAGAKLYDLVDERFLEDKRVDVEVSLAK 202
QY	180	GLADLAIKDSLNVLTCKWDLDDFNRIFCWQSQKLAERVDSWKEDALFGYQFLNGANPVV 239
DB	203	GLADLAIKDSLNVLTCKWDLDDFNRIFCWQSQKLAERVDSWKEDALFGYQFLNGANPVV 262
QY	240	LRRSAHLPARLVPPPGMEELQALEKELEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 299
DB	263	LRRSAHLPARLVPPPGMEELQALEKELEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 322
QY	300	VMLKLPQDGKLLPMVTLQQLPRGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 359
DB	323	VMLKLPQDGKLLPMVTLQQLPRGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 382
QY	360	LLRGHLMAEVIVVATMRCPLSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419
DB	383	LLRGHLMAEVIVVATMRCPLSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 442
QY	420	GGGHHVOLLKQAGAFITYSSFCPPDLDADRGLLGKVSFYAODALRLWEIIRYVEGIVS 479
DB	443	GGGHHVOLLKQAGAFITYSSFCPPDLDADRGLLGKVSFYAODALRLWEIIRYVEGIVS 502
QY	480	LHYKTDAVKDDPELTWCREITEIGLQAGDRGPPVSLQARDQVCHFTVTCIQTGQH 539
DB	503	LHYKTDAVKDDPELTWCREITEIGLQAGDRGPPVSLQARDQVCHFTVTCIQTGQH 562
QY	540	ASVHLGQLDWYSWVPNAPCTMLPPPTTKDATLETVMATLPNFHQASLQMSITWQLRGQ 599
DB	563	ASVHLGQLDWYSWVPNAPCTMLPPPTTKDATLETVMATLPNFHQASLQMSITWQLRGQ 622
QY	600	PVMVAVGQHEEYFSGPEPKAVLKKFREELALDKIEIRNAKLDMPYELRPSVVENS 659
DB	623	PVMVAVGQHEEYFSGPEPKAVLKKFREELALDKIEIRNAKLDMPYELRPSVVENS 682
QY	660	AI 661
DB	683	AI 684
SY	RESULT 7	
SY	ADD47871	standard; protein; 662 AA.
SY	ID	ADD47871 standard; protein; 662 AA.
SY	AC	ADD47871;
SY	DT	02-DEC-2004 (revised)
SY	DT	29-JAN-2004 (first entry)
SY	DE	Rat Protein AAB30132, SEQ ID NO 13567.
SY	KW	Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
SY	KW	chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
SY	OS	Rattus norvegicus.
SY	OS	Unidentified.

PN	WO2003016475-A2.	
XX	27-FEB-2003.	
XX	14-AUG-2002; 2002WO-US025765.	
XX	14-AUG-2001; 2001US-0312147P.	
PR	01-NOV-2001; 2001US-0346382P.	
PR	26-NOV-2001; 2001US-0333347P.	
XX	(GHO ) GEN HOSPITAL CORP.	
PA	(PARB ) BAYER AG.	
XX	Woolf C, D'urso D, Befort K, Costigan M;	
PI	WPI; 2003-268312/26.	
XX	GENBANK; AAB30132.	
DR	New composition comprising two or more isolated polypeptides, useful for	
PT	preparing a medicament for treating pain in an animal.	
PT	Example 1; Page; 1017pp; English.	
PS	The invention discloses a composition comprising two or more isolated rat	
XX	or human polynucleotides or a polynucleotide which represents a fragment,	
CC	derivative or allelic variation of the nucleic acid sequence. Also	
CC	claimed are a vector comprising the novel polynucleotide, a host cell	
CC	comprising the vector, a method for identifying a nucleotide sequence	
CC	which is differentially regulated in an animal subjected to pain and a	
CC	kit to perform the method, an array, a method for identifying an agent	
CC	that increases or decreases the expression of the polynucleotide sequence	
CC	that is differentially expressed in neuronal tissue of a first animal	
CC	subjected to pain, a method for identifying a compound which regulates	
CC	the expression of a polynucleotide sequence which is differentially	
CC	expressed in an animal subjected to pain, a method for identifying a	
CC	compound that regulates the activity of one or more of the	
CC	polynucleotides, a method for producing a pharmaceutical composition, a	
CC	method for identifying a compound or small molecule that regulates the	
CC	activity in an animal of one or more of the polypeptides given in the	
CC	specification, a method for identifying a compound useful in treating	
CC	pain and a pharmaceutical composition comprising the one or more	
CC	polypeptides or their antibodies. The polynucleotide or the compound that	
CC	modulates its activity is useful for preparing a medicament for treating	
CC	pain (e.g. spinal segmental nerve injury (Chung), chronic constriction	
CC	injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene	
CC	therapy). The sequence presented is a rat protein (described in Table 3	
CC	of the specification) which is differentially expressed during pain.	
CC	Note: The sequence data for this patent did not form part of the printed	
CC	specification, but was obtained in electronic form directly from WIPO at	
CC	ftp.wipo.int/pub/published_pct_sequences.	
XX	Sequence 662 AA;	
SY	Query Match	76.6%; Score 2691; DB 7; Length 662;
SY	Best Local Similarity	74.5%; Pred. No. 1.7e-269;
SY	Matches 493; Conservative	77; Mismatches 90; Indels 2; Gaps 2;
QY	2	GLYRIRVSTGASLYAGSNQVQLMLVGQHGAAALGKRLWPARG-GETELKVEVPEYLGPL 60
DB	1	GVYRIRVSTGSKYAGSNNEVYLMVGQHGASLGLRLRCPEDSAEFKVDVSEYLGPL 60
QY	61	FVKLRKRLHLLKDDAWFCNWIISVQGGAG-AGDEVRFPCYRWVEGNVLSLPEGTGRTVGDP 119
DB	61	FVRVQKHYLTDDAWFCNWIISVQGGAGSEYMFPCYRWVQGRSILSLPEGTGCTWEDS 120
QY	120	QGLFQKHREELERKLYRWGNWKGDLINWAGAKLYDLVDERFLEDKRVDVEVSLAK 179
DB	121	QGLFQKHREELERKLYRWGNWKGDLINWAGAKLYDLVDERFLEDKRVDVEVSLAK 180
QY	180	GLADLAIKDSLNVLTCKWDLDDFNRIFCWQSQKLAERVDSWKEDALFGYQFLNGANPVV 239
DB	181	GVMQTVNPPINTVTCWKSLLDDFNCFKSGHTKMAERVNSWKEDAFPGYQFLNGANPVV 240

QY 240 LRRSAHLPARLVFPFGMELOAQLEKEGGTLPFEADPSLLDGIKANVILCSQOHLAAPL 299  
 Db 241 LKRSTCLPARLVFPFGMEKQALNKLQKGTLPFEADPSLLDGIKANVILCSQOYLAAPL 300  
 QY 300 VMLKLPDQKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLQSH 359  
 Db 301 VMLKLPDQKLLPIALQELPKGTSTPPPIFTPPDPMDLLAKCWRSSDLQLHQLQAH 360  
 QY 360 LLRGLHMAEVIIVATMRCLPSIHPFKLIIPHLRYLTLEINVRARTGLVSDMGIFDQIMST 419  
 Db 361 LLRGLHMAELFAVATMRCLPSVHPFKLIVPHLLYLTMEINVRARSDLSERGFDFKAMST 420  
 QY 420 GGGGHVQLLKQAGAFITYSSFCPPDDLDRLGLGVKSSFYAODARLWEIIRYVVGIVS 479  
 Db 421 GGGGHLDLLKQAGAFITYSSFCPPDDLAERGLDIDTCFYAKDALRLWQIMNRYVVGIFN 480  
 QY 480 LHYKTDVAKDDPELQIETWCREITTEIGLOAQDRGFPVSLQARDQVCHFWTWCIFCTCQH 539  
 Db 481 LHYKTDKAVQDDYELQSWCREITDGLQAGDRGFTSLQSPAQACYFITWCIFCTTAQH 540  
 QY 540 ASVHLGOLDWYSWVPNAPCTMRLPPTTKDATLETVMATLPNFHQAQSLQMSITWOLGRRQ 599  
 Db 541 SSVHLGOLDWYFVWVNPACTMRLPPTTKDATLETVMATLPNFHQAQSLQMSITWOLGRRQ 600  
 QY 600 PWWAVGQHEEYFSGPEPKAVLKKFRELAALDKKEIRNKLDMPEYELRPSVWVNSV 659  
 Db 601 AVMPVLGQHSSEHFPNPEAKAVLKKFRELAALDKKEIRNKLDMPEYELRPSVWVNSV 660  
 QY 660 AI 661  
 Db 661 AI 662  
 RESULT 8  
 ID ADJ76170 standard; protein; 663 AA.  
 XX ADJ76170;  
 AC ADJ76170;  
 DT 20-MAY-2004 (first entry)  
 XX Marker gene related amino acid sequence SEQ ID NO:1422.  
 DE bronchial asthma; chronic obstructive pulmonary disease;  
 KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;  
 KW gene therapy; marker.  
 XX Mus musculus.  
 OS EPI394274-A2.  
 FN 03-MAR-2004.  
 XX 04-AUG-2003; 2003EP-00254857.  
 XX 06-AUG-2002; 2002JP-00229312.  
 PR 20-MAR-2003; 2003JP-00077212.  
 XX (GENO-) GENOX RES INC.  
 PA Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;  
 PI WPI; 2004-193155/19.  
 DR Testing for bronchial asthma or chronic obstructive pulmonary disease by  
 PT comparing the expression level of a marker gene in a biological sample  
 PT from a subject with the expression level of the gene in a sample from a  
 PT healthy subject.  
 XX Claim 16; SEQ ID NO 1422; 241pp; English.  
 PS The present invention describes a method of testing for bronchial asthma  
 CC or chronic obstructive pulmonary disease. The method comprises

CC determining the expression level of a marker gene in a biological sample  
 CC from a subject, comparing the expression level determined with the  
 CC expression level of the marker gene in a biological sample from a healthy  
 CC subject, and judging whether the subject has bronchial asthma or chronic  
 CC obstructive pulmonary disease. The marker gene comprises: (a) a group of  
 CC genes (S1) whose expression levels increase when respiratory epithelial  
 CC cells are stimulated with interleukin-13; or (b) a group of genes (S2)  
 CC whose expression levels decrease when respiratory epithelial cells are  
 CC stimulated with interleukin-13. Also described: (1) a reagent (1) for  
 CC testing for bronchial asthma or chronic obstructive pulmonary disease;  
 CC (2) a kit for screening for a candidate compound for a therapeutic agent  
 CC to treat bronchial asthma or chronic obstructive pulmonary disease; (3)  
 CC an animal model for bronchial asthma or chronic obstructive pulmonary  
 CC disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a  
 CC method for producing an animal model for bronchial asthma or chronic  
 CC obstructive pulmonary disease; (6) a therapeutic agent for bronchial  
 CC asthma or chronic obstructive pulmonary disease, comprising the compound,  
 CC a marker gene or an antisense nucleic acid corresponding to a portion of  
 CC the marker gene, a ribozyme, a polynucleotide that suppresses the  
 CC expression of the gene through an RNAi effect or an antibody recognising  
 CC a protein encoded by a marker gene; and (7) a DNA chip for testing for  
 CC bronchial asthma or a chronic obstructive pulmonary disease, on which a  
 CC probe has been immobilised to assay a marker gene. (1) has respiratory  
 CC and antiasthmatic activities, and can be used in gene therapy. The method  
 CC is useful for testing for or screening for a therapeutic agent for  
 CC bronchial asthma or chronic obstructive pulmonary disease. The present  
 CC sequence is used in the exemplification of the present invention.  
 XX Sequence 663 AA;

Query Match 76.2%; Score 2676; DB 8; Length 663;  
 Best Local Similarity 73.6%; Pred. No. 6.3e-268;  
 Matches 488; Conservative 80; Mismatches 93; Indels 2; Gaps 2;  
 QY 1 MGLYRIVSTGASLYAGSNNOVLVQGHGEAALGKRLMPAR-GETELKVEVPEYLGL 59  
 Db 1 MGVTIRIVSTGDSVYAGSNNEVILVQGHGEASLGKLFRCRNSAEAFKVDSEYLGL 60  
 QY 60 LFVKLRHLLKDDAWFCNWTISVQGP-AGDEVFPFCYRVWVEGVLSLPGTGTGTGVED 118  
 Db 61 LFRVQKWHYLKEDAWFCNWTISVQGPQDQSEYTFPCYRVWVQGTSLNLPSTGCTTVED 120  
 QY 119 PQGLFQKHREBELEERKLYRWGNWKGDLILNAGAKLYDLVDERFLEDRKVDPEVSLA 178  
 Db 121 SQGLFRHREBELEERSLYRWGNWKGDTILNVAATSSIDLPVQDRFREDKLEFEASQV 180  
 QY 179 KGLADLAIKDSLNVLTCTWKDLDDFNRIFWCQSKLAERVDSWKEDALFGYQFLNGANPV 238  
 Db 181 LGTMDTVINFPKNTVTCWKSLLDDENYFKSHTKAAERVNSWKEDAFFGYQFLNGANPM 240  
 QY 239 VLRRSAHLPARLVFPFGMEELQALQLEKEGGTLPFEADPSLLDGIKANVILCSQOHLAAP 298  
 Db 241 VLKSTCLPARLVFPFGMEKQALQLEKEGGTLPFEADPSLLDGIKANVILCSQOYLAAP 300  
 QY 299 LVMLKLPDQKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFOLHELOS 358  
 Db 301 LVMLKLPDQKLLPIALQELPKGTSTPPPIFTDPPMDLLAKCWRSSDLQLHQLQAH 360  
 QY 359 LLRGLHMAEVIIVATMRCLPSIHPFKLIIPHLRYLTLEINVRARTGLVSDMGIFDQIMST 418  
 Db 361 LLRGLHMAELFAVATMRCLPSVHPFKLIVPHLLYLTMEINVRARSDLSERGFDFKMS 420  
 QY 419 TGGGGHVQLLKQAGAFITYSSFCPPDDLDRLGLGVKSSFYAODARLWEIIRYVVGIV 478  
 Db 421 TGGGGHLDLLKQAGAFITYSSFCPPDDLAERGLDIDTCFYAKDALRLWQIMNRYVVGIFN 480  
 QY 479 SLHYKTDVAKDDPELQIETWCREITTEIGLOAQDRGFPVSLQARDQVCHFWTWCIFCTCQH 538  
 Db 481 DLYYKTDQAVQDDYELQSWCREITTEIGLOAQDRGFTSLQSPAQACYFITWCIFCTTAQ 540  
 QY 539 HASVHLGOLDWYSWVPNAPCTMRLPPTTKDATLETVMATLPNFHQAQSLQMSITWOLGRR 598  
 Db 541 HSSVHLGOLDWYFVWVNPACTMRLPPTTKDATLETVMATLPNFHQAQSLQMSITWOLGRR 600





XX WO2004058052-A2.  
 XX 15-JUL-2004.  
 XX 22-DEC-2003; 2003WO-US040978.  
 XX 20-DEC-2002; 2002US-0434778P.  
 XX 10-MAR-2003; 2003US-0453135P.  
 XX 30-APR-2003; 2003US-0466412P.  
 XX 23-SEP-2003; 2003US-0504955P.  
 XX (APPL-) APPLERA CORP.  
 XX Cargill M, Devlin JJ, Iakoubova O;  
 XX WPI; 2004-533949/51.  
 XX N-PSDB; ADQ39008.  
 XX Identifying an individual who has an altered risk for developing  
 PT myocardial infarction by detecting a single nucleotide polymorphism in  
 PT the individual's nucleic acids.  
 XX Claim 10; SEQ ID NO 1499; 145pp; English.  
 XX The invention relates to a novel method for identifying an individual who  
 CC has an altered risk for developing myocardial infarction. The method  
 CC comprises detecting a single nucleotide polymorphism (SNP) in any one of  
 CC the nucleotide sequences given in the specification in the individual's  
 CC nucleic acids, where the presence of the SNP is correlated with an  
 CC altered risk for myocardial infarction in the individual. The invention  
 CC further comprises: an isolated nucleic acid molecule comprising at least  
 CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
 CC the specification or its complement and encoding any one of the amino  
 CC acid sequences given in the specification; an isolated polypeptide  
 CC comprising an amino acid sequence given in the specification; an antibody  
 CC that specifically binds to the polypeptide or its antigen-binding  
 CC fragment; an amplified polynucleotide containing an SNP given in the  
 CC specification and which is between about 16 and 1000 nucleotides in  
 CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
 CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
 CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
 CC method for identifying an agent useful in treating or preventing  
 CC myocardial infarction. The novel detection method has cardiant activity.  
 CC The nucleic acids of the invention may be used in gene therapy. The  
 CC method is useful in identifying an individual who has an increased or  
 CC decreased risk for developing myocardial infarction and for preparing a  
 CC composition for treating or preventing myocardial infarction. This  
 CC sequence represents the protein of a human myocardial infarction-  
 CC associated gene containing one or more SNPs of the invention. Note: This  
 CC sequence was not shown in the specification. The sequence has come from  
 CC an electronic sequence listing downloaded from the WIPO website.  
 XX Sequence 563 AA;  
 SQ  
 Query Match 65.9%; Score 2316; DB 8; Length 663;  
 Best Local Similarity 65.5%; Pred. No. 1.6e-230;  
 Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;  
 QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVQGHGAALGKRLWPARG-ETELKVEVEYLGPL 59  
 DB 1 MGRYRIRVATGAWLFGSGYRNQVQLWLVGTRGAELEQLRPARGBEEFDHDAEDLGL 60  
 QY 60 LFLVLRKRLKDDAWFCNWLISVQSGAGDEVRFPFCYRWEGNVLSPGEGTRVGRDGP 119  
 DB 61 QFVRLKRLHVLVDDAWFCORITVQSGACAEVAFPCYRWQGEDILSLPEGTARLPDGA 120  
 QY 120 QGLFQKREELERKLYRMGNWKGILNAGAKLYDLPVDERFLDKRVDVEVSLAK 179  
 DB 121 LDMFQKREKELKDRQYICWATWKEGLPLTIAADRKDDLPPNMFHEEKLDFEWTLKA 180  
 QY 180 GLADIAIKDNLVTCWKDLDLDFNIFWCGSGKLAERVRDWSKEDALLFGYQFLNGANPV 239  
 XX

DB 181 GALEWALKRVYVTLSSWNCLDEPDQIFWGQKSALEAKVRQCMQDDELFSYQFLNGANPWL 240  
 QY 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGOTLFEADFSLLDGIKANVILCSQOHLAAPL 299  
 DB 241 LRRSTSLPSRLVLPSPGMEELQAQLEKELEGOTLFEADFSLLDGIKANVIRGEKQYLAAPL 300  
 QY 300 VMLKLOPDGKLLPMVIOQLPRTGSPPPPLPDTDPMAWLLAKCWVRSSDFQLHQLQSH 359  
 DB 301 VMLKMEENGKLPQVVIQIQPNPSSPTTLPSPDPPLAWLLAKSWVRNSDFQLHEIQYH 360  
 QY 360 LLRGLHMAEVIVVATMRLCLPSIHPFKLIIPLHRYTLEINVRARTGLVSDMGIFDQIMST 419  
 DB 361 LLNTHLVAEVIATVATMRLCLPGLHPIFKFLPHIRYTWMEINTRANTQLISDGGIPDKAVST 420  
 QY 420 GGGHVQLLQOAGAFLYTSFPCPPDDLADRGLLGVKSSFYAQDALRLWEIIRYVVEGIVS 479  
 DB 421 GGGHVQLLRRRAAQLTYCSLCPDDDLADRGLLGALYAHDAHLRLWEIIRYVVEGIVH 480  
 QY 480 LHYKTDVAVKDDPELQWTCREITEIGLQAGDRGFPVSLQARDQVCHPVTWCIFTCTGQH 539  
 DB 481 LFYRDDIVKGDPELQWTCREITEVGLCAQDRGFPVFSQSQCCHFTWCVFTCTAQH 540  
 QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPPTTK-DATLETVMATLNFHQASLQMSITWQLGRR 598  
 DB 541 AAINQGLDWYAVVPNAPCTMRLPPPTTKEDVTWATVWGS�PDVROACLQMAISWHLSSR 600  
 QY 599 QPVMVAVQHEEYFSGPEPKAVLKFREEALADKXIEIRNAKLDMPEYILRPSVWENS 658  
 DB 601 QPDMVPLGHKKEKYFSGPKAVLNQFRTOLEKLEITARNEQLDMDPEYILKPSCIENS 660  
 QY 659 VAI 661  
 DB 661 VTI 663  
 RESULT 11  
 ADS10679  
 ID ADS10679 standard; protein; 647 AA.  
 AC ADS10679;  
 DT 16-DEC-2004 (first entry)  
 XX Human therapeutic protein - SEQ ID 916.  
 DE antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;  
 KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;  
 KW aplastic anaemia; cancer; wound healing; gene therapy.  
 XX Homo sapiens.  
 OS WO2004080148-A2.  
 PN 23-SEP-2004.  
 PD 30-SEP-2003; 2003WO-US030720.  
 PF 02-OCT-2002; 2002US-0416186P.  
 PR (NUVE-) NUVELO INC.  
 PA Tang YT, Asundi V, Ren F, Zhang J, Zhang J, Wehrman T, Wang Z, Ma Y; Zhou P;  
 PI Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;  
 XX WPI; 2004-668857/65.  
 DR N-PSDB; ADS09995.  
 XX New polynucleotide, useful in preparing a composition for diagnosing or  
 PT treating inflammatory, neurodegenerative or stem cell disorders, e.g.,  
 PT aplastic anemia or cancer for promoting wound healing.  
 XX Claim 20; SEQ ID NO 916; 718pp; English.  
 XX

CC The invention relates to a novel isolated polynucleotide and the encoded  
CC polypeptide. The molecules of the invention demonstrate antiinflammatory,  
CC neuroprotective, antianemic, cytostatic and vulnerary activities and may  
CC be useful in preparing a composition for diagnosing or treating  
CC inflammatory, haematopoietic, immune, neurodegenerative or stem cell  
CC disorders, such as aplastic anemia or cancer, as well as for promoting  
CC wound healing. The molecules may also be utilised during gene therapy  
CC procedures. The current sequence is that of a human therapeutic protein  
CC of the invention. The current sequence is not shown explicitly within the  
CC specification but can be accessed from the WIPO web-site.

XX  
SQ Sequence 647 AA;

Query Match 65.4%; Score 2298.5; DB 8; Length 647;  
Best Local Similarity 67.8%; Pred. No. 1e-228;  
Matches 442; Conservative 83; Mismatches 120; Indels 7; Gaps 6;

QY 1 MGLYRIRVSTGASLYAGSNQVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 59  
DB 1 MGKYTRVATGDLALLAGSPNLVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 60  
QY 60 LFVKLRKHLLKDDAWFCNWIISVQPGAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 119  
DB 61 LMVKLRKHVLLSLDMFCNWIISVQPGAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 120  
QY 120 QGLFQKHREELERKLYRNKGNWKGDLILNMGAKLYDLPVDERFLEDKRVDPEVSLA 178  
DB 121 QNLFKYRQELERKLYRNKGNWKGDLILNMGAKLYDLPVDERFLEDKRVDPEVSLA 180  
QY 179 KGLADLAIKDSLNLVLCWKDLDNFNIFWCGOSKLAERVRDSWKEDALFGYQFLNGANPV 238  
DB 181 KG-DLAIKGTLDLFNCVRLDEPKIPPHGKTVLAERVYDSWKNDAPFGYQFLNGANPV 238  
QY 239 VLRSAPHLPARLVPPGMELOAQLEKEGTLFEADPSLIDGKIKANVILCSQOHLAAP 298  
DB 239 LLRCSRLPACLVPPGMELOAQLEKEGTLFEADPSLIDGKIKANVILCSQOHLAAP 298  
QY 299 LVMLKLPDQKLLPMVLIQOLPRTGSPPLFLPTDPPMAWLLAKWVRSSDFQLHELQS 358  
DB 299 LVMLKLPDQKLLPMVLIQOLPRTGSPPLFLPTDPPMAWLLAKWVRSSDFQLHELQS 357  
QY 359 HLLRGHLMAEVIVATMRCLPSIHPIFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMS 418  
DB 358 HLLRGHLMAEVIVATMRCLPSIHPIFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMS 417  
QY 419 TGGGHVQLLKQAGAFITVSSCPDDIADRLGLGVKSSFYAQDALRLWEIIVRYVEGIV 478  
DB 418 TGGGHVQLLKQAGAFITVSSCPDDIADRLGLGVKSSFYAQDALRLWEIIVRYVEGIV 476  
QY 479 SLHYKTDVAVKDDPELOTWCRETTEIGLQAGDORGFVSLQARDQVCHFTVTCIFCTGQ 538  
DB 477 GLFYNSDQAMKDDLEQANCREWTEGLQADQGFLLSLESAQLCHFTVTCIFCTGQ 536  
QY 539 HASVHLGQLDWYSWVFNAPCTMLRPLPTTKDATLETWATLPNFHQAQSLQMSITWLQGR 598  
DB 537 HASNHLGQLDWYSWVFNAPCTMLRPLPTTKDATLETWATLPNFHQAQSLQMSITWLQGR 596  
QY 599 QPVMVAVGQHEEYFSGPPKAVLKFKFREBELAALDKIEIRNAKLDMPYEYL 650  
DB 597 QPVMVR-SKHEEKYFSGPPKAVLKFKFREBELAALDKIEIRNAKLDMPYEYL 647

RESULT 12  
AAB24019  
ID AAB24019 standard; protein; 663 AA.

XX AAB24019;  
XX AAB24019;  
XX AAB24019;  
DT 25-JAN-2001 (first entry)  
DE Arachidonic acid metabolism related protein sequence #653.  
XX Human; biallelic marker; arachidonic acid metabolism; genotyping;

KW detection; hybridisation; phenotype; haplotype; SNP; polymorphic base;  
KW single nucleotide polymorphism; hybridisation assay; sequencing assay;  
KW specific amplification assay; identification; ERM; 12-LO-RBM;  
XX eicosanoid-related biallelic marker; 12-LO-related biallelic marker.

OS Homo sapiens.

XX WO200047771-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-1B000184.

XX 12-FEB-1999; 99US-0119917P.

XX 23-MAR-1999; 99US-00275267.

XX 07-MAY-1999; 99US-0133200P.

XX (GEST ) GENSET.

XX Blumenfeld M, Bougueleret L, Chumakov I;

XX WPI; 2000-571881/53.

XX N-PSDB; AAC58018.

PT Novel biallelic markers useful for detecting conditions and genotypes  
associated with arachidonic acid metabolism.

PS Claim 75; Page 800-801; 802pp; English.

XX The present invention describes polynucleotides including biallelic  
markers derived from genes involved in arachidonic acid metabolism and  
from genomic regions flanking those genes. Methods from the present  
invention may be used to select individuals for clinical trials and  
predict responses to treatment with drugs. The polynucleotides may be  
used in hybridisation assays, sequencing assays and specific  
amplification assays for identifying an eicosanoid-related biallelic  
segment of nucleotides containing an ERM. The polynucleotides are useful  
in diagnostic kits. The markers may be used to detect conditions and  
genotypes associated with arachidonic acid metabolism. AAC57367 to  
AAC58018 and AAB24019 and AAB24020 represent sequences used in the  
exemplification of the present invention

XX Sequence 663 AA;

Query Match 64.9%; Score 2280; DB 3; Length 663;  
Best Local Similarity 64.7%; Pred. No. 8.e-227; Indels 2; Gaps 2;  
Matches 429; Conservative 92; Mismatches 140;

QY 1 MGLYRIRVSTGASLYAGSNQVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 59  
DB 1 MGKYTRVATGDLALLAGSPNLVQLMVLVGHGSAALGKRLMPARG-ETELKVEVPYLGPL 60

QY 60 LFVKLRKHLLKDDAWFCNWIISVQPGAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 119  
DB 61 QPVLRLKHVLLSLDMFCNWIISVQPGAGDEVRFCYRWVEGNGVLSLPEGTGRTVGEDP 120

QY 120 QGLFQKHREELERKLYRNKGNWKGDLILNMGAKLYDLPVDERFLEDKRVDPEVSLA 179  
DB 121 LDMFKHREELERKLYRNKGNWKGDLILNMGAKLYDLPVDERFLEDKRVDPEVSLA 180

QY 180 GLADLAIKDSLNLVLCWKDLDNFNIFWCGOSKLAERVRDSWKEDALFGYQFLNGANPV 239  
DB 181 GALEVALXXVYVTLSSWNCLEDFDQIFWQKSALEKVRQCQWDXELFSYQFLNGANPV 240

QY 240 LRSAPHLPARLVPPGMELOAQLEKEGTLFEADPSLIDGKIKANVILCSQOHLAAP 299  
DB 241 LRSAPHLPARLVPPGMELOAQLEKEGTLFEADPSLIDGKIKANVILCSQOHLAAP 300

QY 300 VMLKLPDQKLLPMVLIQOLPRTGSPPLFLPTDPPMAWLLAKWVRSSDFQLHELQS 359  
DB 301 VMLKLPDQKLLPMVLIQOLPRTGSPPLFLPTDPPMAWLLAKWVRSSDFQLHELQS 360

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QY 360 LLRGLHMAEVIVATMRCLPSIHPIFKLIIPHLRYTLINVRARTGLVSDMGIFDQIMST 419
DB 361 LLNTHLVAEVIVATMRCLPGLHPFKFLPHIRYTMETRARTQLISDGGIFDKAVST 420
QY 420 GGGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAQDALRLWEIIRYVVEGIVS 479
DB 421 GGGGHVQLLRRAAQITVCSLCPPDDADRGLLGLPGALYAHADALRLWEIIRYVVEGIVH 480
QY 480 LHYKTDVAVKDDPELOTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQH 539
DB 481 LFYQRDDIVKGDPELQACWREITEVGLCOAQDRGFPVSLQARDQVCHFTVTCIQH 540
QY 540 ASVHLGOLDWYSWPNACTWRLPPTTK-DATLETVMATLNPFOASLQMSITWQLGRR 598
DB 541 AAINQGOLDWYAWPNAPCTWRMPPTTKXEDVTATVNGSLPDRQACLOMAISHLSRR 600
QY 599 QPVMVAVGQHEEYFSGPEKAVLKPFREELAAIDKEIERNAKLDMPEYLRPSVWENS 658
DB 601 QPDMVPLGHHKEKYPGPKAVLNQFRITDLEKEITARNEQOLDWYEVILKPSCIENS 660
QY 659 VAI 661
DB 661 VTI 663

RESULT 13
ADSI11946
ID ADSI11946 standard; protein; 632 AA.
XX
AC ADSI11946;
XX
DT 16-DEC-2004 (first entry)
DE Human therapeutic contig protein - SEQ ID 2183.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
FT Misc-difference 1..632
FT /label= Unknown, OTHER
FT /note= "OTHER = In-frame STOP codon"
XX
XX WO2004080148-A2.
XX
PD 23-SEP-2004.
XX
PF 30-SEP-2003; 2003WO-US030720.
XX
PR 02-OCT-2002; 2002US-0416186P.
XX
XX (NUVE-) NUVELO INC.
XX
XX Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y;
XX Wang D, Chen R, Zhao QA, Wang J, Ghosh M, Xue AJ, Weng G, Zhou P;
XX
XX WPI; 2004-668957/65.
XX N-PSDB; ADSI1348.
XX
XX New polynucleotide, useful in preparing a composition for diagnosing or
XX treating inflammatory, neurodegenerative or stem cell disorders, e.g.,
XX aplastic anemia or cancer for promoting wound healing.
XX
XX Example 2; SEQ ID NO 2183; 718pp; English.
XX
XX The invention relates to a novel isolated polynucleotide and the encoded
XX polypeptide. The molecules of the invention demonstrate antiinflammatory,
XX neuroprotective, antianaemic, cytostatic and vulnerary activities and may
XX be useful in preparing a composition for diagnosing or treating
XX inflammatory, haematopoietic, immune, neurodegenerative or stem cell
```

```
CC disorders, such as aplastic anaemia or cancer, as well as for promoting
CC wound healing. The molecules may also be utilised during gene therapy
CC procedures. The current sequence is that of a human therapeutic contig
CC protein of the invention.
XX
XX Sequence 632 AA;
SQ
Query Match 63.5%; Score 2230.5; DB 8; Length 632;
Best Local Similarity 64.8%; Pred. No. 1.1e-221;
Matches 430; Conservative 80; Mismatches 119; Indels 35; Gaps 4;
QY 1 MGLYRIIVSTGASLYAGSNNOVLWLVGQHGEEAALGKRLWPARG-ETELKKEVEPEYLGPL 59
DB 1 MGKTVRVATGDLLLAGSPNLVQLWVGEEADLGKQLPPVWKEAEFEIDVPLHLGRL 60
QY 60 LFLVKLRHLKDDAWFCNMTISVQPGAGDVRFPFCYRWVEGNGVLSLPEGTGRTVSDP 119
DB 61 LMVVKLRHNVLLSDWFCMKMISVQPGTQGAFFPCYRWVQGHGIIICPEGT----- 112
QY 120 QGLFQKREBELEERRKLYRWGNWKDGLILNMAKALYDLVDERFLEDKRVDFEVSIAK 179
DB 113 -----RWGSKWKGILLPFIAGNRQPDLPDRERFLEDKOLDNFVSLAK 153
QY 180 GLADLAIKDSLNLVLTCKWLDLDFNRIFWCGQSCLAERVDSWKEDALFGYQFLNGANPVV 239
DB 154 GKDLALIKGTLDIFNCVRLEDFKKIPHGKTVLAERVYDSWKNDADFFGYQFLNGANPML 213
QY 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGGTFLFEADFSLLDGIKANVILCSQQHLAAPL 299
DB 214 LRCSRLPACILVLPFGMEDLKTQLEKELOAGSLFEVDLSLDGKPNVLIIFKQOCVAAAPL 273
QY 300 VMLKLQPDGKLLPMVIOQLPRTGSPPPPLPLPTDPPMAWLLKACWVRSSDFQLHELOSH 359
DB 274 VVLKLQPDGKLLPMVIOQLPRTGSPPPPLPLPSHPPMAWLLKATWVRSSDFQLQLOSH 333
QY 360 LLRGLHMAEVIVATMRCLPSIHPIFKLIIPHLRYTLINVRARTGLVSDMGIFDQIMST 419
DB 334 LLRGLHMAEVIVATMRCLPSIHPIFKLIIPHLRYTMAINTLAQSSLSVSEWGFIDLVVST 393
QY 420 GGGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAQDALRLWEIIRYVVEGI 477
DB 394 GSGSHVDILQRAMACTYHSLCPDDADRGLLGVKSSFYCKDAIRLWGLISREXYVEGM 453
QY 478 VSLHYKTDVAVKDDPELOTWCREITEIGLQAGDRGFPVSLQARDQVCHFTVTCIQH 537
DB 454 VGLFYNSDQAMKDDLELQACWRETEGLQARQDQGGFLISLESRAQLCHFVTMCTICTG 513
QY 538 QHASVHLGOLDWYSWPNACTWRLPPTTKDATLETVMATLNPFOASLQMSITWQLGR 597
DB 514 QHASNHLGOLDWYSWIPNGPCTMQKPPISKDVTEKDIVDILLPNLHQARMOKTFTKFLGR 573
QY 598 RQPMVAVGQHEEYFSGPEKAVLKPFREELAAIDKEIERNAKLDMPEYLRPSVVEN 657
DB 574 RQPMV-----HEEKYFSGPEQAVLRQFQELASMDKEIEVRNAVILNLPCEYLXESMVEN 628
QY 658 SVAI 661
DB 629 SVTI 632

RESULT 14
ADSI11947
ID ADSI11947 standard; protein; 632 AA.
XX
AC ADSI11947;
XX
PT 16-DEC-2004 (first entry)
DE Human therapeutic contig protein - SEQ ID 2184.
XX
KW antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary;
KW inflammatory; haematopoiesis; immunity; neurodegenerative; stem cell;
KW aplastic anaemia; cancer; wound healing; gene therapy.
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2005, 21:41:37 ; Search time 111.649 Seconds  
(without alignments)  
3031.690 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLYRIRVSTGASLYAGSNN.....KLDMPYELRPSVSVNSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3498.5	99.6	661	1 LOX1_HUMAN	P16050 homo sapien
2	3085	87.8	662	1 LOXP_BOVIN	P27479 bos taurus
3	3054	86.9	662	1 LOXP_PIG	P16469 sus scrofa
4	2891	82.3	662	1 LOX1_RABIT	P12530 oryctolagus
5	2889	82.2	662	1 LOXP_RABIT	O19043 oryctolagus
6	2891	76.6	662	1 LOX2_RAT	O02759 rattus norv
7	2882	76.3	663	2 Q6PHB2	Q6phb2 mus musculus
8	2671	76.0	662	1 LOXL_MOUSE	P39654 mus musculus
9	2352.5	66.9	662	1 LOXE_MOUSE	P55249 mus musculus
10	2350.5	66.9	662	2 Q91YW6	Q91yw6 mus musculus
11	2312	65.8	663	2 Q6ISF8	Q6isf8 homo sapien
12	2310	65.7	662	1 LOXP_HUMAN	P18054 homo sapien
13	2258	64.3	663	2 QBHG4	Q8bhg4 m mus muscu
14	2247	63.9	662	1 LOXP_MOUSE	P39655 mus musculus
15	1905.5	54.2	555	2 Q95103	Q95103 bos taurus
16	1442	41.0	670	2 Q7T2A9	Q7t2a9 brachydanio
17	1298.5	37.0	673	1 LOX5_MOUSE	P48999 mus musculus
18	1297.5	36.9	673	1 LOX5_HUMAN	P09917 homo sapien
19	1290	36.7	672	1 LOX5_RAT	P12527 rattus norv
20	1271	36.2	672	1 LOX5_MESAU	Q8c587 mus musculus
21	1255.5	35.7	390	2 Q8C587	Q8c587 mus musculus
22	1213.5	34.5	686	2 Q6GJ24	Q6gj24 xenopus lae
23	1203.5	34.2	676	2 Q81YQ2	Q81yq2 homo sapien
24	1202.5	34.2	676	1 LX1B_HUMAN	O15296 homo sapien
25	1198.5	34.1	667	2 Q9XT59	Q9xt59 bos taurus
26	1184	33.7	677	1 LX1B_MOUSE	Q35936 mus musculus
27	1153	32.8	711	1 LX3_HUMAN	Q9byj1 homo sapien
28	1150	32.7	711	1 LX3_MOUSE	Q9wv07 mus musculus
29	1143	32.5	677	2 Q84F2	Q84f2 rattus norv
30	1124	32.0	701	1 LOXR_HUMAN	Q75342 homo sapien
31	1113	31.7	234	2 Q6SYC4	Q6syc4 bos taurus

32	1093	31.1	701	1 LOXR_MOUSE	O70582 mus musculus
33	947	26.9	238	2 Q64042	Q64042 rattus sp.
34	863.5	24.6	1066	1 AOSL_PLEHO	O16025 plexaura no
35	816.5	23.2	430	2 Q9BEG3	Q9beg3 bos taurus
36	522.5	14.9	917	2 Q9CAG3	Q9cag3 arabidopsis
37	508	14.5	922	2 Q93YA9	Q93ya9 sebania ro
38	502.5	14.3	565	2 Q82V62	Q82v62 nitrosomona
39	500.5	14.2	896	1 LX23_HORVU	Q8gsm2 hordeum vul
40	498.5	14.2	133	2 Q9UQM4	Q9uqm4 homo sapien
41	497	14.1	912	2 Q9LQJ5	Q9lqj5 arabidopsis
42	497	14.1	919	2 Q9LNR3	Q9lnr3 arabidopsis
43	497	14.1	919	2 Q9SMW1	Q9smw1 arabidopsis
44	496.5	14.1	865	2 Q93W22	Q93w22 gossypium h
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#### ALIGNMENTS

#### RESULT 1

ID LOX1\_HUMAN STANDARD; PRT; 661 AA.  
AC P16050; Q8N6R7; Q99657;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Arachidonate 15-lipoxygenase (EC 1.13.11.33) (Arachidonate omega-6  
DE lipoxygenase) (15-LOX).  
GN Name=ALOX15; Synonyms=LOG15;  
OS Homo sapiens (Human)  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
RX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
EX MEDLINE=89076270; PubMed=3202857;  
RA Sigal E., Craik C.S., Highland E., Grumberger D., Costello L.L.,  
RA Dixon R.A.F., Nadel J.A.;  
RT "Molecular cloning and primary structure of human 15-lipoxygenase.";  
RL Biochem. Biophys. Res. Commun. 157:457-464(1988).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Kritzik M.R., Zlobner A.F., Sigal E., Conrad D.J.;  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A., AND VARIANTS HIS-89; LYS-102 AND GLN-204.  
RA Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,  
RA Rajkumar N., Yi Q., Nickerson D.A.;  
RT "SeattlesNPS. NHLBI HL66682 program for genomic applications, UW-  
FHCRRC, Seattle, WA (URL: http://pga.gs.washington.edu).";  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain, and Lung;  
RX MEDLINE=22382625; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strauberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
FAhey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [5]  
 RP SEQUENCE OF 1-45 FROM N.A.  
 RX MEDLINE=98363633; PubMed=9700053; DOI=10.1023/A:1006813009006;  
 RA Kelavkar U.; Wang S.; Montero A.; Murrigh J.; Shah K.; Badr K.;  
 RT "Human 15-lipoxygenase gene promoter: analysis and identification of  
 RT DNA binding sites for IL-13-induced regulatory factors in monocytes.";  
 RL Mol. Biol. Rep. 25:173-182 (1998).  
 RN [6]  
 RP SEQUENCE OF 1-15.  
 RX MEDLINE=89186828; PubMed=3356688;  
 RA Sigal E.; Grumberger D.; Craik C.S.; Caughey G.H.; Nadel J.A.;  
 RT "Arachidonate 15-lipoxygenase (omega-6 lipoxygenase) from human  
 RT leukocytes. Purification and structural homology to other mammalian  
 RT lipoxygenases.";  
 RL J. Biol. Chem. 263:5328-5332 (1988).  
 RN [7]  
 RP SEQUENCE OF 1-30; 37-44; 156-167 AND 625-630.  
 RX TISSUE=Eosinophil, and Leukocyte;  
 RA MEDLINE=92111501; PubMed=1662607;  
 RA Izumi T.; Raadmark O.; Joernvall H.; Samuelsson B.;  
 RT "Purification of two forms of arachidonate 15-lipoxygenase from human  
 RT leukocytes.";  
 RL Eur. J. Biochem. 202:1231-1238 (1991).  
 RN [8]  
 RP MUTAGENESIS OF MET-417.  
 RX MEDLINE=92049779; PubMed=1944593; DOI=10.1038/354149a0;  
 RA Sloane D.L.; Leung R.; Craik C.S.; Sigal E.;  
 RT "A primary determinant for lipoxygenase positional specificity.";  
 RL Nature 354:149-152 (1991).  
 CC -!- FUNCTION: Converts arachidonic acid to 15S-  
 CC hydroperoxyicosatetraenoic acid. Also acts on C-12 of  
 CC arachidonate as well as on linoleic acid.  
 CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,11Z,13E)-(15S)-  
 CC 15-hydroperoxyicoso-5,8,11,13-tetraenoate.  
 CC -!- COFACTOR: Iron.  
 CC -!- PATHWAY: Leukotrienes biosynthesis.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the lipoxygenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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 DR EMBL; M23892; AAA36182.1; -;  
 DR EMBL; U88317; AAB49305.1; -;  
 DR EMBL; AY051111; AAR84235.1; -;  
 DR EMBL; BC029032; AAB29032.1; -;  
 DR EMBL; U63384; AAC52118.1; -;  
 DR PIR; A31349; A31349.  
 DR HSSP; P12530; ILOX.  
 DR Genew; HGNC:433; ALOX15.  
 DR H-InvDB; HIX0013446; -;  
 DR MIM; 152392; -;  
 DR GO; GO:0016165; F:lipoxygenase activity; TAS.  
 DR GO; GO:0006954; P:inflammatory response; TAS.  
 DR InterPro; IPR000907; Lipoxygenase.  
 DR InterPro; IPR001024; Lipoxygenase\_LH2.  
 DR InterPro; IPR001885; Mam\_lipoxygenase.  
 DR Pfam; PF00305; Lipoxygenase\_1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00467; MAMLIPOXGNASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS50095; PLAT; 1.

Dioxygenase; Direct protein sequencing; Iron;  
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 FT METAL 364 364 Iron (By similarity).  
 FT METAL 539 539 Iron (By similarity).  
 FT METAL 661 661 Iron (By similarity).  
 FT VARIANT 89 89 D -> H.  
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 FT VARIANT 102 102 N -> K.  
 FT /FTID=VAR\_018747.  
 FT VARIANT 204 204 R -> Q.  
 FT /FTID=VAR\_018748.  
 FT MUTAGEN 417 417 M->V: Catalyzes 15- and 12-  
 FT lipoxygenation.  
 FT CONFLICT 45 45 E -> V (in Ref. 5).  
 FT CONFLICT 460 460 A -> P (in Ref. 4).  
 FT SEQUENCE 661 AA; 74673 MW; 1A4B9087DB11B130 CRC64;  
 Query Match 99.6%; Score 3498.5; DB 1; Length 661;  
 Best Local Similarity 99.8%; Pred. No. 8.4e-265;  
 Matches 660; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 QY 2 GLYRIRVSTGASLYAGSNQVQLMLVGQHGAAALGKRLWPARG-ETELKVEVPEYLGPLL 60  
 DB 1 GLYRIRVSTGASLYAGSNQVQLMLVGQHGAAALGKRLWPARGKETELKVEVPEYLGPLL 60  
 QY 61 FVKLRKRLHLLKDDAWFCNWSVQGGAGDEVPFCYRWVEGVNLSLPGTGRTVGEDPQ 120  
 DB 61 FVKLRKRLHLLKDDAWFCNWSVQGGAGDEVPFCYRWVEGVNLSLPGTGRTVGEDPQ 120  
 QY 121 GLFQGHREEELEERKLYRWGNWKGDLINMAGAKLYDLVDERFLEKRVDFEYSLAKG 180  
 DB 121 GLFQGHREEELEERKLYRWGNWKGDLINMAGAKLYDLVDERFLEKRVDFEYSLAKG 180  
 QY 181 LADLAIKDSLNLVTCWKDLDDFNRIFWCQSKLAERVDSWKEDALFGYQFLNGANPVVL 240  
 DB 181 LADLAIKDSLNLVTCWKDLDDFNRIFWCQSKLAERVDSWKEDALFGYQFLNGANPVVL 240  
 QY 241 RRSALHPARLVPPPGMEELQAQLEKELEGGTTFEADFSLLDGIKANVLCSQQHAAPLV 300  
 DB 241 RRSALHPARLVPPPGMEELQAQLEKELEGGTTFEADFSLLDGIKANVLCSQQHAAPLV 300  
 QY 301 MLKLPDQCKLLPMVLIQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHLSHL 360  
 DB 301 MLKLPDQCKLLPMVLIQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHLSHL 360  
 QY 361 LRGHLMAEVIVVATWRCPLSPHPIPKLIIPHLYTLEINVRARTGLVSDMGIFDQIMSTG 420  
 DB 361 LRGHLMAEVIVVATWRCPLSPHPIPKLIIPHLYTLEINVRARTGLVSDMGIFDQIMSTG 420  
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 DB 421 GGGHVQLLKQAGAFITYSSFCPPDDLADRLGLGVKSSFYAODALRLWEIYRYVGVLSL 480  
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 DB 481 HYKTDVAVKDDPELQWCREITEIGLQAGQDRGFVPSLQARDQVCHFVTCMCTCTGQHA 540  
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 DB 541 SVHLQGLDWYSWVPNAPCTMRLPPPTTKDATLETVMATLPNPHQASLQMSITWQLGRROP 600  
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 DB 601 VMVAVGOHEEYFSGPEPKAVLKKFREELALDKEIERNAKLDMPEYELRPSVVNSVA 660  
 QY 661 I 661  
 DB 661 I 661

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RESULT 2
ID LOXP BOVIN STANDARD; PRT; 662 AA.
AC P27479;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX).
GN Name=ALOX12;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Tracheal epithelium;
RX MEDLINE=92170942; PubMed=1539676;
RA de Marzo N., Sloan D.L., Dicharry S., Highland E., Sigal E.;
RT "Cloning and expression of an airway epithelial 12-lipoxygenase.";
RL Am. J. Physiol. 262:L198-L207(1992).
CC - FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.
CC - CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-
CC 12-hydroperoxyicoso-5,8,10,14-tetraenoate.
CC - COFACTOR: Iron.
CC - PATHWAY: Leukotrienes biosynthesis.
CC - SUBCELLULAR LOCATION: Cytoplasmic.
CC - SIMILARITY: Belongs to the lipoxygenase family.
CC - SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC -----
DR EMBL; M81320; AAA30346.1; -.
DR EMBL; M62516; AAC41614.1; -.
DR EMBL; S96247; AAB21522.2; ALT_SEQ.
DR PIR; S32825; S32825.
DR HSP; P12530; ILOX.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase LH2.
DR InterPro; IPR001885; Mam.lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF04777; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0 By similarity.
FT DOMAIN 1 114 PLAT.
FT METAL 360 360 Iron (By similarity).
FT METAL 365 365 Iron (By similarity).
FT METAL 540 540 Iron (By similarity).
FT METAL 662 662 Iron (By similarity).
SQ SEQUENCE 662 AA; 74910 MW; 09C6B7BE91133E61 CRC64;
Query Match 87.8%; Score 3085; DB 1; Length 662;
Best Local Similarity 86.1%; Pred. No. 1.9e-232;
Matches 570; Conservative 48; Mismatches 42; Indels 2; Gaps 2;
QY 2 GLYIRVSTGASLYAGSNQVWLVGQHGGAALGKRLWPARG-ETELKVEYPEYLGPLL 60
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DQ 1 GLYIRVSTGSGFCAGSNQVHMLVGEHGAALGWAVRARGKEVERQVDVSEYLGRL 60
QY 61 FVKLKRHLKDDAWFCNWISVQGGASGNEFRPCYRWVEGNSVLSLPEGTGRTVDDP 119
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Db 61 FVKLKRHLKDDAWFCNWISVQGGASGNEFRPCYRWVEGNSVLSLPEGTGRTVDDP 120
QY 120 QGLFKHREELERRKLYRGNWKGILNMGAKLYDLVPDERFLBDRKVDVFEVSLAK 179
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QY 240 LRRSAHLPARLVFPFGMBELQAQLEKELEGCTLFEADFSLDGKANKVILCSQQHAAAPL 299
DQ 241 LRRSVRLPARLEFPFGMGELQAQLEKELEGCTLFEADFSLDGKANKVILCTQYVAAPL 300
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QY 420 GGGGHVOLLKQAGAFVLTYSFPCPPDDADRGLLGVKSSFYAQDADLRLEWIIYRYVEGIVS 479
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DQ 541 SSTHLGQLDWTWVNPAPCTWRLPPPTTKDLETWMTATLNFHQASLQMSITWQLGRRQ 600
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RESULT 3
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AC P16469;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX).
GN Name=ALOX12;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
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RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Leukocyte; PubMed=2315307;
RX MEDLINE=90192763; PubMed=2315307;
RA Yoshimoto T., Suzuki H., Yamamoto S., Takai T., Yokoyama C.,
RA Tanabe T.;
RT "Cloning and sequence analysis of the cDNA for arachidonate 12-
RT lipoxygenase of porcine leukocytes.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:2142-2146(1990).
RN [2]
RP MUTAGENESIS.
RX MEDLINE=94137772; PubMed=8305485; DOI=10.1016/0005-2760(94)90234-8;
RA Suzuki H., Kishimoto K., Yoshimoto T., Yamamoto S., Kanai F.,
RA Ebina Y., Miyatake A., Tanabe T.;
RT "Site-directed mutagenesis studies on the iron-binding domain and the
RT determinant for the substrate oxygenation site of porcine leukocyte
RT arachidonate 12-lipoxygenase.";

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RT "Structure of the mRNA and of the gene coding for the rabbit erythroid  
RL 15-lipoxygenase.";   
RN Biomed. Biochim. Acta 49:S17-S24 (1990).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).  
RX MEDLINE=98069648; PubMed=9406550;  
RA Gillmor S.A., Villaseñor A., Fletcher R., Sigal E., Browner M.P.;  
RT "The structure of mammalian 15-lipoxygenase reveals similarity to the  
RT lipases and the determinants of substrate specificity.";  
RL Nat. Struct. Biol. 4:1003-1009 (1997).  
CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,11Z,13E)-(15S)-  
CC 15-hydroperoxyicoso-5,8,11,13-tetraenoate.  
CC -!- COFACTOR: Iron.  
CC -!- PATHWAY: Leukotrienes biosynthesis.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- SIMILARITY: Belongs to the lipoxygenase family.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
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CC -----  
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DR PDB; 1LOX; X-ray; @=1-662.  
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DR InterPro; IPR001024; Lipoxygenase\_LH2.  
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DR Pfam; PF01477; PLAT; 1.  
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DR PRINTS; PRO0467; MAMLIPOXGNASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00095; PLAT; 1.  
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FT METAL 662 662 Iron.  
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FT TURN 536  
FT HELIX 538  
FT TURN 545  
FT HELIX 547  
FT HELIX 554  
FT HELIX 573  
FT TURN 583  
FT TURN 596  
FT STRAND 605  
FT TURN 606  
FT HELIX 617  
FT TURN 643  
FT TURN 650  
FT TURN 651  
FT TURN 653  
FT STRAND 657  
SQ SEQUENCE 662 AA; 75178 MW; 92F99AF10E241B0A CRC64;

Query Match

82.3%; Score 2891; DB 1; Length 662;

Best Local Similarity 81.0%; Pred. No. 2.9e-217; Matches 536; Conservative 59; Mismatches 65; Indels 2; Gaps 2;			
Qy	2	GLYRVRVSTGASIVAGSNNOVLWVGQGEALGKRLWPARG-ETELKVEVPEYLGPLL	60
Db	1	GVYRVCVSTGASIVAGSNKVELWVGQGEVGLGSLRPNKKEEFKVNYSKYLGLL	60
Qy	61	FVKLRKRLHLLKDDAWFCNWSVQGPAG-DEVRFPCYRWVEGNGVLSLPEGTGRTVGDP	119
Db	61	FVRLRKKHFLKEDAWFCNWSVQALGAEDKYWFCYRWVVGQVQSLPVGTCITVGDP	120
Qy	120	QGLFQKHREELERKLYRWGNWQGLILNAGAKLYDLPVDERFLEDKRVDVEVSLAK	179
Db	121	QGLFQKHREELERKLYRWGNWQGLILNAGAKLYDLPVDERFLEDKRVDVEVSLAK	180
Qy	180	GLADLAIKDNLVITCKDLDDFNRIFWCGSKLAERVRDSWKEDALFCYQFLNGANPV	239
Db	181	GLAELALKNSLILAPWKTLDDFNRIFWCGSKLARVRDSWQEDSLFGYQFLNGANPML	240
Qy	240	LRRSAHLPARLVFPFGMEELQALEKELEGGTFLFADFSLLDGIKANVILCSQQHLAAPL	359
Db	241	LRRSVQLPARLVFPFGMEELQALEKELEGGTFLFADFSLLDGIKANVILCSQQHLAAPL	360
Qy	360	LRRGHLMARVIVVATMRCPLSPHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST	419
Db	361	LRRGHLMARVIVVATMRCPLSPHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST	420
Qy	420	GGGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALRLWELIYRYVEGIVS	479
Db	421	GGGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALRLWELIYRYVEGIVS	480
Qy	480	LHYKTDAVKDDPELTWCREITEIGLQAGQGRFPVSVLQARDQVCHFTVMCIFTCTGQH	539
Db	481	LHYKTDAVKDDPELTWCREITEIGLQAGQGRFPVSVLQARDQVCHFTVMCIFTCTGQH	540
Qy	540	ASVHLGOLDWYSVVRNAPCTMRLPPPTTKDATTLETVMATLPHFQASLQMSITWOLGRQ	599
Db	541	SSHLGOLDWFTVWVNPACTMRLPPPTTKDATTLETVMATLPHFQASLQMSITWOLGRQ	600
Qy	600	PVAVAVGOHEEYFSGPEPAVLKFRBELAALDKIEIRNAKLDMPYELRPSVVVENS	659
Db	601	PVAVAVGOHEEYFSGPEPAVLKFRBELAALDKIEIRNAKLDMPYELRPSVVVENS	660
Qy	660	AI 661	
Db	661	AI 662	
RESULT 5			
LOXP RABIT			
ID	LOXP RABIT	STANDARD;	PRT; 662 AA.
AC	O19043;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	05-JUL-2004 (Rel. 44, Last annotation update)		
DE	Arachidionate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX).		
GN	Names=ALOX12;		
OS	Oryctolagus cuniculus (Rabbit).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.		
OX	NCBI_TaxID=9986;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RP	MEDLINE=98263260; PubMed=9600854; DOI=10.1006/jmbi.1998.1737;		
RA	Berger M., Schwarz K., Thiele H., Reimann I., Huth A., Borngraeber S.,		
RA	Kuehn H., Thiele B.J.;		
RT	"Simultaneous expression of leukocyte-type 12-lipoxygenase and		
RT	reticulocyte-type 15-lipoxygenase in rabbits."		
RL	J. Mol. Biol. 278:935-948 (1998).		

CC	-!	FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.	
CC	-!	CAATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-	
CC	-!	12-hydroperoxyicoso-5,8,10,14-tetraenoate.	
CC	-!	COFACTOR: Iron.	
CC	-!	PATHWAY: Leukotrienes biosynthesis.	
CC	-!	SUBCELLULAR LOCATION: Cytoplasmic.	
CC	-!	SIMILARITY: Belongs to the lipoxygenase family.	
CC	-!	SIMILARITY: Contains 1 PLAT domain.	
CC	-!	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	-!	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	-!	the European Bioinformatics Institute. There are no restrictions on its	
CC	-!	use by non-profit institutions as long as its content is in no way	
CC	-!	modified and this statement is not removed. Usage by and for commercial	
CC	-!	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	-!	or send an email to license@isb-sib.ch).	
CC	-!	EMBL; 297654; CABL0746.1; -.	
CC	-!	HSP; P12530; LLOX.	
DR	InterPro; IPR000907; Lipoxygenase.		
DR	InterPro; IPR001024; Lipoxygenase LH2.		
DR	InterPro; IPR001885; Mam.lipoxygenase.		
DR	InterPro; IPR008976; PLAT_LH2.		
DR	Pfam; PF00305; Lipoxygenase; 1.		
DR	Pfam; PF01477; PLAT; 1.		
DR	PRINTS; PR00087; LIPOXYGENASE.		
DR	PRINTS; PR00467; MAMLOXYGENASE.		
DR	SMART; SM00308; LH2; 1.		
DR	PROSITE; PS00711; LIPOXYGENASE_1; 1.		
DR	PROSITE; PS00881; LIPOXYGENASE_2; 1.		
DR	PROSITE; PS00995; PLAT; 1.		
KW	Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.		
FT	INIT MET 0	By similarity.	
FT	DOMAIN 1	114	PLAT.
FT	METAL 360	360	Iron (By similarity).
FT	METAL 365	365	Iron (By similarity).
FT	METAL 540	540	Iron (By similarity).
FT	METAL 662	662	Iron (By similarity).
SQ	SEQUENCE 662 AA; 75102 MW; 48A780ED859F013E CRC64;		
Query Match 82.2%; Score 2889; DB 1; Length 662;			
Best Local Similarity 81.0%; Pred. No. 4.1e-217;			
Matches 536; Conservative 59; Mismatches 65; Indels 2; Gaps 2;			
Qy	2	GLYRVRVSTGASIVAGSNNOVLWVGQGEALGKRLWPARG-ETELKVEVPEYLGPLL	60
Db	1	GVYRVCVSTGASIVAGSNKVELWVGQGEVGLGSLRPNKKEEFKVNYSKYLGLL	60
Qy	61	FVKLRKRLHLLKDDAWFCNWSVQGPAG-DEVRFPCYRWVEGNGVLSLPEGTGRTVGDP	119
Db	61	FVRLRKKHFLKEDAWFCNWSVQALGAEDKYWFCYRWVVGQVQSLPVGTCITVGDP	120
Qy	120	QGLFQKHREELERKLYRWGNWQGLILNAGAKLYDLPVDERFLEDKRVDVEVSLAK	179
Db	121	QGLFQKHREELERKLYRWGNWQGLILNAGAKLYDLPVDERFLEDKRVDVEVSLAK	180
Qy	180	GLADLAIKDNLVITCKDLDDFNRIFWCGSKLAERVRDSWKEDALFCYQFLNGANPV	239
Db	181	GLAELALKNSLILAPWKTLDDFNRIFWCGSKLARVRDSWQEDSLFGYQFLNGANPML	240
Qy	240	LRRSAHLPARLVFPFGMEELQALEKELEGGTFLFADFSLLDGIKANVILCSQQHLAAPL	299
Db	241	LRRSVQLPARLVFPFGMEELQALEKELEGGTFLFADFSLLDGIKANVILCSQQHLAAPL	300
Qy	300	VMLKLPDQGLKPMVITQLOLPRGTGSPPLFLPTDPPMALLAKCWRVSSDQFQHLNASH	359
Db	301	VMLKLPDQGLKPMVITQLOLPRGTGSPPLFLPTDPPMALLAKCWRVSSDQFQHLNASH	360
Qy	360	LRRGHLMARVIVVATMRCPLSPHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST	419
Db	361	LRRGHLMARVIVVATMRCPLSPHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST	420
Qy	420	GGGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALRLWELIYRYVEGIVS	479



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Db 421 GGGHVVQLQAGAFITVRSFPPDDLADRGLLGVSEFYAQDALRLWEIISRYVQGLMG 480
Qy 480 LHYKTDVAVKDDPELOTWCRREITEIGLQAGQDRGFPVSLQARDQVCHFTVMCIPTCTGQH 539
Db 481 LYYKTDVAVKDDPELOTWCRREITEIGLQAGQDRGFPVSLQARDQVCHFTVMCIPTCTGQH 540
Qy 540 ASVHLGOLDWYSWVSNAPCTMRLPPTTKDLETVMATLNFHQASLOMSITWGLGRQ 599
Db 541 SSIHLGOLDWYSWVSNAPCTMRLPPTTKDLETVMATLNFHQASLOMSITWGLGRQ 600
Qy 600 PMVAVGQHEEYFSGPPEKAVLKFRLELAALDKIEIRNAKLDMPEYELRPSVVENS 659
Db 601 PMVPLGQHEEYFSGPPEKAVLKFRLELAALDKIEIRNAKLDMPEYELRPSVVENS 660
Qy 660 AI 661
Db 661 AI 662

RESULT 6
LOX2 RAT STANDARD; PRT; 662 AA.
ID AC LOX2 RAT STANDARD; PRT; 662 AA.
AD Q02759;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Arachidonate 12-lipoxygenase (BC 1.13.11.31) (12-LOX).
DN Name=ALOX12;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93185682; PubMed=8444196;
RA Watanabe T., Medina J.F., Haegstroem J.Z., Raadmark O.P.,
RA Samuelsson B.;
RT "Molecular cloning of a 12-lipoxygenase cDNA from rat brain.";
RL Eur. J. Biochem. 212:605-612(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pineal gland;
RX MEDLINE=94162305; PubMed=8117750; DOI=10.1016/0005-2760(94)90272-0;
RA Hada T., Hagiya H., Suzuki H., Arakawa T., Nakamura M., Matsuda S.,
RA Yoshimoto T., Yamamoto S., Azekawa T., Morita Y., Ishimura K.,
RA Kim H.Y.;
RT "Arachidonate 12-lipoxygenase of rat pineal glands: catalytic
properties and primary structure deduced from its cDNA.";
RL Biochim. Biophys. Acta 1211:221-228(1994).
CC -!- FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.
CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = [5Z,8Z,10E,14Z]-(12S)-
CC 12-hydroperoxyicoso-5,8,10,14-tetraenoate.
CC -!- COFACTOR: Iron.
CC -!- PATHWAY: Leukotrienes biosynthesis.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the lipoxygenase family.
CC -!- SIMILARITY: Contains 1 PLAT domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06040; AAA41532.1; -.
DR EMBL; S69383; AAB30132.1; -.
DR PIR; S30051; S30051.
DR HSP; P12530; ILOX2.
DR RGD; 70493; Alox12.
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DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR001024; Lipoxygenase_LH2.
DR InterPro; IPR001885; Mam_lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR PRINTS; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00881; LIPOXYGENASE_2; 1.
DR PROSITE; PS00895; PLAT; 1.
KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0
FT DOMAIN 1 114 PLAT.
FT METAL 360 360 Iron (By similarity).
FT METAL 365 365 Iron (By similarity).
FT METAL 540 540 Iron (By similarity).
FT METAL 662 662 Iron (By similarity).
FT CONFLICT 54 54 E -> G (in Ref. 2).
FT CONFLICT 370 370 L -> V (in Ref. 2).
SQ SEQUENCE 662 AA; 75260 MW; C0187FAA27FBBF38 CRC64;

Query Match 76.6%; Score 2691; DB 1; Length 662;
Best Local Similarity 74.5%; Pred. No. 1.3e-201;
Matches 493; Conservative 77; Mismatches 90; Indels 2; Gaps 2;

Qy 2 GLYIRVSTGSLVAGSNNQVLMVGHQGBAALKRLWPAR-GETELKVEVPEYLGPI 60
Db 1 GYIRVSTGSKVAGSNNVYLMVGHQGBAALKRLPCRDSEAFKVDVSEYLGPI 60
Qy 61 FVLRKRLHLLKDDAFCNWSVQGGP-AGDEVRFPCYRWEGNGLSLPEGTRTGEDP 119
Db 61 FVRQKHYLTDADFCNWSVQGGDQSGSEYFPCYRWQGRSLSLPEGTRTGEDP 120
Qy 120 QGLFQKREELERKLYRWGNWKGILNAGAKLYDLVDERFLEDKRVDVEVSLAK 179
Db 121 QGLFRKREELERSLYRWGNWKGSLNVAASISDLVDQRFREDKRIEFASQVI 180
Qy 180 GLADLAIKDSLNLVTCWKDDFNRIFCWGSGSKLAERVDSWKEDALFGYQLNGANPV 239
Db 181 GWMDTVNVFPINTVTCWKSLDDFNCVFKSGHTKMAERVRNSWKEDAFFGYQLNGANPV 240
Qy 240 LRRSHLPARLVFPFGMEELQALEKEGGTLFEADFSLLDGIKANVILCSQQHLA 299
Db 241 LKRSTCLPARLVFPFGMEKLAQNLKELQKGTLEADFFLLDGIKANVILCSQQYLA 300
Qy 300 VMLKLQPDGKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELO 359
Db 301 VMLKLPDQQLPPIAIQLPRTGSPPPPIPTSPDPMDWLLAKCWVRSSDLQLHELO 360
Qy 360 LLRGLHMAEVIWATMRCPLSIHPFIKLIIPHLRYLLEINVRARTGLVSDMGIFDQIM 419
Db 361 LLRGLHMAELPAVATMRCPLSVHPVFKLLVPHLLYTMELNVRARSDILSERGF 420
Qy 420 GGGHVVQLQAGAFITVRSFPPDDLADRGLLGVSEFYAQDALRLWEIISRYVQGL 479
Db 421 GGGHLLDLKQAGAFITVRSFPPDDLAERGLDICTCYAKDALRLWQIMRYVGMFN 480
Qy 480 LHYKTDVAVKDDPELOTWCRREITEIGLQAGQDRGFPVSLQARDQVCHFTVMCIPTCTGQH 539
Db 481 LHYKTDVAVKDDPELOTWCRREITEIGLQAGQDRGFPVSLQARDQVCHFTVMCIPTCTGQH 540
Qy 540 ASVHLGOLDWYSWVSNAPCTMRLPPTTKDLETVMATLNFHQASLOMSITWGLGRQ 599
Db 541 SSVHLGOLDWYSWVSNAPCTMRLPPTTKDLETVMATLNFHQASLOMSITWGLGRQ 600
Qy 600 PMVAVGQHEEYFSGPPEKAVLKFRLELAALDKIEIRNAKLDMPEYELRPSVVENS 659
Db 601 PMVPLGQHEEYFSGPPEKAVLKFRLELAALDKIEIRNAKLDMPEYELRPSVVENS 660
Qy 660 AI 661
Db 661 AI 662
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RESULT 7
Q6PHB2
ID Q6PHB2 PRELIMINARY; PRT; 663 AA.
AC Q6PHB2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Alox15 protein.
GN Name=Alox15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3, and FVB/N; TISSUE=Mammary tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner F.S., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Ziesberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywicki M.I., Skalak U., Smillius D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N-3; TISSUE=Mammary tumor;
RA Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;
RA Director MGC Project;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: Iron (By similarity).
CC -1- SIMILARITY: Belongs to the lipoygenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
DR EMBL; BC056625; AAH56625.1; -.
DR EMBL; BC081546; AAH81546.1; -.
DR GO; GO:0005506; F:iron ion binding; IEA.
DR GO; GO:0016165; F:lipoygenase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR GO; GO:0006691; P:leukotriene metabolism; IEA.
DR InterPro; IPR001547; Glyco_hydro_5.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR000907; Lipoygenase.
DR InterPro; IPR001024; Lipoygenase LH2.
DR InterPro; IPR001885; Mam_lipoygenase.
DR Pfam; PF00305; Lipoygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGNASE.
DR PRINTS; PR00467; MAMLIPOXGNASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.

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DR PROSITE; PS00095; PLAT; 1.
KW Dioxigenase; Oxidoreductase.
SQ SEQUENCE 663 AA; 75417 MW; 86D7AA8FD380C787 CRC64;

Query Match 76.3%; Score 2682; DB 2; Length 663;
Best Local Similarity 73.8%; Pred. No. 6.5e-201;
Matches 489; Conservative 80; Mismatches 92; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNNNOVLWVGQHGGAALGKRLWPAR-GETELKRVVPEYLGPL 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MGVRIRVSTGDSVYAGSNNNEVLWLGQHGSEASLGKLFRCNSEAEFKVDVSEYLGPL 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 60 LFKVLKRHLKDDAWFCNWSVQGP-AGDEVRFPCYRVWEGNVLSPEGTGRTVGSD 118
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 LFRVQKWHYLKEDAWFCNWSVQGPQGSSEYTFPCYRWVQGTSLNLPSTGCTVVD 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 119 PQGLFKHREEREERKLYRWGNWKGGLINMAGAKLYDLVPDERFELEDKEDVFEVSLA 178
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 SQGLFRNHREREERSLYRWGNWKGDTILNVAATSDLPVDQRFREKDKLEFEASOV 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 179 KGLADLAIKDSLNVLTCKWDLDDFNRIFCWGOSKLAERVRDSWKEDALFGYQFLNGANPV 238
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 LGTMDTVINFPKNTVTCNKLDDFNVYFKSGHTKWAERVNSWKEDAFPGYQFLNGANPM 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 239 VLRRSAHLPARLVFPFGMEELQAQLEKELEGTLFEADFSLLDGIKANVILCSQQHLAAP 298
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 VLKRSTCLPARLVFPFGMEKLAQQLDEELKKGTLFEADFFLLDGIKANVILCSQQYLAAP 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 299 LVMLKLQDQKLLPMVIOLOLPRTCSPPLPLPTDPPMAMLLAKCWVRSSDFOLHELQAS 358
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 301 LVMLKLQDQGLPLTAIOLELPKTSPPPIPTDPPMDMLLAKCWVRSSDLQLLHELQA 360
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 359 HLLRGLMAEVIVWATMRCPLSIHPIFKLIIPLHRYTLEINVRARTGLVSDMGIFDQIMS 418
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 361 HLLRGLVAEVAFAVATMRCPLSVHVFVKLLVPHLLYTWEINVRASDLISERGFDFKVM 420
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 419 TGGGHVQLLKQAQAFITYSSFCPPDDADRLGLLVKVSFYAQADLRRLWEIYRYVEGV 478
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 421 TGGGGHLLKQAQAFITYSSLCPPDDLAERGLLDDTCFYAKDALQLWQVNNRYVGNMF 480
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 479 SLHYKTDVAVKDDPHLOTWCREITIGLQAGDQRFVSVLQARDQVCHVTWCIFCTCGQ 538
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 481 DLYYKTDQAVDDYELQSWCQBITEIGLQAGDQRFVSVLQARDQVCHVTWCIFCTCGQ 540
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 539 HASVHLGOLDWYSWVNPACTMRLPPTTKDATTLETVMATLNFHQAISLQMSITWOLGRR 598
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 541 HSSIHLGQLDWFYVWNPACTMRLPPTTKDATMELMATLFPNPGSTLQINWVWMLGRR 600
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 599 QPVMVAVQGHSEEEYFSGPEPKAVLKFKFREELAAALDKEIERNKALDMPYEYLRPSVENS 558
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 601 QAVWVPLGQHSBEHFPNPEAKAVLKFKFREELAAALDKEIERNKSLDIPYEYLRPSLVENS 660
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 659 VAI 661
   |||
Db 661 VAI 663

RESULT 8
LOXL_MOUSE
ID LOXL_MOUSE STANDARD; PRT; 662 AA.
AC P39654;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Arachidonate 12-lipoxygenase, leukocyte-type (EC 1.13.11.31) (12-LOX).
GN Name=Alox12; Synonyms=Alox15;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6, and ICR; TISSUE=Spleen;

```

RA MEDLINE=94245713; PubMed=8188678;  
 RA Chen X.-S., Kurre U., Jenkins N.A., Copeland N.G., Funk C.D.;  
 RT "cDNA cloning, expression, mutagenesis of C-terminal isoleucine,  
 RT genomic structure, and chromosomal localizations of murine 12-  
 RT lipoxigenases.";  
 RN J. Biol. Chem. 269:13979-13987(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Macrophage;  
 RX MEDLINE=95110857; PubMed=7811740; DOI=10.1016/0005-2760(94)00199-9;  
 RA Freire-Moar J., Alavi-Nassab A., Ng M., Mulkins M., Sigal E.;  
 RT "Cloning and characterization of a murine macrophage lipoxigenase.";  
 RL Biochim. Biophys. Acta 1254:112-116(1995).  
 CC -!- FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.  
 CC Converts arachidonic acid to 12(S)-hydro(pero)xyeicosatetraenoic  
 CC acid (12-HPETE) and 15-hydro(pero)xyeicosatetraenoic acid in a 3:1  
 CC ratio. Converts as well linoleic acid to 13-hydro-  
 CC (pero)xyoctadecadienoic acid.  
 CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-  
 CC 12-hydroperoxyicoso-5,8,10,14-tetraenoate.  
 CC -!- COFATOR: Iron.  
 CC -!- PATHWAY: Leukotrienes biosynthesis.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: Found in pituitary and pineal glands as well  
 CC as leukocytes, kidney, aorta and small intestine.  
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U04331; AAA20658.1; -;  
 DR EMBL; L34570; AAA64930.1; -;  
 DR FIR; B54075; B54075.  
 DR HSSP; P12530; 1LOX.  
 DR MGD; MGI:87997; Alox15.  
 DR InterPro; IPR000907; Lipoxigenase.  
 DR InterPro; IPR001024; Lipoxigenase\_LH2.  
 DR InterPro; IPR001885; Mam\_lipoxigenase.  
 DR Pfam; PF00305; Lipoxigenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00467; MAMLIPOXGNASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.  
 FT INIT\_MET 0  
 FT DOMAIN 1 114  
 FT METAL 360 360 Iron (By similarity).  
 FT METAL 365 365 Iron (By similarity).  
 FT METAL 540 540 Iron (By similarity).  
 FT METAL 662 662 Iron (By similarity).  
 FT CONFLICT 36 36 K -> N (in Ref. 2).  
 FT CONFLICT 118 118 E -> Q (in Ref. 2).  
 FT CONFLICT 396 396 T -> N (in Ref. 2).  
 SQ SEQUENCE 662 AA; 75313 MW; 5C94965B30767C2C CRC64;

Query Match 76.0%; Score 2671; DB 1; Length 662;  
 Best Local Similarity 73.6%; Pred. No. 4.7e-200;  
 Matches 487; Conservative 80; Mismatches 93; Indels 2; Gaps 2;  
 2 GLYIRVSTGSLVAGSNVQVGLVGGHGAALGKRLWPAR-GTELKVPEVYLGPLL 60  
 1 GYIRVSTGSLVAGSNVNEVYLVGGHGAALGKRLWPAR-GTELKVPEVYLGPLL 60  
 61 FVLRKRHLKDDAWFCNWNISVQGGF-AGDEVRFPCYRWEGNGVLSLPEGTGRTVGSDP 119

Db 61 FVRVQKHYLKEDAWFCNWNISVQGGFSEYTFPCYRWVGGTSILNLPSTGCTVVEDS 120  
 Qy 120 QGLFQKREEREELEBRKLYRWGNWKGGLILNMAAGKLYDLVPDERFLEDKRVDREVSIAK 179  
 Db 121 QGLFNRHREEREELEBRKLYRWGNWKGGLILNMAAGKLYDLVPDERFLEDKRVDREVSIAK 180  
 Qy 180 GLADLAIKDSINVLTCWKDLDDFNRIFWCGSKLAERVRDSWKEDALRGYQFLANGANPVV 239  
 Db 181 GTMTVINFPKNTVTCWKSLDDFNYPKSGHTKWAERVRNSWKEDAFGYQFLANGANPMV 240  
 Qy 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGFTLEAFPSLLDGIKANVILCSQQHLAAPL 299  
 Db 241 LKRSTCLPARLVFPFGMEELQAQLEKELEGFTLEAFPSLLDGIKANVILCSQQHLAAPL 300  
 Qy 300 VMLKLPDQKGLPMVIQLPRTGSPPPPLPLPTDPPMAWLLAKCWVRSSPQLHELOSH 359  
 Db 301 VMLKLPDQGLPLTAIQLELPKGTSTPPPIFTPLDPPMDWLLAKCWVRSSDQLHELOAH 360  
 Qy 360 LLRGHLMAEVIVVATMRCCLPSIHDFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419  
 Db 361 LLRGHLVAEFAVATMRCCLPSVHFVFKLLVPHLLYTWEINVRASDLISERGFDFKVMST 420  
 Qy 420 GGGGHVOLLKQAGAFLLTVSSPCPPDDADRLGLGVKSSFYAODALRLWEIYRYVEGIVS 479  
 Db 421 GGGGHLLDLKQAGAFLLTVSSPCPPDDADRLGLGLDITCFYADALQLQVWNRVYVGMFD 480  
 Qy 480 LHYTVDVAVKDDPBLQTCREITBGLQGAQDRGFPVSLQARDQVCHFVTWCIFCTCQH 539  
 Db 481 LYYKTDQAVDDYELQSWCQBEITBGLQGAQDRGFPVSLQSAQAQCHITWCIFCTCAQH 540  
 Qy 540 ASVHLGQLDVYVWVNPAPCTWRLPPPTKATLETVMATLPNFHQASLQMSITWOLGRRQ 599  
 Db 541 SSIHLGQLDVYVWVNPAPCTWRLPPPTKATLETVMATLPNFHQASLQMSITWOLGRRQ 600  
 Qy 600 PMYAVAGHREHEEYSGPEPKAVLKKFREELAAALDKIEIRNAKMDPVEYLRPSVVENSV 659  
 Db 601 AMVPLGQHSSEHPNPEAKAVLKKFREELAAALDKIEIRNAKMDPVEYLRPSVVENSV 660  
 Qy 660 AI 661  
 Db 661 AI 662

RESULT 9  
 LOXE\_MOUSE STANDARD; PRT; 662 AA.  
 ID LOXE\_MOUSE STANDARD; PRT; 662 AA.  
 AC P55249;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Arachidonate 12-lipoxigenase, epidermal-type (EC 1.13.11.31) (12-LOX).  
 GN Name=Alox12e; Synonyms=Alox12-p82, Alox2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CS7BL/6 X 129/Sv; TISSUE=Epidermis;  
 RX MEDLINE=96394429; PubMed=8798535; DOI=10.1074/jbc.271.38.23338;  
 RA Funk C.D., Keeney D.S., Olliv E.H., Boeglin W.E., Braah A.R.;  
 RT "Functional expression and cellular localization of a mouse epidermal  
 RT lipoxigenase.";  
 RL J. Biol. Chem. 271:23338-23344(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129/Sv; TISSUE=Epidermis;  
 RX MEDLINE=96085100; PubMed=7492614; DOI=10.1016/0005-2760(95)00158-9;  
 RA van Dijk K.W., Steketee K., Havekes L., Frants R., Hofker M.;  
 RT "Genomic and cDNA cloning of a novel mouse lipoxigenase gene.";  
 RL Biochim. Biophys. Acta 1259:4-8(1995).  
 RN [3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=NMRI; TISSUE=Skin;  
 RX MEDLINE=9718602; PubMed=9037187; DOI=10.1016/S0014-5793(96)01517-7;  
 RA Kinzig A., Fuerstenberger G., Mueller F., Vogel S., Mueller-Decker K.,  
 RA Mincheva A., Lichtenberger P., Marks P., Krieg P.;  
 RT "Murine epidermal lipoxigenase (Aloxe) encodes a 12-lipoxygenase  
 isoform.";  
 RL FEBS Lett. 402:162-166(1997).  
 CC - CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-  
 CC 12-hydroperoxyicoso-5,8,10,14-tetraenoate.  
 CC - COFACTOR: Iron.  
 CC - PATHWAY: Leukotrienes biosynthesis.  
 CC - SUBCELLULAR LOCATION: Cytoplasmic (Potential).  
 CC - TISSUE SPECIFICITY: Epidermal.  
 CC - SIMILARITY: Belongs to the lipoxygenase family.  
 CC - SIMILARITY: Contains 1 PLAT domain.  
 CC - CAUTION: Was originally thought to be an arachidonate 8-  
 CC lipoxygenase and was called LOX8.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC  
 CC -----  
 DR EMBL; U19200; AAC52869.1; -  
 DR EMBL; U24181; AAC52324.1; -  
 DR EMBL; X99252; CAA67625.1; -  
 DR HSSP; P12530; ILOX.  
 DR MGI; MGI:1274790; Aloxi2e.  
 DR InterPro; IPR000907; Lipoxygenase.  
 DR InterPro; IPR001024; Lipoxygenase LH2.  
 DR InterPro; IPR001885; Mam\_lipoxygenase.  
 DR Pfam; PF00305; Lipoxygenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00467; MAMLIPOXYGNASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS50095; PLAT; 1.  
 KW Diorygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.  
 FT DOMAIN 2 114  
 FT METAL 360 360 Iron (By similarity).  
 FT METAL 365 365 Iron (By similarity).  
 FT METAL 540 540 Iron (By similarity).  
 FT METAL 662 662 Iron (By similarity).  
 FT CONFLICT 619 619 P -> A (in Ref. 2).  
 SQ SEQUENCE 662 AA; 75455 MW; D67768415BE988F7 CRC64;  
 Query Match 66.9%; Score 2352.5; DB 1; Length 662;  
 Best Local Similarity 66.5%; Pred. No. 3.9e-175;  
 Matches 438; Conservative 97; Mismatches 123; Indels 1; Gaps 1;  
 QY 4 YRIVSTGASLVAGSNVQVLVGVGHGAALCKRLWPARG-ETELKVEVPYVLGLLFFV 62  
 DB 4 YKILVATGVSFVAGSANVHLMLVGEHAGLQKRLPLGRKTELEVDVPLHGLLAV 63  
 QY 63 KLKRHLKDDAWFCNWNISVQGGAGDEVRFPCCYRWVGVNGVLSLPEGTGRTVGEDPQGL 122  
 DB 64 KLKQKGLLSDWFFCKSIITVQGGTQGEAFFPCYSWVQGGKETTICTLTGALKVTDQTNL 123  
 QY 123 FQKHREELERKRLRWGNKDKGLLNAGAKLYDLVDERFLEPKRVDVFEVSLAKGLA 182  
 DB 124 FRKYRQELERNRNVYRWGSWKLEGLPLTAGSTERDLPRNQRPMKDLDFSLSLVKELK 183  
 QY 183 DLIAKDLNLVLCWKDLDFNRIFWCGSKLAERVDKSWKEDALFGYQFLNGANPVVLR 242  
 DB 184 NFAIKGTLDVSVRQKLEDYQKVPHTKTALPERVAGSKWEDALFGYQFLNGANPMLRR 243  
 QY 243 SAHLPARLVFPQGMELQALEKELEGGTLFEADFSLLDGIKANVILCSQQLAAPLVML 302

DB 244 SMRLPARLVLPQGMEDVOTQLEKELKAGSLFEVDFSLDDGVKPNIIIFKQYVTPVLVWL 303  
 QY 303 KLPDQKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKWVRSSDFQLHLOSHLIR 362  
 DB 304 KLPDGRLLPMVIOQLPRTGSPPPPLFLPSDPPMAWLLAKIWRSSDFQLHLOSHLIR 363  
 QY 363 GHLMAEVLVATMRCPLSIHPIFKLIIPHLYTYLEINVRARTGLVSDMGIDQIMSTGGG 422  
 DB 364 GHLMAEVLVATMRCPLSIHPIFKLIIPHLYTYLEINVRARTGLVSDMGIDQIMSTGGG 423  
 QY 423 GHVOLLKOAGAFITYSSFCPPDDADRLGLGVKSSFYAQDALRLWEILYRYVEGIVSLHY 482  
 DB 424 GHVDILQRTATSLTYRSPCPDDADRLGLGVKSSLYAQDALRLWEILYRYVERWELFY 483  
 QY 483 KTDVAVKDDPELQTWCREITEIGLQGAQDRGFPVLSQARDQVCHFTVTCIFTCTQHASV 542  
 DB 484 RSDTDVKEDPELQVWCREVTEVGLLGAQDRGFPLSLESAELCRFVAMCIFTCTQHASV 543  
 QY 543 HLGQLDWTSWPNAPCTWRLLPPPTTKDATLETVMATLENFQASLOMSITWOLGRQPMV 602  
 DB 544 HLGQLDWTSWPNAPCTWRLLPPPTTKDATLETVMATLENFQASLOMSITWOLGRQPMV 603  
 QY 603 VAVGQHEEYSGPPEKAVLKKFREELAAALDKIEIRNAKLDMPYELRPSVVENSVAI 661  
 DB 604 VALGQHEEYSGPPEKAVLKKFREELAAALDKIEIRNAKLDMPYELRPSVVENSVAI 662  
 RESULT 10  
 Q91YW6 PRELIMINARY; PRT; 662 AA.  
 ID Q91YW6  
 AC Q91YW6;  
 DT 01-DEC-2001 (TREMELrel. 19, Created)  
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)  
 DT 25-OCT-2004 (TREMELrel. 28, Last annotation update)  
 DE Arachidonate lipoxygenase, epidermal.  
 GN Name=Aloxi2e;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor; DOI=10.1073/pnas.242603899;  
 RX MEDLINE=23388257; PubMed=12477932; Grouse L.H., Derge J.G.,  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A.C., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor;

RA Strausberg R.;  
 RL Submitted (APR-2003) to the EMBL/GenBank/DBSJ databases.  
 CC -!- COFACTOR: Iron (By similarity).  
 CC -!- SIMILARITY: Belongs to the lipoxxygenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 DR EMBL; BC013751; AAH13751.1; -.  
 DR EMBL; BC051047; AAH51047.1; -.  
 DR HSSP; P12530; ILOX.  
 DR MGD; MGI:1274790; Alox12e.  
 DR GO; GO:0005506; F:iron ion binding; IEA.  
 DR GO; GO:0016165; F:lipoxxygenase activity; IEA.  
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0006691; P:leukotriene metabolism; IEA.  
 DR Pfam; PF00305; Lipoxxygenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00467; MAMLOXGNASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Dioxygenase; Oxidoreductase.  
 SQ SEQUENCE 662 AA; 75473 MW; 831C038037D3745D CRC64;  
 Query Match 66.9%; Score 2350.5; DB 2; Length 662;  
 Best Local Similarity 66.6%; Pred. No. 5.7e-175;  
 Matches 439; Conservative 95; Mismatches 124; Indels 1; Gaps 1;  
 QY 4 YRIVSTGASLVAGSNNOVLVGHGEAALGKRLWPARG-ETELKVEVEYLGPLLPV 62  
 DB 4 YKILVATGDSVFGASNLVHMLVHGHEADLGKRLPLGRKTSLEVDVPLHGLRLAV 63  
 QY 63 KLRKRLKLDKDAWFCNWTISVQGFAGDEVRFCYRWVEGNGVLSPEGTGRTVGDPOGL 122  
 DB 64 KLRKQGLLDLDFCKSIYVQGPQGEAFFCYSMVQGEKICITETGALKVTDITQNL 123  
 QY 123 FOKHREBELERKULYRWGNWKGILINMAGAKLYDLVDERFLDKRVDPEVSLKGLA 182  
 DB 124 FRKYREQELENNRYRWGSKWKEGLITPLAGSTERDLPRNORFMKDKDLSLSVKELK 183  
 QY 183 DLAIKDSNLVTCWLDODFNRIFCWGQSKLAERVDSKEDALRGYQFLNAGNPVLLRR 242  
 DB 184 NFAIKGTLDVFSRVOKLEDYQVFPHTKTALPERVVRGSKEDALRGYQFLNAGNPVLLRR 243  
 QY 243 SAHLPARLVFPFGMELOAQLEKEGGTLFEADFLSLDGKIKANVILCSQQHAAPLVWL 302  
 DB 244 SNRLPARLVLPFGMEDLQTLQLEKELKAGSLFEVDFSLDGVKPNIIIFKQIVTAPLWL 303  
 QY 303 KLQPGKLLPMVLIQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSHLLR 362  
 DB 304 KLQPDGRLLPMVLIQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSHLLR 363  
 QY 363 GHLMAEVIVATMRCPLPSHTPIFKLIIPHLRVTLEINVRARTGLVSDMGIFDQINSTGG 422  
 DB 364 GHLMAEVIVATMRCPLPSHTPIFKLIIPHLRVTLEINVRARTGLVSDMGIFDQINSTGG 423  
 QY 423 GHVQLLKQAGFLTYSSFCPPDDLDLADRGLLGVKSSFYAQDALRLWEIITYRYVEGVLSHL 482  
 DB 424 GHVDILQRTSCLTYSFCPPDDLDLADRGLLGVKSSLYAQDALRLWEIISRYVERVVELFY 483  
 QY 483 KTDVAVKDDPELQVTCREITEIGLQAGDQRPVPSLQADQVCHVFTWCIFCTCOHASV 542  
 DB 484 RSDTDVKEDPELQVTCREITEIGLQAGDQRPVPSLQADQVCHVFTWCIFCTCOHASV 543  
 QY 543 HLGQLDWISWVNACTWRLPPTTKDLETVMATLNFHQAOSLMSITWOLGRQPM 602  
 DB 544 HLGQLDWAWIENGCTWRKPPFISVTERDIDVSLPCLQOQARMQITVTKFLGRQPM 603  
 QY 603 VAVGQHEERYGSGPKAVLKFRLEALDKXIEIRNAKLMDPYEYLRPSVVENSVAI 661  
 DB 604 VALGQHEERYGSGRPRVLDKQFQBELAIMDKXIEIRNAKLMDPYEYLRPSVVENSVAI 662

RESULT 11  
 Q6ISF8 PRELIMINARY; PRT; 663 AA.  
 ID Q6ISF8;  
 AC Q6ISF8;  
 DT 05-JUL-2004 (TREMBlrel. 27, Created)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)  
 DE Arachidonate 12-lipoxygenase.  
 GN Name=ALOX12;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Stapleton L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Wozley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Wozny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Rodriguez A.C., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PCR rescued clones;  
 RA Director MGC Project;  
 RL Submitted (APR-2004) to the EMBL/GenBank/DBSJ databases.  
 CC -!- COFACTOR: Iron (By similarity).  
 CC -!- SIMILARITY: Belongs to the lipoxxygenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 DR EMBL; BC069557; AAH69557.1; -.  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0004052; P:arachidonate 12-lipoxygenase activity; ISS.  
 DR GO; GO:0047977; F:hoxillin-epoxide hydrolase activity; ISS.  
 DR GO; GO:0019870; P:potassium channel inhibitor activity; ISS.  
 DR GO; GO:0019369; P:arachidonic acid metabolism; ISS.  
 DR GO; GO:0046456; P:icosanoid biosynthesis; ISS.  
 DR GO; GO:0045794; P:negative regulation of cell volume; ISS.  
 DR GO; GO:0008284; P:positive regulation of cell proliferation; ISS.  
 DR GO; GO:0042391; P:regulation of membrane potential; ISS.  
 DR InterPro; IPR003006; Ig MHC.  
 DR InterPro; IPR000907; Lipoxxygenase.  
 DR InterPro; IPR001024; Lipoxxygenase LH2.  
 DR InterPro; IPR001885; Mam\_lipoxygenase.  
 DR Pfam; PF00305; Lipoxxygenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00467; MAMLOXGNASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; UNKNOWN\_1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Dioxygenase; Oxidoreductase.  
 SQ SEQUENCE 663 AA; 75721 MW; 39E7350F62D4C9E7 CRC64;  
 Query Match 65.8%; Score 2312; DB 2; Length 663;

Best Local Similarity 65.3%; Pred. No. 5.8e-172; Matches 433; Conservative 94; Mismatches 134; Indels 2; Gaps 2;	
QY 1	MGLYRVRVSTGSLVAGSNVQVLVGVGHQAAKGLRWLPARG-ETELKRVVPEVLGLP 59
DB 1	MGRYRIRVATGAWLFGSGSNRVQLMLVGVTRGAELELQLRPARGEEEDHVDVADLGLL 60
QY 60	LFVKLRKRLHLLKDDAWFCNWIISVQSGAGDEVRFPCTRWVEGVNGLSLPEGTGRTVGEDP 119
DB 61	QFVLRKKEHVLVDDAWFCDFRITVQSGCAEAVAFPCYRWVQGEDILSLPEGTARLPGDNA 120
QY 120	QGLFQKHREELERKLYRWGNWKDGLILNAGAKLYDLVDPERFLEKRVDFEVSLLAK 179
DB 121	LDMFQKHREKELDRQYICWATWKEGLEFLTTAADRKKDLPNMRPHEEKRLDFEWTLLKA 180
QY 180	GLADLAIKDSLNLVLTCKWLDLDFNRFVCGQSKLAERVDSKEDALFCYQFLNGANPVV 239
DB 181	GALEMALKRVYILLSSWNCLEDQFLFWGQKALAEKVRQOCWDELFSYQFLNGANPML 240
QY 240	LRRSAHLPARLVFPFGMEELQALEKELEGGLTFEADFSLLDGIKANVILCSQOHLAAPL 299
DB 241	LRRSTSLPSRLVLPSCMEELRAQLEKELQNGSLFEADPILLDGIPIANVIRGEKQVLAAPL 300
QY 300	VMLKLPDQKLLPMVJLOLPRTGSPDPPLFLPTDPPMAWLLAKCWVRSSDQLHELQSH 359
DB 301	VMLKMEPNKLPQMVJQIOPPNPSSPTTLFLPSDPLAWLLAKSWVRNSDFQLHEIQYH 360
QY 360	LLRGLHMAEIVVATWRCILPSHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFQIMST 419
DB 361	LNLTHLVAEIVAVIATWRCPLGHLPIFKFLPHIRYITMEINTRATQLISDGGIFDKAVST 420
QY 420	GGGGHVQLLKQAGAFITYSSFCPPDDLADRLGLGVKSSFYAODALRLMEIIRYVEGIVS 479
DB 421	GGGGHVQLLRRAAAQLTYCSLCPDPLADRLGLGALYAHDALRLMEIIRYVEGIVH 480
QY 480	LHYKTDVAVKDDELQVTCWRETEIGLQAGADRFPVSVLQARDQVCHFTVTCIGTQGH 539
DB 481	LFYQRDDIVKGDPELQAWCREITEVGLCAQDRGFVFSQSQSLCHFTMCTVCTTAQH 540
QY 540	ASVHLGQLDWYSVNPVNACTMLRPPTTK-DATLETVMATLNFHQASLQMSITTWOLGR 598
DB 541	AALNQQLDWAYVNPVNACTMREMPPTTKEDVTVMATVMSGLPFDVRCQLQMAISLWLSRR 600
QY 599	QPVMAVGOHEEYFSGPPKAVLKFRBELAALDKIEIRNAKLDMPEYILRPSVENS 658
DB 601	QPMVPLGHHKXYFSGPRKPAVLNQRFTDLEKLEIKETARNEQLDWPVEYLKPSCIENS 660
QY 659	VAI 661
DB 661	VTI 663
RESULT 12	
LOXP_HUMAN STANDARD; PRT; 662 AA.	
ID	AC P18054; C95569;
DT	01-NOV-1990 (Rel. 16, Created)
DT	01-NOV-1991 (Rel. 20, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Arachidonate 12-lipoxygenase, 12S-type (EC 1.13.11.31) (12-LOX)
DE	(Platelet-type lipoxygenase 12).
GN	Name=ALOX12; Synonyms=LOG12;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	MEDLINE=90332636; PubMed=2377602;
RX	Funk C.D., Furci L., Fitzgerald G.A.;
RT	"Molecular cloning, primary structure, and expression of the human
RT	platelet/erythrocyte cell 12-lipoxygenase.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:5638-5642(1990).
[2]	
RN	SEQUENCE FROM N.A., AND VARIANTS ARG-260 AND ASN-321.
RP	MEDLINE=91017529; PubMed=2217179;
RA	Izumi T., Hoshiko S., Raadmark O., Samuelsson B.;
RT	"Cloning of the cDNA for human 12-lipoxygenase.";
RL	Proc. Natl. Acad. Sci. U.S.A. 87:7477-7481(1990).
[3]	
RN	SEQUENCE FROM N.A.
RP	MEDLINE=91058562; PubMed=2244907;
RA	Yoshimoto T., Yamamoto Y., Arakawa T., Suzuki H., Yamamoto S.,
RA	Yokoyama C., Tanabe T., Toh H.;
RT	"Molecular cloning and expression of human arachidonate 12-
RT	lipoxygenase.";
RL	Biochem. Biophys. Res. Commun. 172:1230-1235(1990).
[4]	
RN	SEQUENCE FROM N.A., AND VARIANTS ARG-260; ASN-321 AND HIS-429.
RP	Rieder M.J., Daniels R.L., da Ponte S.H., Hastings N.C., Ahearn M.O.,
RA	Rajkumar N., Yi Q., Nickerson D.A.;
RT	"SeattlesNPS. NHLBI HL6682 program for genomic applications, UW-
RT	PHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL	Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
[5]	
RN	SEQUENCE OF 1-111 FROM N.A.
RP	MEDLINE=93077582; PubMed=1447217;
RA	Yoshimoto T., Arakawa T., Hada T., Yamamoto S., Takahashi E.;
RT	"Structure and chromosomal localization of human arachidonate 12-
RT	lipoxygenase gene.";
RL	J. Biol. Chem. 267:24805-24809(1992).
[6]	
RN	SEQUENCE OF 1-44 FROM N.A.
RP	MEDLINE=92237289; PubMed=1570320;
RA	Funk C.D., Funk L.B., Fitzgerald G.A., Samuelsson B.;
RT	"Characterization of human 12-lipoxygenase genes.";
RL	Proc. Natl. Acad. Sci. U.S.A. 89:3962-3966(1992).
[7]	
RN	SEQUENCE OF 339-426 FROM N.A.
RC	TISSUE=Skin;
RA	MEDLINE=94136572; PubMed=8304420;
RA	Hussein H., Shornick L.P., Shannon V.R., Wilson J.D., Funk C.D.,
RA	Pentland A.P., Holtzman M.J.;
RT	"Epidermis contains platelet-type 12-lipoxygenase that is
RT	overexpressed in germinal layer keratinocytes in psoriasis.";
RL	Am. J. Physiol. 266:C243-C253(1994).
CC	- FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.
CC	- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-
CC	12-hydroperoxyicoso-5,8,10,14-tetraenoate.
CC	- COFACTOR: Iron.
CC	- PATHWAY: Leukotrienes biosynthesis.
CC	- SUBCELLULAR LOCATION: Cytoplasmic.
CC	- SIMILARITY: Belongs to the lipoxygenase family.
CC	- SIMILARITY: Contains 1 PLAT domain.
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CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	or send an email to license@isb-sib.ch).
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DR	EMBL; M35418; AAA60056.1; -
DR	EMBL; M58704; AAA59523.1; -
DR	EMBL; M62982; AAA51533.1; -
DR	EMBL; AY527817; AAS00094.1; -
DR	EMBL; D12638; BAA02162.1; -
DR	EMBL; M87004; AAA51587.1; -
DR	EMBL; S68587; AAD14020.1; -
DR	PIR; A38283; A38283.
DR	HSSP; P12530; 1LOX.
DR	Genew; HGNC:429; ALOX12.
DR	MIM; 152391; -
DR	GO; GO:0004052; F:arachidonate 12-lipoxygenase activity; TAS.
DR	GO; GO:0006631; P:fatty acid metabolism; TAS.



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DR InterPro; IPR000907; Lipoxigenase.
DR InterPro; IPR001024; Lipoxigenase_LH2.
DR InterPro; IPR001885; Mam lipoxigenase.
DR Pfam; PF00305; Lipoxigenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPOXYGENASE.
DR PRINTS; PR00467; MAMLIPOXYGENASE.
DR SMART; SM00308; LH2; 1.
DR PROSITE; PS00711; LIPOXYGENASE_1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS00095; PLAT; 1.
DR Diogenase; Iron; Leukotriene biosynthesis; Oxidoreductase;
KW Polymorphism.
FT INIT_MET 0
FT DOMAIN 1 113 PLAT.
FT METAL 359 359 Iron (By similarity).
FT METAL 364 364 Iron (By similarity).
FT METAL 539 539 Iron (By similarity).
FT METAL 662 662 Iron (By similarity).
FT VARIANT 260 260 Q -> R.
FT VARIANT 297 297 /FTID=VAR_018743.
FT VARIANT 321 321 /FTID=VAR_004279.
FT VARIANT 321 321 S -> N.
FT VARIANT 429 429 /FTID=VAR_018744.
FT VARIANT 429 429 R -> H.
FT CONFLICT 188 191 /FTID=VAR_018745.
FT CONFLICT 344 344 RYVT -> PCLH (in Ref. 3).
FT CONFLICT 388 388 S -> C (in Ref. 3).
FT CONFLICT 388 388 L -> P (in Ref. 1).
FT SEQUENCE 662 AA; 75535 MW; B7FFDCFC66F8CFB CRC64;

Query Match 65.7%; Score 2310; DB 1; Length 662;
Best Local Similarity 65.4%; Pred. No. 8.4e-172;
Matches 433; Conservative 93; Mismatches 134; Indels 2; Gaps 2;

QY 2 GLYRIVSTGSLVYAGSNVQLVGVQGENALGRWLPARG-RTELKVEVPEVLGPLL 60
DB 1 GRYRIVATGAWLFGSSYRVLVGVTRGEAELELRPARGEEEDHDVDAEDLGLLQ 60
QY 61 FVLRKHLLKDDAFWCFWISVQGGAGDEVFPFCYRWVGVNGLSLPEGTGRTVGEDPQ 120
DB 61 FVLRKHHLVDDAFWCFDRIIVQGGAGCAEAFPCYRWVQGGEDILSLPEGTARLPEDNAL 120
QY 121 GLFQKHREELERKLYRWGNKDGILNMGAKLYLDPVDERFLEDRKVDVFEVSLAKG 180
DB 121 DMFQKHREKELKDRQIYCWATKKEGLPLTTAADRKDDLPPNMRFEKRLDFEWTLAG 180
QY 181 LADLAIKDSLNVLTCKDLDNRIFWCGQSKLAERVRDSWKEDALFGYQFLNGANPVVL 240
DB 181 ALEMALKRVYTLSSWNCLEDPDQIFWQKGSALAEKVRQCWDDELFSYQFLNGANPMLL 240
QY 241 RPSAHLPARLVPPGMEELQALEKELSGTTFEADFSLLDGIKANVLCSQOHLAAPLV 300
DB 241 RRSTSLPSRLVPSGMEELQALEKELQNGSLFEADFIILDGIPANVRIGEKYLAAPLV 300
QY 301 MLKLPQDGKLLPMVITQLQPLRTGSPPLPLFTDPPMAWLLAKCVRSSDFOLHELQSHL 360
DB 301 MLKMEPNGLQPMVITQIPSPSSPTPLFLPSDPLAWLLAKSVNRNSDQLHEIQYHL 360
QY 361 LRGHMAEVIVVATVRCPLPSIHPKLIPIHLYTLINVRARTGLVDMGIFDQIMSTG 420
DB 361 LNTHLVAEVIAVATVRCPLPGLHPFKFLPHIRYTMETINRARTQLISDGGIFDKAVSTG 420
QY 421 CGGHVQLLKQACAFITYSSFCPPDDLADRLGLLVKSSFYAQDALRLWIIYRYVEGIVSL 480
DB 421 CGGHVQLLRRAAAQULTYCSLCPDDLADRLGLLVKSSFYAQDALRLWIIYRYVEGIVSL 480
QY 481 HYKTDVAVKDDPELQWCKREITEIGLQAGQDRGFPVLSQARDQVCFHVTWICTCTGQHA 540
DB 481 FYQRDDIVKGDPELQWCKREITEVEGLCQQRDRGFPVLSQSQQLCFHVTWICTCTGQHA 540
QY 541 SVHLQGLDWYSVWVPNAPCTMLRPPTTK-DATLETVMATLPNFHOASLQMSITWQGRGQ 599
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Db 541 AINQGLQDWTANVENAFCTWRMPPTTKEDVTMTATVMSGLSDPVQACLOMAISWHLSRQ 600
QY 600 PMVAVQGHHEEYFSGPEPKAVLKFKFRELAALDKIEIRNAKLDMPEYLYRPSVVENS 659
DB 601 PMVPLGLHKKYFSGPKAVLNQFRTDLEKLEKEITARNEQLDWPPEYLYLKPSCIENS 660
QY 660 AI 661
DB 661 TI 662

RESULT 13
Q8BHG4 Q8BHG4 PRELIMINARY; PRT; 663 AA.
AC Q8BHG4;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Mus musculus adult female vagina cDNA, RIKEN full-length enriched
DE library, clone:9930022G08 product:arachidonate 12-lipoxygenase, full
DE insert sequence (Mus musculus 2 days pregnant adult female ovary cDNA,
DE RIKEN full-length enriched library, clone:E330011M05
DE product:arachidonate 12-lipoxygenase, full insert sequence).
GN Name=alox12;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Ovary, and Vagina;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata K., Hayashizaki Y., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,
RA Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yanamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujiwaka S., Inoue K., Togawa Y., Izawa Y., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
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Genome Res. 10:1757-1771 (2000).

16] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Vagina;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Tanaka A., Tanaka T., Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

17] SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Ovary;

RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H., Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Tanaka A., Tanaka T., Tomaru A., Taya T., Yasunishi A., Muramatsu M., Hayashizaki Y.; Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

CC -I- COFACTOR: Iron (By similarity).

CC -I- SIMILARITY: Belongs to the lipoxigenase family.

CC -I- SIMILARITY: Contains 1 PLAT domain.

DR EMBL; AK036898; BAC29629.1; -.

DR HSSP; P12530; 1LOX.

DR MGD; MGI:87998; Alox12.

DR GO; GO:0005829; C:cytosol; ISS.

DR GO; GO:0042383; C:sarcolemma; ISS.

DR GO; GO:0004052; F:arachidonate 12-lipoxygenase activity; ISS.

DR GO; GO:0047977; F:hypoxilin-epoxide hydrolase activity; ISS.

DR GO; GO:0019870; F:potassium channel inhibitor activity; ISS.

DR GO; GO:0006916; P:anti-apoptosis; IMP.

DR GO; GO:0006916; P:anti-apoptosis; ISS.

DR GO; GO:0019369; P:arachidonic acid metabolism; ISS.

DR GO; GO:0019395; P:fatty acid oxidation; ISS.

DR GO; GO:0046456; P:icosanoid biosynthesis; ISS.

DR GO; GO:0045794; P:negative regulation of cell volume; ISS.

DR GO; GO:0006800; P:oxygen and reactive oxygen species metabolism; ISS.

DR GO; GO:0030307; P:positive regulation of cell growth; ISS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; IMP.

DR GO; GO:0042391; P:regulation of membrane potential; ISS.

DR GO; GO:0042554; P:superoxide release; ISS.

DR InterPro; IPR003006; IG\_MHC.

DR InterPro; IPR000907; Lipoxigenase.

DR InterPro; IPR01024; Lipoxigenase\_LH2.

DR InterPro; IPR01885; Mam\_lipoxygenase.

DR Pfam; PF00305; Lipoxigenase; 1.

DR Pfam; PF01477; PLAT; 1.

DR PRINTS; PR00087; LIPOXYGNASE.

DR PRINTS; PR00467; MAMLIPOXYGNASE.

DR SMART; SM00308; LH2; 1.

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DR PROSITE; PS00081; LIPOXYGNASE\_2; 1.

DR PROSITE; PS50095; PLAT; 1.

KW Dioxxygenase; Oxidoreductase.

SQ SEQUENCE 663 AA; 75389 MW; 205BE32BE2CF3E87 CRC64;

Query Match 64.3%; Score 2258; DB 2; Length 663;

Best Local Similarity 63.5%; Pred. No. 9.8e-168;

Matches 421; Conservative 97; Mismatches 143; Indels 2; Gaps 2;

RP SEQUENCE FROM N.A.  
 RX MEDLINE=96052410; PubMed=7576099;  
 RA Krieg P., Kinzig A., Rees-Joschke M., Vogel S., Vanlandingham B.,  
 RA Stephan M., Lehmann W.D., Marks F., Furstemberger G.;  
 RT "12-lipoxygenase isoenzymes in mouse skin tumor development.";  
 RL Mol. Carcinog. 14:118-129(1995).  
 RN [3]  
 RP SEQUENCE OF 125-217 FROM N.A.  
 RC TISSUE=Lung;  
 RX MEDLINE=95312654; PubMed=7792391; DOI=10.1016/0090-6980(94)00005-H;  
 RA Hagnann W., Gao X., Zacharek A., Wojciechowski L.A., Honn K.V.;  
 RT "12-lipoxygenase in Lewis lung carcinoma cells: molecular identity,  
 RT intracellular distribution of activity and protein, and Ca(2+)-  
 RT dependent translocation from cytosol to membranes.";  
 RL Prostaglandins 49:49-62(1995).  
 CC -1- FUNCTION: Oxygenase and 14,15-leukotriene A4 synthase activity.  
 CC -1- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,10E,14Z)-(12S)-  
 CC 12-hydroperoxyicoso-5,8,10,14-tetraenoate.  
 CC -1- COFACTOR: Iron.  
 CC -1- PATHWAY: Leukotrienes biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: Found primarily in platelets and in microsomal  
 CC and cytosolic fractions of the epidermis.  
 CC -1- SIMILARITY: belongs to the lipoxygenase family.  
 CC -1- SIMILARITY: Contains 1 PLAT domain.  
 CC -----  
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U04334; AAA20659.1; -;  
 DR EMBL; S80446; AAB36013.1; -;  
 DR EMBL; S77511; AAB34667.1; -;  
 DR PIR; A54075; A54075.  
 DR HSP; P12530; ILOX.  
 DR MGD; MGI:87998; Alox12.  
 DR InterPro; IPR000907; Lipoxygenase.  
 DR InterPro; IPR001024; Lipoxygenase\_LH2.  
 DR InterPro; IPR001885; Mam\_lipoxygenase.  
 DR Pfam; PF00305; Lipoxygenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00457; MAMLIPOXGNASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; FALSE\_NEG.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS0095; PLAT; 1.  
 KW Dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.  
 FT INIT MET 0 0 By similarity.  
 FT DOMAIN 1 113 PLAT.  
 FT METAL 359 359 Iron (By similarity).  
 FT METAL 364 364 Iron (By similarity).  
 FT METAL 539 539 Iron (By similarity).  
 FT METAL 662 662 Iron (By similarity).  
 FT MUTAGEN 662 662 I->D,R,K,G: Loss of activity.  
 FT MUTAGEN 662 662 I->S,N: Little activity (8-15%).  
 FT MUTAGEN 662 662 I->V: Nearly full activity.  
 FT CONFLICT 2 2 A -> R (in Ref. 2).  
 SQ SEQUENCE 662 AA; 75214 MW; ACS62C1EDC5049B5 CRC64;  
 Query Match 63.9%; Score 2247; DB 1; Length 662;  
 Best Local Similarity 63.3%; Pred. No. 7.1e-167;  
 Matches 419; Conservative 96; Mismatches 145; Indels 2; Gaps 2;  
 QY 2 GUYRVRVSTGSLVAGSNNOVLWVGHGAEALGRLPARG-ETELKVEYVIGPLL 60  
 DB 1 GAYRVRVSTGSLVAGSNNOVLWVGHGAEALGRLPARG-ETELKVEYVIGPLQ 60  
 QY 61 FVKLRKRLKDDAFCNFWISVQGPCAGDEVFPFCYRWVWEGNVLSPETGRTGVGDPLQ 120

Db 61 FVKLRKHTVDDAFCNLTIVQPGTSAEAVFCYRWVWEGNVLSPETGQARLAGDNAL 120  
 QY 121 GLFQKHREELERKRYRWGNWKGILNMGAKLYDLVDPDERFLEDKRVDFEVLAKG 180  
 Db 121 DVFKYREKELKERQCYWATWKEGLPQTIAADCKDDLPNMRPHEEKRLDFEWTLAG 180  
 QY 181 LADLAIKDSLNVLTCKWDLDPNRIFWCGQSKLAERVDSWKEDALFCYQFQYGLNANPVVL 240  
 Db 181 VLENGLRVYTLRSWNHLEDFQIFWQKSALEAKVHCQWOEDLFGYQFGLNANPMLL 240  
 QY 241 RRSALHLPARLVFPFPMELQALQLEKEGGLTFADFSLLDGIIKANVILCSQOHLAAPLV 300  
 Db 241 RRSLSLSRLVLPFPMELQALQLEKEGGLTFADFSLLDGIIKANVILCSQOHLAAPLV 300  
 QY 301 MLKLQDPGKLPVMIQQLPRTGSPPLFLPTDPPMAWLAKCWVRSSDFQLHQLSHL 360  
 Db 301 MLRMDPGKLLPMAIQIPPNPSPAPTLFLPSPDPLAWLLAKIWRNSDFQLQLPQL 360  
 QY 361 LRGLHMAEIVVATMRCCLPSHPHFKLIIPLHRLTLEINVRARTGLVSDMGIFDQIMSTG 420  
 Db 361 LNTHLVAEIVATMRCCLPGHPIFKLVPHRYTMEINTRTQLISDGGIFDQVWSTG 420  
 QY 421 GGGHVQLLKQAGAFITYSSFCPPDDLDLADRGILGVKVSFYAODALRLWELIIVRYVGVISL 480  
 Db 421 GGGHVQLLUTRAVQLTSHSLCPPDDLANRGLRIPSAUYARDALQWETARYVKGWHL 480  
 QY 481 HYKTDVAVKDDPELQTCREITEIGLQAGADRGFPVSLQARDQVCHFVTCMCTCTGQHA 540  
 Db 481 FYQSDDIVRGDPELQAMCREITEVGLCHADRGFPVSPQSRALCHFLTMCVFTCTAQAHA 540  
 QY 541 SVHLQGLDWSVWPNAPCTMLPPTTK-DATLETVMATLNFHQASLOMSITWOLGRRQ 599  
 Db 541 AINQGLDWSVWPNAPCTMRMPPTSKDDVTMETVMSGLPDVQKACIQMTITWHLGRILQ 600  
 QY 600 PMVAVGQHEEYRSGPEPKAVLKKFREELAAALDKEIEIRNAKLDMPYEYLRPSVVSNSV 659  
 Db 601 PMVPLGHHTKTFSDPRTKAVLSQFQADLONLEKEITARNEQLDPLPYELKPSRIENSI 660  
 QY 660 AI 661  
 Db 661 TI 662  
 RESULT 15  
 Q95103 PRELIMINARY; PRT; 555 AA.  
 AC Q95103;  
 DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE 12-lipoxygenase (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cornea;  
 RA Hornsten L.M.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: Iron (By similarity).  
 CC -1- SIMILARITY: belongs to the lipoxygenase family.  
 CC EMBL; Y08829; CAA70062.1; -;  
 DR HSRP; P12530; ILOX.  
 DR GO; GO:0005829; C:cytosol; ISS.  
 DR GO; GO:0004052; F:arachidonate 12-lipoxygenase activity; ISS.  
 DR GO; GO:0047977; F:hexokinase-epoxide hydrolase activity; ISS.  
 DR GO; GO:0019870; F:potassium channel inhibitor activity; ISS.  
 DR GO; GO:0019369; P:arachidonic acid metabolism; ISS.  
 DR GO; GO:0046456; P:icosanoid biosynthesis; ISS.  
 DR GO; GO:0045794; P:negative regulation of cell volume; ISS.

DR GO; GO:0008284; P:positive regulation of cell proliferation; ISS.  
DR GO; GO:0042391; P:regulation of membrane potential; ISS.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR001885; Mam\_lipoxigenase.  
DR InterPro; IPR001005; Myb\_DNA\_binding.  
DR Pfam; PF00305; Lipoxigenase; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR PRINTS; PR00467; MAMLPXGNASE.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; UNKNOWN\_1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00037; MYB\_1; UNKNOWN\_1.  
KW Dioxigenase; Oxidoreductase.  
FT NON\_TER 1  
FT NON\_TER 555 555  
SQ SEQUENCE 555 AA; 63266 MW; A030B1871173D3AC CRC64;  
  
Query Match 54.2%; Score 1905.5; DB 2; Length 555;  
Best Local Similarity 63.7%; Pred. No. 2.9e-140;  
Matches 352; Conservative 81; Mismatches 119; Indels 1; Gaps 1;  
  
QY 102 NGVLSPEGTGRTVGEDPQGLFQKHREERLEERRKLYRWGNKDGILINMAGAKYLDLPV 161  
DB 1 DGVLCLEPRTARLAGNNALDVFORHREKELKERHKIYRWATWKEGLPLTIAAGSEDDLLPA 60  
  
QY 162 DERFLEDKRVDPRVSLAKGLADLAIKDSLNLVTCWKDLDDFNRIFWCGOSKLAERVDSW 221  
DB 61 NRRFHEEKRLDFEWTLKAGTLEMLVLRVYTLSSWTSLEDFDLIFWGQKSPLAEKVHCW 120  
  
QY 222 KEDALFGYQFLNGANPVVLRSAHLPARLVFPFGMEELQAQLEKELEGGTLFEADFSLLD 281  
DB 121 RODELFYQFLNGANPMLLRRCCTSLRLVLPSPGMEELRAQLERELQNGSLFEADFIILD 180  
  
QY 282 GIKANVILCSQQHAAPIVMLKLQDPGKLLPMVLIQLPRTGSPPPPLFLPTDPPMALL 341  
DB 181 GIPANVIRGEKQYLAAPVMLKMDPSKLLPMVIQIPSPISPTPPPLFLPSDPLAWLL 240  
  
QY 342 AKCWVRSSDFQLHELQSHLLRGLHMAEVIWATMRCLPSIHPIFKLIIPHLYTLEINVR 401  
DB 241 AKTWVRNSDFQLHQLQYHLNTHLLAEVIAVATMRCLPGLHPVFKLLMHIHYTWEINTR 300  
  
QY 402 ARTGLVSDMGIFDQIMSTGGGHVQLLKQAGAPLYTSFSCPDDDLADRGLLGVKGSFYAQ 461  
DB 301 ARTQLISDGGIFDKAVSTGGGHVHLRRALAQLYRSLCPLDLLADRELLGTPGALYAC 360  
  
QY 462 DALRLWEIIRYVEGIVSLHYKTDVAVKDDPELQWCREITRIGLQGAQDRGFPVSLQAR 521  
DB 361 DALRLWEITARYVEGIVVHLFYHGDDVYVKGDPPELQAWCREITEVGLPQAQERGFVVSFQSQ 420  
  
QY 522 DOVCHFTVTCIFTCTGSHASVHLGQLDWYSWPNAPCTMRLPPPTTK-DATLETVMATLP 580  
DB 421 NQLCHFLTWCVFTCTAQHGAINGQGLDWYAWVNPACTMWRMPPTTKEDVTWATVNGSLP 480  
  
QY 581 NFHQASLQMSITWQLGRRQPMVAVGQHEEEYFSGPEPKAVLKKFREELAAALDKKEIERN 640  
DB 481 DVRQACIQMAITWHLGRRQPMVPLGHKKEKYFSDPKAKSVLNQFQTDLENLEREITARN 540  
  
QY 641 AKLDMPEYILRPS 653  
DB 541 EQLDLPEYVLKPS 553

Search completed: July 18, 2005, 22:01:11  
Job time : 115.649 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:49:42 ; Search time 27.6652 Seconds  
(without alignments)  
2298.893 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLRIRVSTGASLYAGSNN.....KLDMPYELRPSVENSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3503.5	99.7	662	1 A31349	arachidonate 15-li
2	3090	87.9	663	2 S32825	arachidonate 12-li
3	3060	87.1	663	1 A35087	arachidonate 12-li
4	2896	82.4	663	1 JQ0018	arachidonate 15-li
5	2696	76.7	663	2 S30051	arachidonate 12-li
6	2692	76.6	663	2 I52462	arachidonate 12-li
7	2676	76.2	663	1 B54075	arachidonate 12-li
8	2312	65.8	663	1 A38283	arachidonate 12-li
9	2252	64.1	663	1 A54075	arachidonate 12-li
10	1299.5	37.0	674	2 I49479	arachidonate 5-lip
11	1298.5	37.0	674	1 DAUHAL	arachidonate 5-lip
12	1270	36.1	670	1 A30882	arachidonate 5-lip
13	947	26.9	238	2 I56977	arachidonate 12-li
14	863.5	24.6	1066	2 T30903	arachidonate 8-lip
15	522.5	14.9	917	2 B96699	probable lipoxigen
16	490.5	14.0	896	2 T07408	lipoxigenase (EC 1
17	490.5	14.0	914	2 T07065	probable lipoxigen
18	489.5	13.9	862	2 S57964	probable lipoxigen
19	487.5	13.9	908	2 T07409	lipoxigenase (EC 1
20	484.5	13.8	926	2 E96749	probable lipoxigen
21	483	13.7	865	2 T11852	lipoxigenase (EC 1
22	482	13.7	899	2 T11578	probable lipoxigen
23	478	13.6	858	2 T12142	lipoxigenase (EC 1
24	477.5	13.6	862	2 T07775	lipoxigenase (EC 1
25	476.5	13.6	899	2 T07062	probable lipoxigen
26	475	13.5	859	2 T06339	lipoxigenase (EC 1
27	474	13.5	859	2 T06352	lipoxigenase (EC 1
28	472.5	13.4	862	2 S22153	lipoxigenase (EC 1
29	470	13.4	859	2 T06429	lipoxigenase (EC 1

30	470	13.4	876	2 T07101	lipoxigenase (EC 1
31	470	13.4	896	2 J02391	lipoxigenase (EC 1
32	467.5	13.3	866	2 T06454	probable lipoxigen
33	466	13.3	857	2 S01864	lipoxigenase (EC 1
34	460	13.1	861	2 S44940	lipoxigenase (EC 1
35	459.5	13.1	864	1 S07075	lipoxigenase (EC 1
36	456.5	13.0	861	1 S01142	lipoxigenase (EC 1
37	454.5	12.9	876	2 T05943	probable lipoxigen
38	453.5	12.9	877	2 T10085	lipoxigenase (EC 1
39	448.5	12.8	862	2 T05941	lipoxigenase (EC 1
40	448	12.7	868	2 T06827	lipoxigenase (EC 1
41	445.5	12.7	859	1 J02267	lipoxigenase (EC 1
42	445.5	12.7	864	2 T05945	lipoxigenase (EC 1
43	445.5	12.6	864	2 S13381	lipoxigenase (EC 1
44	442	12.6	865	1 DAS1L1	lipoxigenase (EC 1
45	439	12.5	856	2 T06596	lipoxigenase (EC 1

## ALIGNMENTS

### RESULT 1

A31349

arachidonate 15-lipoxygenase (EC 1.13.11.33) - human

N:Alternate names: arachidonate omega-6 lipoxygenase

C:Species: Homo sapiens (man)

C>Date: 31-Mar-1990 #sequence revision 07-Feb-1997 #text change 09-Jul-2004

C:Accession: A31349; A28192; S19625; S19577; A61164; B61164

R:Signal, E.; Craik, C.S.; Highland, E.; Grunberger, D.; Costello, L.L.; Dixon, R.A.F.; Nadel, J.A.

Biochem. Biophys. Res. Commun. 157, 457-464, 1988

A:Title: Molecular cloning and primary structure of human 15-lipoxygenase.

A:Reference number: A31349; MUID:89076270; PMID:3202857

A:Accession: A31349

A:Molecule type: mRNA

A:Residues: 1-662 <SIG>

A:Cross-references: UNIPROT:P16050; GB:M23892; NID:g187190; PIDN:AAA36182.1; PID:g307135

A:Experimental source: reticulocyte

R:Signal, E.; Grunberger, D.; Craik, C.S.; Caughey, G.H.; Nadel, J.A.

J. Biol. Chem. 263, 5328-5332, 1988

A:Title: Arachidonate 15-lipoxygenase (omega-6 lipoxygenase) from human leukocytes. Purifi

A:Reference number: A28192; MUID:88186828; PMID:3356688

A:Accession: A28192

A:Molecule type: protein

A:Residues: 3-16 <SI2>

A:Experimental source: leukocyte

R:izumi, T.; Radmark, O.; Joernvall, H.; Samuelsson, B.

Eur. J. Biochem. 202, 1231-1238, 1991

A:Title: Purification of two forms of arachidonate 15-lipoxygenase from human leukocytes.

A:Reference number: S19577; MUID:92111501; PMID:1662607

A:Accession: S19625

A:Molecule type: protein

A:Residues: 'X', 3-4, 'X', 6, 'X', 8-22; 38-45; 157-162, 'XX', 165-168; 627-631 <IZU>

A:Accession: S19577

A:Molecule type: protein

A:Residues: 'X', 3-25; 27-31 <IZ1>

A>Note: there appear to be distinct chromatographic forms, at least one each from reticul

teor

R:izumi, T.; Radmark, O.; Samuelsson, B.

Adv. Prostaglandin Thromboxane Leukotriene Res. 21, 101-104, 1990

A:Title: Purification of 15-lipoxygenase from human leukocytes, evidence for the presence

A:Reference number: A61164

A:Accession: A61164

A:Molecule type: protein

A:Residues: 'X', 3-4, 'X', 6, 'X', 8-12, 'X', 14-19, 'T', 21-22 <IZ2>

A:Experimental source: leukocyte

A:Accession: B61164

A:Molecule type: protein

A:Residues: 'X', 3-25; 27-31 <IZ3>

A:Experimental source: leukocyte

C:Genetics:

A:Gene: GDB:ALOX15

A:Cross-references: GDB:132454

A:Map position: 17pter-17qter

C:Function:  
A:Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,11Z,13E)-(15S)-15-h  
A:Pathway: leukotriene biosynthesis  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidore  
F:360,365,540,544,662/Binding site: iron (His, His, His, His, His, Ile) #status predicted

Query Match 99.7%; Score 3503.5; DB 1; Length 662;  
Best Local Similarity 99.8%; Pred. No. 6e-279; Mismatches 0; Indels 1; Gaps 1;  
Matches 661; Conservative 0;

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QY 1 MGLYRIRVSTGASLYAGSNQVQLMWVGQHGAAALGKRLWPARG-ETELKVEVPEYLGPL 59
DB 1 MGLYRIRVSTGASLYAGSNQVQLMWVGQHGAAALGKRLWPARGKETELKVEVPEYLGPL 60
QY 60 LFVKLRKRLHLLKDDAWFCNWIISVQGGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGEDP 119
DB 61 LFVKLRKRLHLLKDDAWFCNWIISVQGGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRDVDFEVSIAK 179
DB 121 QGLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRDVDFEVSIAK 180
QY 180 GLADLAIKDSLNLVTCWKDLDDFNRIFWCGQSKLAERVRDSWKEDALFGYQFLNGANPVV 239
DB 181 GLADLAIKDSLNLVTCWKDLDDFNRIFWCGQSKLAERVRDSWKEDALFGYQFLNGANPVV 240
QY 240 LRRSAHLPARLVPPPGMEELQALEKELEGTLFEADFSLLDGIKANVILCSQOHLAAPL 299
DB 241 LRRSAHLPARLVPPPGMEELQALEKELEGTLFEADFSLLDGIKANVILCSQOHLAAPL 300
QY 300 VMLKLPDQDKLLPMVLIQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 359
DB 301 VMLKLPDQDKLLPMVLIQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOSH 360
QY 360 LLRGHLMAEVIVVATMRCPLSIHPFKLIIPHLYLTLEINVRARTGLVSDMGIFDQIMST 419
DB 361 LLRGHLMAEVIVVATMRCPLSIHPFKLIIPHLYLTLEINVRARTGLVSDMGIFDQIMST 420
QY 420 GGGGHVQLLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIYYRVVEGIVS 479
DB 421 GGGGHVQLLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIYYRVVEGIVS 480
QY 480 LHYKTDAVKDDPELQTCREITEIGLOAQDRGFVPSLQARDQVCHFTVTCIETCTGQ 539
DB 481 LHYKTDAVKDDPELQTCREITEIGLOAQDRGFVPSLQARDQVCHFTVTCIETCTGQ 540
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATLETVMATLPNFHQASLQMSITWQLGRRQ 599
DB 541 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATLETVMATLPNFHQASLQMSITWQLGRRQ 600
QY 600 PNMVAVQOHEEYFSGPEPKAVLKKFREELAAALDKEIEIRNAKLDMPYELRPSVVENS 659
DB 601 PNMVAVQOHEEYFSGPEPKAVLKKFREELAAALDKEIEIRNAKLDMPYELRPSVVENS 660
QY 660 AI 661
DB 661 AI 662
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RESULT 2  
S32825  
arachidonate 12-lipoxygenase (EC 1.13.11.31), tracheal - bovine  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 13-Jan-1995 #sequence\_revision 29-Aug-1997 #text\_change 09-Jul-2004  
C:Accession: S32825; S77975; A56770  
R:de Marzo, N.; Sloane, D.L.; Dicharry, S.; Highland, E.; Sigal, E.  
Am. J. Physiol. 262, L198-L207, 1992  
A:Title: Cloning and expression of an airway epithelial 12-lipoxygenase.  
A:Reference number: A56770; PMID:52170942; PMID:1539676  
A:Contents: tracheal epithelium  
A:Accession: S32825  
A:Molecule type: mRNA

A:Residues: 1-663 <ACC>  
A:Cross-references: UNIPROT:P27479; EMBL:S96247; NID:g246172; PIDN:AAB21522.1; PID:g2461;  
A:Note: in the authors' translation residues 441-460 do not match the nucleotide sequence  
A:Note: sequence extracted from NCBI backbone (NCBIN:96247)  
R:de Marzo, N.; Sloane, D.L.; Dicharry, S.; Highland, E.; Sigal, E.  
submitted to the EMBL Data Library, December 1993  
A:Reference number: S77975  
A:Accession: S77975  
A:Molecule type: mRNA  
A:Residues: 1-440, 'GLLGKSSFY', 441-450, 461-663 <DEM>  
A:Cross-references: EMBL:S96247  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: leukotriene biosynthesis; oxidoreductase

Query Match 87.9%; Score 3090; DB 2; Length 663;  
Best Local Similarity 86.1%; Pred. No. 4.8e-245;  
Matches 571; Conservative 48; Mismatches 42; Indels 2; Gaps 2;

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QY 1 MGLYRIRVSTGASLYAGSNQVQLMWVGQHGAAALGKRLWPARG-ETELKVEVPEYLGPL 59
DB 1 MGLYRIRVSTGSSFCAGSNQVHLWVGEGEAAALGWAVRPARGKEVEFQVDVSEYLGRL 60
QY 60 LFVKLRKRLHLLKDDAWFCNWIISVQGGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVGED 118
DB 61 LFVKLRKRLHLLSDDAWFCNWIISVQGGAGDEVRFPFCYRWVEGNGVLSLPEGTGRTVDD 120
QY 119 PQGLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRDVDFEVSIA 178
DB 121 PQGLFQKHREELERKLYRWGNWKGDLINMAGAKLYDLPVDERFLEDKRDVDFEVSIA 180
QY 179 KGLADLAIKDSLNLVTCWKDLDDFNRIFWCGQSKLAERVRDSWKEDALFGYQFLNGANPV 238
DB 181 KGLADLAIKDSLNLVTCWKDLDDFNRIFWCGQSKLAERVRDSWKEDALFGYQFLNGANPV 240
QY 239 VLRRSAHLPARLVPPPGMEELQALEKELEGTLFEADFSLLDGIKANVILCSQOHLAAP 298
DB 241 LLRRSVRLPARLEFPFGMGELQAELEKELQOQTLFEADFSLLMGIKANVILCTQOYVAP 300
QY 299 LVMLKLPDQDKLLPMVLIQOLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELOS 358
DB 301 LVMLKLPDQDKLLPMVLIQOLPHKGSPPPPPLFLPTDPPMTWLLAKCWRSSDFQLHELHS 360
QY 359 LLRGHLMAEVIVVATMRCPLSIHPFKLIIPHLYLTLEINVRARTGLVSDMGIFDQIMS 418
DB 361 LLRGHLMAEVIVATVATMRCPLSIHPFMFKLIPHLYTMEINIRARTGLVSDSGVDFQVVS 420
QY 419 TGGGHVQLLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIYYRVVEGIV 478
DB 421 TGGGHVQLLKQAGAFITYSSFCPPDDADRLGKLVKSSFYAODALRLWEIYYRVVEGIV 480
QY 479 SLHYKTDAVKDDPELQTCREITEIGLOAQDRGFVPSLQARDQVCHFTVTCIETCTGQ 538
DB 481 SLHYKTDSVRDDIELOQWCRDITEIGLLGAQDRGFVPSLQAKOQCHFTVTCIETCTGQ 540
QY 539 HASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATLETVMATLPNFHQASLQMSITWQLGR 598
DB 541 HSSVHLGQLDWYSWVPNAPCTMRLPPPTTKDVTLEKVMATLPNFHQASLQMSITWQLGR 600
QY 599 QNMVAVQOHEEYFSGPEPKAVLKKFREELAAALDKEIEIRNAKLDMPYELRPSVVENS 658
DB 601 QPIMVALQOHEEYFSGPEPKAVLKKFREELAAALDKEIEIRNAQLDMPYELRPSVLVENS 660
QY 659 VAI 661
DB 661 VAI 663
```

RESULT 3  
A35087  
arachidonate 12-lipoxygenase (EC 1.13.11.31) - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A35087



R.Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.; Tanabe, T.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 2142-2146, 1990  
 A>Title: Cloning and sequence analysis of the cDNA for arachidonate 12-lipoxygenase of B  
 A:Reference number: A35087; MUID:90192763; PMID:2315307  
 A:Accession: A35087  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-663 <YOS>  
 A:CROSS-references: UNIPROT:P16469; GB:M31417  
 C:Superfamily: arachidonate 5-lipoxygenase  
 C:Keywords: oxidoreductase

```

Query Match      87.1%; Score 3060; DB 1; Length 663;
Best Local Similarity 86.1%; Pred. No. 1.4e-242;
Matches 571; Conservative 40; Mismatches 50; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNQVQLVWGQHGAAALGKRLWPARG-ETELKVEVPYLGPL 59
DB 1 MGLYRIRVSTGSSFYAGSQVQLVWGQHGAAALGKRLWPARGKETEFSDVSEYLGPL 60
QY 60 LFLVLRKRLHLLKDDAWFCNWIISVQGPAG-GDEVRFPCYRWVGNVGLSPECTGRTVGED 118
DB 61 LFLVLRKRLHLLKDDAWFCNWIISVQGPAGGDEFRPCYRWVGNVGLSPECTARTVDD 120
QY 119 PQGLFQKHREELERRKLYRWGNKDGILINMAGAKLYDLVDFERFLEDKRVDPEVSLA 178
DB 121 PQGLFQKHREELERRKLYRWGNKDGILINMAGAKLYDLVDFERFLEDKRIDFEASLA 180
QY 179 KGLADLAIKDSLNLVTCWKDLDDFNRIFCWGOSKLAERVRDSWKEDALFGYQFLNGANPV 238
DB 181 KGLADLAIKDSLNLVTCWKDLDDFNRIFCWGOSKLAERVRDSWKEDALFGYQFLNGANPV 240
QY 239 VLRRSAHLPARLVPPPGMEELQAQLEKELEGTLFEADFSLLDGKANKVILCSQOHLAAP 298
DB 241 LLRHSVELPARLKFPFGMEELQAQLEKELEGTLFEADFSLLDGKANKVILCSQOHLAAP 300
QY 299 LVMLKLQDPGKLLPMVIOQLPRTGSPPPPLPLPTDPPMAMLLAKCWRSSDFQLHELQS 358
DB 301 LVMLKLQDPGKLLPMVIOQLPRTGSPPPPLPLPTDPPMAMLLAKCWRSSDFQLHELQS 360
QY 359 HLLRGLHMAEIVTAVTMCPLSIHPIFKLILPHRYTLLEINVRTGLVSDMGIDQIMS 418
DB 361 HLLRGLHMAEIVTAVTMCPLSIHPIFKLILPHRYTLLEINVRTGLVSDMGIDQIMS 420
QY 419 TGGGGHVOLLKQAGAFVLTYSFPCPPDDADRLGLGVKSFYAQDALRLWEIIRYVEGIV 478
DB 421 TGGGGHVOLLKQAGAFVLTYSFPCPPDDADRLGLGVKSFYAQDALRLWEIIRYVEGIV 480
QY 479 SLHYKTDVAVKDDPELQVTCREITIGLQAGQDRGFPVSLQARDQVCHFTVMCIPTCTGQ 538
DB 481 SLHYKTDVAVKDDPELQVTCREITIGLQAGQDRGFPVSLQARDQVCHFTVMCIPTCTGQ 540
QY 539 HASVHLGQLDWYSWVNPACTNRLPPPTTKDNLLETVATLNPFHQASLQMSITWQLGR 598
DB 541 HSSNHLGQLDWYSWVNPACTNRLPPPTTKDNLLETVATLNPFHQASLQMSITWQLGR 600
QY 599 QPVMVAVGQHEEYFSGPEPKAVLKFFREELAAALDKETEIRNAKLDMPVEYLRPSSVNS 658
DB 601 QPVMVAVGQHEEYFSGPEPKAVLKFFREELAAALDKETEIRNAKLDMPVEYLRPSSVNS 660
QY 659 VAI 661
DB 661 VAI 663

```

RESULT 4  
 JQ0018  
 arachidonate 15-lipoxygenase (EC 1.13.11.33), erythroid-specific - rabbit  
 N:Alternate names: carotene oxidase; lipoxidase  
 N:Contains: lipoxygenase peptides  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: JQ0018; A61060; A27327; A61568; JC1513

R.Fleming, J.; Thiele, B.J.; Chester, J.; O'Prey, J.; Janetzki, S.; Aitken, A.; Anton, I.  
 Gene 79, 181-188, 1989  
 A>Title: The complete sequence of the rabbit erythroid cell-specific 15-lipoxygenase mRNA  
 A:Reference number: JQ0018; MUID:89378774; PMID:2777088  
 A:Accession: JQ0018  
 A:Molecule type: mRNA  
 A:Residues: 1-663 <FILE>  
 A:CROSS-references: UNIPROT:P12530; GB:M27214; NID:92642134; PIDN:AAS86978.1; PID:g16490;  
 R:Thiele, B.J.; Fleming, J.; Chester, J.; O'Prey, J.; Prehn, S.; Janetzki, S.; Rapoport,  
 Biomed. Biochim. Acta 49, s17-s24, 1990  
 A>Title: Structure of the mRNA and of the gene coding for the rabbit erythroid 15-lipoxyg  
 A:Reference number: A61060; MUID:90351403; PMID:2386503  
 A:Accession: A61060  
 A>Status: not compared with conceptual translation  
 A:Molecule type: mRNA; DNA  
 A:Residues: 2-605,'F',607-663 <THI>  
 A>Note: nucleotide sequence is given only for intron/exon boundaries  
 R:Thiele, B.J.; Fleming, J.; Kasturi, K.; O'Prey, J.; Black, E.; Chester, J.; Rapoport, S.  
 Gene 57, 111-119, 1987  
 A>Title: Cloning of a rabbit erythroid-cell-specific lipoxygenase mRNA.  
 A:Reference number: A27327; MUID:88112854; PMID:3123326  
 A:Accession: A27327  
 A:Molecule type: mRNA  
 A:Residues: 1-31 <TH2>  
 A:CROSS-references: GB:M33291  
 R:Thiele, B.J.; Black, E.; Fleming, J.; Nack, B.; Rapoport, S.M.; Harrison, P.R.  
 Biomed. Biochim. Acta 46, S120-S123, 1987  
 A>Title: Cloning of reticulocyte lipoxygenase mRNA.  
 A:Reference number: A61568; MUID:87241419; PMID:3109402  
 A:Accession: A61568  
 A:Molecule type: mRNA  
 A:Residues: 1-40,'SHEH',540-582,'S' <TH3>  
 A>Note: this clone was reevaluated in reference JQ0018 and is thought to represent a clor  
 R:O'Prey, J.; Chester, J.; Thiele, B.J.; Janetzki, S.; Prehn, S.; Fleming, J.; Harrison,  
 Gene 84, 493-499, 1989  
 A>Title: The promoter structure and complete sequence of the gene encoding the rabbit ery  
 A:Reference number: JC1513; MUID:90128296; PMID:2612916  
 A:Accession: JC1513  
 A:Molecule type: DNA  
 A:Residues: 1-112,'T',114-189,'N',191-193,'I',195-663 <OPR>  
 A:CROSS-references: GB:M33291; NID:g164731; PIDN:AAA75014.1; PID:g164732  
 C:Comment: Rabbit reticulocyte lipoxygenase plays a role in the degradation of mitochond  
 C:Comment: This enzyme catalyzes the dioxygenation of polyenoic fatty acids containing at  
 C:Genetics:  
 A:Gene: 15-Lox  
 A:Introns: 45/3; 114/1; 141/2; 182/2; 217/1; 270/3; 318/3; 388/3; 417/3; 474/2; 515/1; 54  
 C:Superfamily: arachidonate 5-lipoxygenase  
 C:Keywords: erythrocyte; iron; oxidoreductase

```

Query Match      82.4%; Score 2896; DB 1; Length 663;
Best Local Similarity 81.1%; Pred. No. 3.9e-229;
Matches 538; Conservative 57; Mismatches 66; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNQVQLVWGQHGAAALGKRLWPARG-ETELKVEVPYLGPL 59
DB 1 MGLYRIRVSTGASLYAGSNQVQLVWGQHGAAALGKRLWPARG-ETELKVEVPYLGPL 60
QY 60 LFLVLRKRLHLLKDDAWFCNWIISVQGPAG-GDEVRFPCYRWVGNVGLSPECTGRTVGED 118
DB 61 LFLVLRKRLHLLKDDAWFCNWIISVQGPAGGDEFRPCYRWVGNVGLSPECTARTVDD 120
QY 119 PQGLFQKHREELERRKLYRWGNKDGILINMAGAKLYDLVDFERFLEDKRVDPEVSLA 178
DB 121 PQGLFQKHREELERRKLYRWGNKDGILINMAGAKLYDLVDFERFLEDKRIDFEASLA 180
QY 179 KGLADLAIKDSLNLVTCWKDLDDFNRIFCWGOSKLAERVRDSWKEDALFGYQFLNGANPV 238
DB 181 KGLADLAIKDSLNLVTCWKDLDDFNRIFCWGOSKLAERVRDSWKEDALFGYQFLNGANPV 240
QY 239 VLRRSAHLPARLVPPPGMEELQAQLEKELEGTLFEADFSLLDGKANKVILCSQOHLAAP 298
DB 241 LLRHSVELPARLKFPFGMEELQAQLEKELEGTLFEADFSLLDGKANKVILCSQOHLAAP 300

```



Db 361 HLLRGHLMAEVAVATMCLPSVHFVFKLLVPHLLYTWEINVRARSDLISERGFFDKMS 420  
 Qy 419 TGGGGHVLKQAGAFITYSSFCPPDDLDADRLGLGVKSSFYAQDALRLWEIYYRVEGIV 478  
 Db 421 TGGGGHLLDLKQAGAFITYSSFCPPDDLDADRLGLGVKSSFYAQDALRLWEIYYRVEGIV 480  
 Qy 479 SLHYKTDVAVKDDPELOTWCREITIGLQAGQDRGFVSLQARDQVCHFTVTCITCTGQ 538  
 Db 481 NLHYKTDKAVQDDYELQSWCREITIGLQAGQDRGFVSLQARDQVCHFTVTCITCTGQ 540  
 Qy 539 HASVHLGOLDWYSVWPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRR 598  
 Db 541 HSSVHLGOLDWYSVWPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRR 600  
 Qy 599 QPVMVAVGQHEEYFSGPEPKAVLKKFREELAALDKETIEIRNAKLDMPYEYLRPSVENS 658  
 Db 601 QAVMVPLGQHSSEHFPNPEAKAVLKKFREELAALDKETIEIRNAKLDMPYEYLRPSVENS 660  
 Qy 659 VAI 661  
 Db 661 VAI 663

## RESULT 7

arachidonate 12-lipoxygenase (EC 1.13.11.31), leukocyte [validated] - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
 C:Accession: B54075; 149439  
 R:Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.  
 J. Biol. Chem. 269, 13979-13987, 1994  
 A:Title: cDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure  
 A:Reference number: A54075; MUID:94245713; PMID:8188678  
 A:Accession: B54075  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-663 <CHE>  
 A:Cross-references: UNIPROT:P39654; GB:U04331; NID:9467216; PIDN:AAA20658.1; PID:9467217  
 A:Experimental source: strains C57BL/6 and ICR, spleen leukocytes  
 A:Note: removal or substitution of Ile-663 abolished enzyme activity  
 R:Freire-Moar, J.; Alavi-Nassab, A.; Ng, M.; Mulkins, M.; Sigal, E.  
 Biochim. Biophys. Acta 1254, 112-116, 1995  
 A:Title: Cloning and characterization of a murine macrophage lipoxygenase.  
 A:Reference number: 149439; MUID:95110857; PMID:7811740  
 A:Accession: 149439  
 A>Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-36, 'N', 38-118, 'Q', 120-396, 'N', 398-663 <RES>  
 A:Cross-references: GB:L34570; NID:9509607; PIDN:AAA64930.1; PID:9763530  
 C:Comment: A second arachidonate 12-lipoxygenase from mouse platelets is shown in (PIR:A  
 C:Genetics:  
 A:Map position: 11  
 C:Superfamily: arachidonate 5-lipoxygenase  
 C:Keywords: oxidoreductase

Query Match 76.2%; Score 2676; DB 1; Length 663;  
 Best Local Similarity 73.6%; Pred. No. 4.3e-211;  
 Matches 488; Conservative 80; Mismatches 93; Indels 2; Gaps 2;  
 Qy 1 MGLYRIRVSTGASLYAGSNVQVLIVGQHGGAALGKRLWPAR-CETELKVEVPYILGPL 59  
 Db 1 MGVIYRIVSTGDSVYAGSNNEVYLLIGQHGGAALGKRLWPAR-CETELKVEVPYILGPL 60  
 Qy 60 LFLVLRKRLKDDDAWFCNWIISVQGP-AGDVRFPYVWEGNGLVSLPEGTGRTGVED 118  
 Db 61 LFRVQKRWYLLKEDDAWFCNWIISVQGPQGGSYTFPCIRVWQGTSLMDPEGTGCTVVED 120  
 Qy 119 PQGLFKQKREELERRLKLYRGNKWDGLILNMAGAKLYDLVDFRFRLEDKRVDFEVL 178  
 Db 121 SQGLFRNREELERRLKLYRGNKWDGLILNMAGAKLYDLVDFRFRLEDKRVDFEVL 180  
 Qy 179 KGLADLAIKOSLNVLTCKWDLDFNRFWCGOSKLAERVRSWKSDALFGYQFLNGANPV 238

Db 181 LGTMDTVINPPKNTVTCKWSLDDFNYYVFKSGHTKMAERVRNSWKEDAFPGYQFLNGANPM 240  
 Qy 239 VLRSASHLPARLVPPPGMEELQALKEKELEGTTFEADFSLLDGKANVILCSQHLAAP 298  
 Db 241 VLKSTCLPARLVPPPGMEELQALKEKELEGTTFEADFSLLDGKANVILCSQHLAAP 300  
 Qy 299 LVMLKLPDQDKLPMVLOLQPLRTGSPPPPLFTPTDPPMAVLLAKCWVRSSDFOLHELQS 358  
 Db 301 LVMLKLPDQDKLPMVLOLQPLRTGSPPPPLFTPTDPPMAVLLAKCWVRSSDFOLHELQS 360  
 Qy 359 HLLRGHLMAEVAVATMCLPSVHFVFKLLVPHLLYTWEINVRARSDLISERGFFDKMS 418  
 Db 361 HLLRGHLMAEVAVATMCLPSVHFVFKLLVPHLLYTWEINVRARSDLISERGFFDKMS 420  
 Qy 419 TGGGGHVLKQAGAFITYSSFCPPDDLDADRLGLGVKSSFYAQDALRLWEIYYRVEGIV 478  
 Db 421 TGGGGHLLDLKQAGAFITYSSFCPPDDLDADRLGLGVKSSFYAQDALRLWEIYYRVEGIV 480  
 Qy 479 SLHYKTDVAVKDDPELOTWCREITIGLQAGQDRGFVSLQARDQVCHFTVTCITCTGQ 538  
 Db 481 NLHYKTDKAVQDDYELQSWCREITIGLQAGQDRGFVSLQARDQVCHFTVTCITCTGQ 540  
 Qy 539 HASVHLGOLDWYSVWPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRR 598  
 Db 541 HSSVHLGOLDWYSVWPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRR 600  
 Qy 599 QPVMVAVGQHEEYFSGPEPKAVLKKFREELAALDKETIEIRNAKLDMPYEYLRPSVENS 658  
 Db 601 QAVMVPLGQHSSEHFPNPEAKAVLKKFREELAALDKETIEIRNAKLDMPYEYLRPSVENS 660  
 Qy 659 VAI 661  
 Db 661 VAI 663

## RESULT 8

arachidonate 12-lipoxygenase (EC 1.13.11.31) - human  
 N:Alternate names: platelet-type 12-lipoxygenase  
 C:Species: Homo sapiens (man)  
 C>Date: 31-May-1991 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004  
 C:Accession: A38283; A36246; A35953; 151906; 164836; A33091  
 R:Fizumi, T.; Hoshiko, S.; Radmark, O.; Samuelsson, B.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 7477-7481, 1990  
 A:Title: Cloning of the cDNA for human 12-lipoxygenase.  
 A:Reference number: A38283; MUID:91017529; PMID:2217179  
 A:Accession: A38283  
 A:Molecule type: mRNA  
 A:Residues: 1-663 <IZU>  
 A:Cross-references: UNIPROT:P18054; UNIPROT:Q16120; GB:M38192; GB:M38792; GB:M58704; NID:  
 A:Experimental source: platelet mRNA  
 A:Note: some sequence heterogeneity was found  
 R:Yoshimoto, T.; Yamamoto, Y.; Arakawa, T.; Suzuki, H.; Yamamoto, S.; Yokoyama, C.; Tanai  
 Biochem. Biophys. Res. Commun. 172, 1230-1235, 1990  
 A:Title: Molecular cloning and expression of human arachidonate 12-lipoxygenase.  
 A:Reference number: A36246; MUID:91058562; PMID:2244907  
 A:Accession: A36246  
 A:Molecule type: mRNA  
 A:Residues: 1-188, 'PCLH', 193-260, 'Q', 262-321, 'S', 323-344, 'C', 346-663 <YOS>  
 A:Cross-references: GB:M62982; NID:9177106; PIDN:AAA51533.1; PID:9177107  
 R:Funk, C.D.; Furci, L.; FitzGerald, G.A.  
 Proc. Natl. Acad. Sci. U.S.A. 87, 5638-5642, 1990  
 A:Title: Molecular cloning, primary structure, and expression of the human platelet/eryth  
 A:Reference number: A35953; MUID:90332636; PMID:2377602  
 A:Accession: A35953  
 A:Molecule type: mRNA  
 A:Residues: 1-260, 'Q', 262-321, 'S', 323-388, 'P', 390-663 <FUN>  
 A:Cross-references: GB:M35418; NID:9189773; PIDN:AAA60056.1; PID:9189774  
 R:Husain, H.; Shornick, L.P.; Shannon, V.R.; Wilson, J.D.; Funk, C.D.; Pentland, A.P.; I  
 Am. J. Physiol. 266, C243-C253, 1994  
 A:Title: Epidermis contains platelet-type 12-lipoxygenase that is overexpressed in germi  
 A:Reference number: 151906; MUID:94135572; PMID:8304420  
 A:Accession: 151906

A>Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 340-427 <RES>

A:Cross-references: GB:S68587; NID:G545223; PIDN:AAAD14020.1; PID:g4261720

A:Experimental source: skin, epidermal cells

A:Accession: I64836

A>Status: translation not shown; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 340-396, 'V', 398-427 <RES>

A:Cross-references: GB:S68588; NID:G545222; PIDN:AAAD14021.1; PID:g4261721

C:Genetics:

A:Gene: GDB:ALOX12

A:Cross-references: GDB:127547; OMIM:152391

A:Map position: 17p13.1-17p13.1

C:Function:

A:Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,10E,14Z)-(12S)-12-H

A:Pathway: leukotriene biosynthesis

C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidoreductase

F:360,365,540,544,663/Binding site: iron (His, His, Asn, Ile) #status predicted

Query Match 65.8%; Score 2312; DB 1; Length 663;  
Best Local Similarity 65.3%; Pred. No. 3e-181;  
Matches 433; Conservative 94; Mismatches 134; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVGQGEAALGKRLWPARG-ETELKVEVPEVLGPL 59

DB 1 MGRYRIRVATGAWLFGSGYNRQLWLVGTRGAELEQLRPARGEEEEFDHVAEDLGLL 60

QY 60 LFFVKLRKRLKDDDAWFCNWIISVQGGAGDEVRFPCYRWVEGNVLSPEGTGRTVGEDP 119

DB 61 QFVLRKXHWLVDDAWFCDDITVQGGACAEAVFPCYRWVQGEDILSLPEGTARLPGDNA 120

QY 120 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLVDERFLEDKRVDFEVSIAK 179

DB 121 LDMFQKHREKELKROQIYCWATWKEGLPLTIAADRKDDLPPNMRPHEEKRLDFEWTLKA 180

QY 180 GLADLAIKDSLNLVTCWKDLDDFNRIFWCGSKLAERVDSWKEDALFGYQFLNGANPVV 239

DB 181 GALEMALKRVYTLSSWNCLEDFDQIFWGQKSALEAKVQCQWDDLELFSYQFLNGANPML 240

QY 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 299

DB 241 LRRSTSLPSRLVLPSCMEELQAQLEKELQNGLSLFEADFLLDGIPANVIRGEKQVLAAPL 300

QY 300 VMLKLOPDGKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 359

DB 301 VMLKMEPNGKLOPMVIOIQPPNPSSPTPLFLPSDPPPLAWLLAKSWVRNSDFQLHEIOYH 360

QY 360 LLRGHLMAEVIIVATWRCPLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 419

DB 361 LINTHLVAEVIIVATWRCPLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 420

QY 420 GGGGHVQLLKOAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWELIIVRYVEGIVS 479

DB 421 GGGGHVQLLRRAAQLTYCSLCPDDLADRGLLGLPGALYAHDAALRLWELIIVRYVEGIVH 480

QY 480 LHYKTDVAVKDDPELQWCREITEIGLOAQDRGFPVSLQARDQVCHFTVTCIPTCTGOH 539

DB 481 LFYQSDDIIVKGDPELQWCREITEVGLCHAQDRGFPVSPQSQSLCHFLTMCVFTCTAQH 540

QY 540 ASVHLGOLDWYSWPNAPCTMRLPPPTTK-DATLETVMATLNFHQAQLQMSITWOLGRR 598

DB 541 AAINQQLQDWYAWPNAPCTMRLPPPTTKEDVTMTVMGSLPDVDRQACIQMAISWHLRR 600

QY 599 QPVMVAVGOHEEYFSGPEPKAVLKKFREELAAALDKKEIIRNAKLDMPYEYLRPSVENS 658

DB 601 QPDMPVLGHKKEKYFSGPKPAVLNQFRITDLEKLEKEITARNEQDLDPYEYLRKPSCIENS 660

QY 659 VAI 661

DB 661 VTI 663

RESULT 9

AS4075

arachidonate 12-lipoxygenase (EC 1.13.11.31), platelet [validated] - mouse

C:Species: Mus musculus (house mouse)

C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004

C:Accession: A54075

R:Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.

J. Biol. Chem. 269, 13979-13987, 1994

A:Title: cDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure

A:Reference number: A54075; MUID:94245713; PMID:8188678

A:Accession: A54075

A:Molecule type: DNA; mRNA

A:Residues: 1-663 <CHE>

A:Cross-references: UNIPROT:P39655; GB:U04334; NID:g467220; PIDN:AAA20659.1; PID:g467221

A:Experimental source: strain C57BL/6, blood platelets

A:Note: removal or substitution of Ile-663 abolished enzyme activity

C:Comment: A second arachidonate 12-lipoxygenase from mouse leukocytes is shown in (PIR: S00001)

C:Genetics:

A:Map position: 11

C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: oxidoreductase

Query Match 64.1%; Score 2252; DB 1; Length 663;

Best Local Similarity 63.3%; Pred. No. 2.5e-176;

Matches 420; Conservative 96; Mismatches 145; Indels 2; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVGQGEAALGKRLWPARG-ETELKVEVPEVLGPL 59

DB 1 MGAYRVRVVTGAWLFGSGSLNLVRLWLVGHEHREAKLEQLRPARGEBEEDFDFVDEDLGPL 60

QY 60 LFFVKLRKRLKDDDAWFCNWIISVQGGAGDEVRFPCYRWVEGNVLSPEGTGRTVGEDP 119

DB 61 QFVKLKHQTVDDAWFCNLLITVQGGTSAEAVFPCYRWVQEGILSLPEGOARLAGDNA 120

QY 120 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLVDERFLEDKRVDFEVSIAK 179

DB 121 LDVFKYREKELKROQTYCWATWKEGLPQTIAADCKDDLPPNMRPHEEKRLDFEWTLKA 180

QY 180 GLADLAIKDSLNLVTCWKDLDDFNRIFWCGSKLAERVDSWKEDALFGYQFLNGANPVV 239

DB 181 GYLEMGLKRVYTLSSWNLHEDFQIFWGQKSALEAKVHCQWQDELFQYQFLNGANPML 240

QY 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGGTLFEADFSLLDGIKANVILCSQQHLAAPL 299

DB 241 LRRSTSLPSRLVLPSCMEELQAQLEKELKNGSLFEADFLLDGIPANVIRGEPPQVLAAPL 300

QY 300 VMLKLOPDGKLLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDFQLHELQSH 359

DB 301 VMLRMDPGKLLPMAIOIQPPNPSSPAPTFLFLPSDPPPLAWLLAKIWNVRNSDFQLQELQSH 360

QY 360 LLRGHLMAEVIIVATWRCPLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 419

DB 361 LINTHLVAEVIIVATWRCPLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMST 420

QY 420 GGGGHVQLLKOAGAFITYSSFCPPDDLADRGLLGVKSSFYAQDALRLWELIIVRYVEGIVS 479

DB 421 GGGGHVQLLTRAVALTYHSLCPDDLANRGLLRIPSALYARDALQLEWTVARYVKGWVH 480

QY 480 LHYKTDVAVKDDPELQWCREITEIGLOAQDRGFPVSLQARDQVCHFTVTCIPTCTGOH 539

DB 481 LFYQSDDIIVKGDPELQWCREITEVGLCHAQDRGFPVSPQSQAQLCHFLTMCVFTCTAQH 540

QY 540 ASVHLGOLDWYSWPNAPCTMRLPPPTTK-DATLETVMATLNFHQAQLQMSITWOLGRR 598

DB 541 AAINQQLQDWYAWPNAPCTMRLPPPTTKDQDVTMTVMGSLPDVQKACIQMTIWHLGRU 600

QY 599 QPVMVAVGOHEEYFSGPEPKAVLKKFREELAAALDKKEIIRNAKLDMPYEYLRPSVENS 658

DB 601 QPDMPVLGHKKEKYFSDPRTKAVLSQFQADLNLKEITARNEQDLDPYEYLRKPSIENS 660

QY 659 VAI 661

DB 661 VTI 663

Db 661 ITI 663

## RESULT 10

I49479  
arachidonate 5-lipoxygenase - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49479  
R:Chen, X.S.; Naumann, T.A.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.  
J. Biol. Chem. 270, 17993-17999, 1995  
A:Title: cDNA cloning, expression, mutagenesis, intracellular localization, and gene characterization of the mouse 5-lipoxygenase.  
A:Reference number: A57186; MUID:95355399; PMID:7629107  
A:Accession: I49479  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-674 <RES>  
A:Cross-references: UNIPROT:P48999; GB:L42198; NID:G886332; PIDN:AAC37673.1; PID:G886333  
C:Genetics:  
C:Superfamily: arachidonate 5-lipoxygenase

Query Match 37.0%; Score 1299.5; DB 2; Length 674;  
Best Local Similarity 39.3%; Pred. No. 3.3e-98;  
Matches 266; Conservative 142; Mismatches 250; Indels 19; Gaps 10;

Qy 1 MGLYRIRVSTGASLYAGSNQVQLVVGQHG---EAALGKRLWP--ARGETE-LKVEYPE 54

Db 1 MPSYTVTVATGQSFAGTDDYIYLSLIGSAGCSKXHLDDKAFYNDFERGAVDSYDVTDE 60

Qy 55 YLGPLLFLVKLRKRLHLLKDDAFCNWIISVQPGAGDEVFPFCYRWVEGNGVSLPFGTGT 114

Db 61 ELGEIYLVKIEKRWKLLHDDWTLKYLTKTP-HGDIYIEFPFCYRWITGEIVLRDGRAL 119

Qy 115 VGEDPQGLFQKHREELERKLYRWGNKQGLILNMGAKLYDLPVDERFLEDKRVDPE 174

Db 120 ARDDQIHLKQHRKELEARQKQYRWMEWNPFGFLSIDAKCHKDLPRDIQFDSEKGVDFV 179

Qy 175 VSLAKGLADLAITKLSNLVLCWKLDDFNRFWCGQSKLARRVRSWKEDALFGYQFLN 233

Db 180 LNYSKAMENLFNRFMEFQSSMHDFADEKIFVKISNTISERVKNHQEDLMFCYQFLN 239

Qy 234 GANPVVLARSALPARLVPPQWEEL----QAQLEKELEGGLFPAESLLDGIKAN-VI 288

Db 240 GCNPVLIRKCTALPKPLPVTTMEVCSLERQLSLQEVEQGNFIVDYELLIDGIDANKTD 299

Qy 289 LCSQQLAALPLVWLKLPQDKLPLWVIOQLPRTGSPPPPLPLPTDPPMALLKCVWS 348

Db 300 PCTHQFLAIPICLLYKLNANKVPIAQLN--QTGCSNPILPLDTSKYDWLLAKIWS 357

Qy 349 SDFQLHELQSHLLRGLHMAEVIWVATMRCPLSIHPILFIPLRYTLEINVRARTGLVS 408

Db 358 SDFHVQITITLRLTHLVSEVFGIAMYRLPAVPLKLLVAHVFTTAINTKAREQLIC 417

Qy 409 DMGIIFDQIMSTGGHVLKQAGFLYVSSPCPPDDADRLGLLVKGS---FYAQDALR 465

Db 418 EYGLDFKANATGGGHVQVQRAVDLTYSLLCFPEAIKARGMDSTEDMPFYFYRDDGIL 477

Qy 466 LWEILYRVVEGVSLHYKTDVAKDDPELOTCWCRITEITGLOGAQRGPPVSLQARDQVC 525

Db 478 VMEALQSFTMEVVSIIYENDQVVEDEQLQDFVKDYVYVMGRKASGFPKSIKREKLS 537

Qy 526 HPVTMCIFCTCQHASVHLGQLDWTSWPNAPCTMRLPPPTTKD-ATLETVMATLPNFHQ 584

Db 538 EYLTIVVIFASQAHAHVNGQYDWCSPINAPPTWRAPPTAKGVVTEIQIVDTLPDRGR 597

Qy 585 ASLQMSITWQLGRRQFVWVAVGQHEEYFSGPEPKAVLKFFRELAALDKETIEINAKLD 644

Db 598 SCWHLGAVWALSQFQENELFLGMYPEEHFIEKPVKEAMIRFRKNLEAITSIAERNKKNK 657

Qy 645 MPEYVLRVSVENSVAI 661

Db 658 LPYIYLSPDRIIPNSVAI 674

## RESULT 11

## DAHUAL

arachidonate 5-lipoxygenase (EC 1.13.11.34) [validated] - human  
C:Species: Homo sapiens (man)  
C>Date: 31-Mar-1989 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004  
C:Accession: A28117; A37017; A28397; A32104; A38410  
R:Dixon, R.A.F.; Jones, R.E.; Diehl, R.E.; Bennett, C.D.; Kargman, S.; Rouzer, C.A.  
Proc. Natl. Acad. Sci. U.S.A. 85, 416-420, 1988  
A:Title: Cloning of the cDNA for human 5-lipoxygenase.  
A:Reference number: A28117; MUID:88124852; PMID:3422434  
A:Accession: A28117  
A:Molecule type: mRNA  
A:Residues: 1-674 <MATS>  
A:Cross-references: UNIPROT:P09917; GB:J03600; NID:g187192; PIDN:AAA36183.1; PID:g187193  
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.  
Adv. Prostaglandin Thromboxane Leukot. Res. 19, 466-469, 1989  
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.  
A:Reference number: A37017; MUID:89320027; PMID:2526519  
A:Accession: A37017  
A:Molecule type: mRNA  
A:Residues: 1-674 <MATS>  
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.  
Proc. Natl. Acad. Sci. U.S.A. 85, 26-30, 1988  
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.  
A:Reference number: A28397; MUID:88124804; PMID:2829172  
A:Accession: A28397  
A:Molecule type: mRNA  
A:Residues: 1-535; PVGVPRGDLHRLPARRGQLRPVRLVLLDPCQPNHASPATDCQ', 581-674 <RF1>  
A:Note: parts of the sequence report, including the amino end, were confirmed by protein sequencing.  
A:Note: This sequence appears to contain a frameshift error  
R:Funk, C.D.; Hoshiko, S.; Matsumoto, T.; Radmark, O.; Samuelsson, B.  
Proc. Natl. Acad. Sci. U.S.A. 86, 2587-2591, 1989  
A:Title: Characterization of the human 5-lipoxygenase gene.  
A:Reference number: A32104; MUID:89202374; PMID:2565035  
A:Accession: A32104  
A:Molecule type: DNA  
A:Residues: 1-50 <FUN>  
A:Cross-references: GB:J04520; NID:g187168; PIDN:AAA59522.1; PID:g187169  
R:Hoshiko, S.; Radmark, O.; Samuelsson, B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 9073-9077, 1990  
A:Title: Characterization of the human 5-lipoxygenase gene promoter.  
A:Reference number: A38410; MUID:91067649; PMID:2251250  
A:Accession: A38410  
A:Molecule type: DNA  
A:Residues: 1-11 <HOS>  
A:Cross-references: GB:M38191  
C:Comment: This calcium- and ATP-requiring enzyme catalyzes the first two steps in the biosynthesis of prostaglandins and thromboxane.  
C:Genetics:

Query Match 37.0%; Score 1298.5; DB 1; Length 674;  
Best Local Similarity 39.7%; Pred. No. 3.9e-98;  
Matches 269; Conservative 140; Mismatches 248; Indels 21; Gaps 11;

Qy 1 MGLYRIRVSTGASLYAGSNQVQLVVGQHG---EAALGKRLWP--ARGETE-LKVEYPE 54

Db 1 MPSYTVTVATGQSFAGTDDYIYLSLIGSAGCSKXHLDDKAFYNDFERGAVDSYDVTDE 60

Qy 55 YLGPLLFLVKLRKRLHLLKDDAFCNWIISVQPGAGDEVFPFCYRWVEGNGVSLPFGTGT 114

Db 61 ELGEIYLVKIEKRWKLLHDDWTLKYLTKTP-HGDIYIEFPFCYRWITGEIVLRDGRAL 119

Qy 115 VGEDPQGLFQKHREELERKLYRWGNKQGLILNMGAKLYDLPVDERFLEDKRVDPE 174

Db 120 ARDDQIHLKQHRKELETRQKQYRWMEWNPFGFLSIDAKCHKDLPRDIQFDSEKGVDFV 179

QY	175	VSLAKGLADLAIKDSLNVL-TCKWLDLDDFNRIFWCQSKLAERVRDSWKEDALFGYQFLN	233
Db	180	LNYSKAMENLFNRMHMFQSSWNDPADPEKIFVKISNTISERVNMHWQEDLMFGYQFLN	239
QY	234	GANPVVLRSAHLPARLVFPFGMEEL-----QAQLEKELEGGLTFEADPSLDDGIKAN-VI	288
Db	240	GNPVLIRRETELPEKLPVTTEMVECSLERQSLSEQVEQGNIFIVDFELLDDIGIDANKTD	299
QY	289	LCSQOHLAAPLVMLKLQPDGKLLPMVIOQLPRTGSPPPPLPLPTDPPMAWLLAKCWVR	348
Db	300	PCTLQFLAAPICLLYKNLANKIVPIAQLNQIP---GDNPIFLPSDAKYDWLLAKIWR	356
QY	348	SSDFQLHELQSHLLRGLHMAEIVVATMRLPSIHPIFKLIIPHLYRTLEINVRARTGLV	407
Db	357	SSDFHVHQITITHLRTHLVSEVFGIAMYRQLPAVHPIFKLLVAHVRFITAINTKAREQLI	416
QY	408	SDMGIFDQIMSTGGGGHVQLLKQAQAFLYSSFCPPDDLADRLGLG---VKSFYAQDAL	464
Db	417	CEGCLFDKANATGGGGHVQVQRAMKDLTYASLCFPEAIKARGMESKEDIPIFYFYRDDGL	476
QY	465	RLWEIIRYVVEGIVSLHYKTDVAVKDDPELQWTCREITEIGLQGAQDRGFPVLSLOARDQV	524
Db	477	LWNEALRTTAEVVDIYYEGDQVVEEDPELQFVNDVYVYVGRKSSGFPKSVKSRQL	536
QY	525	CHFVTWCIFCTGQHASVHLGQLDWYSWVPNAPCTMRLPPPTTKO-ATLETVMATLPNFH	583
Db	537	SEYLTVVIFTASAQAHAANFGQYDWCWIPNAPPTWRAPPTAKGVVTIEQIVDTLPDRG	596
QY	584	QASLQMSITWQLGRROPVMAVGOHEEYFSGPEPKAVLKFRBELAALDKIEIRNAKL	643
Db	597	RSCWHLGAVWALSQFQENELFLGMYPEEHFIEKPVKEAMARFRKNLEAIVSVIAERNKKK	656
QY	644	DMPEYELRPSVENSVAI 661	
Db	657	QLPYLYLSDRIPNSVAI 674	
RESULT 12			
A30882			
arachidonate 5-lipoxygenase (EC 1.13.11.34) - rat			
C:Species: Rattus norvegicus (Norway rat)			
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004			
C:Accession: A30882			
R:Balcarek, J.M.; Theisen, T.W.; Cook, M.N.; Varrichio, A.; Hwang, S.M.; Strohsacker, M.			
J. Biol. Chem. 263, 13937-13941, 1988			
A>Title: Isolation and characterization of a cDNA clone encoding rat 5-lipoxygenase.			
A:Reference number: A30882; MUID:88330933; PMID:3417684			
A:Accession: A30882			
A:Molecule type: mRNA			
A:Residues: 1-670 <BAL>			
A:Cross-references: UNIPROT:P12527; GB:J03960; NID:g205228; PIDN:AAA41538.1; PID:g205229			
C:Superfamily: arachidonate 5-lipoxygenase			
C:Keywords: oxidoreductase			
Query Match 36.1%; Score 1270; DB 1; Length 670;			
Best Local Similarity 38.8%; Pred. No. 8.5e-96;			
Matches 259; Conservative 139; Mismatches 250; Indels 20; Gaps 9;			
QY	1	MGLYRVRVSTGASLYAGSNQVQLWLVQHG---EALGKRILW---PARGETELKVEYVE	54
Db	1	MPSYTVTVATGSQLFAGTDDIYLYSLIGSAGCSEKHLDDKAFYNDPFRGGRSDYVTVD	60
QY	55	YLGPLLVKLRKRHLKDDAFCNWLISVQPGAGDEVFPYRVRWVGNGVLSLPEGTGRT	114
Db	61	ELGEIYLVKIEKKYRLHLDWYLUKYLTKLP--HDYIEFPCTRWITGEIEVLURDCAKL	118
QY	115	VGSDPQGLFOKHREBELEERKLYRWGNWKDGLILNAGAKLYDLVPDRFLDKRVDFE	174
Db	119	ARDDQIHILKHQRKELETRQKYRWMEWNPGLPLSIDAKCHKDLPRDIQFDSEKGVDFV	178
QY	175	VSLAKGLADLAIKDSLNVL-TCKWLDLDDFNRIFWCQSKLAERVRDSWKEDALFGYQFLN	233

Db	179	LNYSKAMENLFNRMHMFQSSWHDPADPEKIFVKISNTISERVNMHWQEDLMFGYQFLN	238
QY	234	GANPVVLRSAHLPARLVFPFGMEEL-----QAQLEKELEGGLTFEADPSLDDGIKAN-VI	288
Db	239	GNPVLIRRETELPEKLPVTTEMVECSLERQSLSEQVEQGNIFIVDYELLDDIGIDANKTD	298
QY	289	LCSQOHLAAPLVMLKLQPDGKLLPMVIOQLPRTGSPPPPLPLPTDPPMAWLLAKCWVR	348
Db	299	PCTHQLAAPTCLLYKNLANKIVPIAQLN--QTPGEKNPIFLPTDSKYDWLLAKIWR	356
QY	349	SDFQLHELQSHLLRGLHMAEIVVATMRLPSIHPIFKLIIPHLYRTLEINVRARTGLVS	408
Db	357	SDFHLHQITITHLRTHLVSEVFGIAMYRQLPAVHPIFKLLVAHVRFITAINTKAREQLNC	416
QY	409	DMGIFDQIMSTGGGGHVQLLKQAQAFLYSSFCPPDDLADRLGLGVKS---SFYAQDALR	465
Db	417	EYGLFDKANATGGGGHVQVQRAVQDLTYSSLCFPEAIKARGMONTEDIPYFYFYRDDGLL	476
QY	466	LWEIIRYVVEGIVSLHYKTDVAVKDDPELQWTCREITEIGLQGAQDRGFPVLSLOARDQVC	525
Db	477	VWEATQSPFTTEVSYIEDDQVVEEDQLQDFVKDQVYVYVYVYVYVYVYVYVYVYVYVYV	536
QY	526	HFVTWCIFCTGQHASVHLGQLDWYSWVPNAPCTMRLPPPTTKO-ATLETVMATLPNFHQ	584
Db	537	EYLTVVIFTASAQAHAANFGQYDWCWIPNAPPTWRAPPTAKGVVTIEQIVDTLPDRGR	596
QY	585	ASLQMSITWQLGRROPVMAVGOHEEYFSGPEPKAVLKFRBELAALDKIEIRNAKLJD	644
Db	597	SCWHLGAVWALSQFQENELFLGMYPEEHFIEKPVKEAMIRFRKNLEAIVSVIAERNKKNK	656
QY	645	MPYEYLRP 652	
Db	657	LPYYLYLP 664	
RESULT 13			
I56977			
arachidonate 12-lipoxygenase (EC 1.13.11.31) - rat (fragment)			
C:Species: Rattus sp. (rat)			
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004			
C:Accession: I56977			
R:Katoch, T.; Lakkis, F.G.; Makita, N.; Badr, K.F.			
Kidney Int. 46, 341-349, 1994			
A>Title: Co-regulated expression of glomerular 12/15-lipoxygenase and interleukin-4 mRNA			
A:Reference number: I56977; MUID:95056840; PMID:7967345			
A:Accession: I56977			
A:Status: preliminary; translated from GB/EMBL/DBJ			
A:Molecule type: mRNA			
A:Residues: 1-238 <RES>			
A:Cross-references: UNIPROT:Q64042; GB:S74450; NID:g765331; PIDN:AAB32449.1; PID:g765332			
C:Superfamily: arachidonate 5-lipoxygenase			
C:Keywords: oxidoreductase			
Query Match 26.9%; Score 947; DB 2; Length 238;			
Best Local Similarity 72.8%; Pred. No. 5.9e-70;			
Matches 169; Conservative 34; Mismatches 29; Indels 0; Gaps 0;			
QY	399	NVRARTGLVSDMGIFDQIMSTGGGGHVQLLKQAQAFLYSSFCPPDDLADRLGLGVKSSF	458
Db	1	NVRARSDLIISERGFPDKAMSTGGGGHLLDLKQAQAFLYCSLCPPDDLAERGLLIETCF	60
QY	459	YAQDALRLWEIIRYVVEGIVSLHYKTDVAVKDDPELQWTCREITEIGLQGAQDRGFPVSL	518
Db	61	YAKDALRLWQIMRVYVWGMFNLHYKTEKAVQDDYELQSWCRBITDGLQGAQDRGFPPTS	120
QY	519	QARDQVCHVPTWCITCTGQHASVHLGOLDWYSWVPNAPCTMRLPPPTTKDLETVMAT	578
Db	121	OSRAQACQFITWCITCTCTAQHSSVHLGOLDWFCWPNAPCTMRLPPPTTKETATMEKML	180
QY	579	LPNFHQASLQMSITWQLGRROPVMAVGOHEEYFSGPEPKAVLKFRBELA 630	
Db	181	LPNPNQSTLQINNVWLLGRQAVWVPLQGHSEHFPNPEAKAVLKFRBELA 232	







GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 12:45:07 ; Search time 1063.87 Seconds  
(without alignments)  
15928.199 Million cell updates/sec

Title: US-10-688-676A-1  
Perfect score: 2671  
Sequence: 1 aaagatgggtctaccgcat.....aaataaaatttggcaaaaag 2671

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 7173243 seqs, 3172129809 residues  
Total number of hits satisfying chosen parameters: 14346486

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications NA:\*

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- 2: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 3: /cgn2\_6/prodata/1/pubpna/US05\_PUBCOMB.seq:\*
- 4: /cgn2\_6/prodata/1/pubpna/US04\_PUBCOMB.seq:\*
- 5: /cgn2\_6/prodata/1/pubpna/US03\_PUBCOMB.seq:\*
- 6: /cgn2\_6/prodata/1/pubpna/US02\_PUBCOMB.seq:\*
- 7: /cgn2\_6/prodata/1/pubpna/US01\_PUBCOMB.seq:\*
- 8: /cgn2\_6/prodata/1/pubpna/US00\_PUBCOMB.seq:\*
- 9: /cgn2\_6/prodata/1/pubpna/US09\_PUBCOMB.seq:\*
- 10: /cgn2\_6/prodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 11: /cgn2\_6/prodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 12: /cgn2\_6/prodata/1/pubpna/US06\_PUBCOMB.seq:\*
- 13: /cgn2\_6/prodata/1/pubpna/US05\_PUBCOMB.seq:\*
- 14: /cgn2\_6/prodata/1/pubpna/US04\_PUBCOMB.seq:\*
- 15: /cgn2\_6/prodata/1/pubpna/US03\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2671	100.0	2671	20	US-10-688-676A-1
2	2660	99.6	3103	21	US-10-498-788-69
3	2644.2	99.0	2844	17	US-10-398-663-13
4	1306	48.9	2048	17	US-10-191-803-178
5	1306	48.9	2048	18	US-10-152-319A-1857
6	1021.2	38.2	2348	18	US-10-240-425-1325
7	1016.4	38.1	2368	21	US-10-741-600-671

8	1016.4	38.1	2867	21	US-10-741-600-672	Sequence 672, App
9	1015.2	38.0	2368	19	US-10-741-601-232	Sequence 232, App
10	1015.2	38.0	2867	19	US-10-741-601-233	Sequence 233, App
11	1013.6	37.9	2343	17	US-10-170-097-652	Sequence 652, App
12	1013.6	37.9	2343	21	US-10-926-684-652	Sequence 652, App
13	515.6	19.3	584	19	US-10-681-818-13	Sequence 13, Appl
14	514	19.2	584	19	US-10-681-818-12	Sequence 12, Appl
15	382.6	14.3	2420	16	US-10-240-305-15	Sequence 15, Appl
16	382.6	14.3	2484	17	US-10-191-997-91	Sequence 91, Appl
17	382.6	14.3	2484	19	US-10-283-975A-296	Sequence 296, App
18	382.6	14.3	2497	9	US-09-964-824A-543	Sequence 543, App
19	382.6	14.3	2497	9	US-09-962-832-97	Sequence 97, Appl
20	382.6	14.3	2497	9	US-09-954-456-942	Sequence 942, App
21	382.6	14.3	2497	16	US-10-240-305-13	Sequence 13, Appl
22	382.6	14.3	2497	18	US-10-641-643-1155	Sequence 1155, Ap
23	382.6	14.3	2497	19	US-10-071-411-3	Sequence 3, Appl
24	382.6	14.3	2497	20	US-10-741-292-1	Sequence 1, Appl
25	382.6	14.3	2497	21	US-10-914-799-3	Sequence 3, Appl
26	382.6	14.3	2497	21	US-10-843-641A-3969	Sequence 3969, Ap
27	382.6	14.3	2497	21	US-10-843-641A-5846	Sequence 5846, Ap
28	382.6	14.3	2497	21	US-10-843-641A-5983	Sequence 5983, Ap
29	381.8	14.3	2076	20	US-10-485-310-21	Sequence 21, Appl
30	373	14.0	2107	20	US-10-741-292-18	Sequence 18, Appl
31	371.4	13.9	2107	20	US-10-741-292-17	Sequence 17, Appl
32	342.8	12.8	2685	9	US-09-764-246-1	Sequence 1, Appl
33	342.8	12.8	2685	10	US-09-960-706-985	Sequence 985, App
34	342.8	12.8	2685	10	US-09-873-319-642	Sequence 642, App
35	342.8	12.8	2685	19	US-10-716-204-1	Sequence 1, Appl
36	332	12.4	3320	9	US-09-862-658-1	Sequence 1, Appl
37	332	12.4	3320	14	US-10-175-696-22	Sequence 22, Appl
38	332	12.4	3320	19	US-10-776-871-22	Sequence 22, Appl
39	332	12.4	3384	16	US-10-422-264-29	Sequence 29, Appl
40	330.4	12.4	2236	16	US-10-422-264-5	Sequence 5, Appl
41	330.4	12.4	2701	16	US-10-422-264-1	Sequence 1, Appl
42	329.4	12.3	2136	9	US-09-862-658-3	Sequence 3, Appl
43	328.4	12.3	2136	14	US-10-175-696-24	Sequence 24, Appl
44	329.4	12.3	2136	19	US-10-776-871-24	Sequence 24, Appl
45	327.8	12.3	2307	18	US-10-302-172-803	Sequence 803, App

ALIGNMENTS

RESULT 1  
US-10-688-676A-1  
; Sequence 1, Application US/10698676A  
; Publication No. US2004024879A1  
; GENERAL INFORMATION:  
; APPLICANT: Alcon, Inc.  
; APPLICANT: Yanni, John M.  
; APPLICANT: Gamache, Daniel A.  
; APPLICANT: Miller, Steven T.  
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo  
; TITLE OF INVENTION: Activity to Ocular Surface Cells  
; FILE REFERENCE: 2394 US  
; CURRENT APPLICATION NUMBER: US/10/688, 676A  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: US 60/435,988  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 1  
; LENGTH: 2671  
; TYPE: DNA  
; ORGANISM: homo sapiens  
US-10-688-676A-1

Query Match 100.0%; Score 2671; DB 20; Length 2671;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2671; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 AAGATGGGTCTTACCGCATCCGGCTGTCCTATCCCGTCCAC 60  
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Db 1 AAGTGGGTCTTACCGCATCCGGGTGTCCACTGGGGCTCGCTCTATGCGCGTTCCAAC 60  
Qy 61 AACCAGGTGACGTGTGGCTGGTCCGACGACGGGAGCGCGCTCGGGAAGCGACTG 120  
Db 61 AACCAAGTGCAGCTGTGGCTGGTCCGACGACGGGAGCGGCGCTCGGGAAGCGACTG 120  
Qy 121 TGGCCCGCA CGGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGCGG 180  
Db 121 TGGCCCGCA CGGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGCGG 180  
Qy 181 CTGCTGTTTGTGAATGCGCAACCGCACCTCTTAAGGACGACGCTGTTCTGCAC 240  
Db 181 CTGCTGTTTGTGAATGCGCAACCGCACCTCTTAAGGACGACGCTGTTCTGCAC 240  
Qy 241 TGGATCTCTGTGACGGGCCCGGAGCGGGACGAGGTCAAGTTCCCTGTTACCGCTGG 300  
Db 241 TGGATCTCTGTGACGGGCCCGGAGCGGGACGAGGTCAAGTTCCCTGTTACCGCTGG 300  
Qy 301 GTGAGGGCAACCGCGTCTGTAGCTTGTGAAGGCAACCGGCGCACTGTGGCGAGGAC 360  
Db 301 GTGAGGGCAACCGCGTCTGTAGCTTGTGAAGGCAACCGGCGCACTGTGGCGAGGAC 360  
Qy 361 CCTCAGGGCTGTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAAAGTTGTAC 420  
Db 361 CCTCAGGGCTGTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAAAGTTGTAC 420  
Qy 421 CGGTGGGAAACTGGAAGGACGGGTAAATCTGAATATGCTGGGGCCAACTATATGAC 480  
Db 421 CGGTGGGAAACTGGAAGGACGGGTAAATCTGAATATGCTGGGGCCAACTATATGAC 480  
Qy 481 CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGCTGGCC 540  
Db 481 CTCCCTGTGATGAGCGATTTCTGGAAGACAAGAGAGTTGACTTTGAGGTTTCGCTGGCC 540  
Qy 541 AAGGGGTGCGCGACCTCGCTATCAAGAATCTCTAAATGTTCTGACTTCTGGAAGAT 600  
Db 541 AAGGGGTGCGCGACCTCGCTATCAAGAATCTCTAAATGTTCTGACTTCTGGAAGAT 600  
Qy 601 CTAGATCACTTCAACCGGATTTCTGTTGGTGTGAGCAAGCTGGTGAAGCGCGTGGG 660  
Db 601 CTAGATCACTTCAACCGGATTTCTGTTGGTGTGAGCAAGCTGGTGAAGCGCGTGGG 660  
Qy 661 GACTCTCTGGAAGGAGTGCCTTATTTGGGTACAGTTCTTAATGGCGCAACCCCGTG 720  
Db 661 GACTCTCTGGAAGGAGTGCCTTATTTGGGTACAGTTCTTAATGGCGCAACCCCGTG 720  
Qy 721 GTGCTGAGGCGCTCTGCTACCTTCTGCTGCGCTAGTGTTCCTCCAGGCATGGAGAA 780  
Db 721 GTGCTGAGGCGCTCTGCTACCTTCTGCTGCGCTAGTGTTCCTCCAGGCATGGAGAA 780  
Qy 781 CTGACGCGCCAGCTGGAGAGGAGCTGGAGGGGACACCTGTTGGAAGCTGACTTCTCC 840  
Db 781 CTGACGCGCCAGCTGGAGAGGAGCTGGAGGGGACACCTGTTGGAAGCTGACTTCTCC 840  
Qy 841 CTGCTGGATGGATCAAGGCCAAGCTCAITCTCTGTAGCCAGCAGCACTGGCTGCCCT 900  
Db 841 CTGCTGGATGGATCAAGGCCAAGCTCAITCTCTGTAGCCAGCAGCACTGGCTGCCCT 900  
Qy 901 CTAGTCATGTGAAATTTGACGCTGTGAGAACTCTTTGGCCCATGTTGTCATGAGTCCAG 960  
Db 901 CTAGTCATGTGAAATTTGACGCTGTGAGAACTCTTTGGCCCATGTTGTCATGAGTCCAG 960  
Qy 961 CTGCCCCGACAGATCCCAACCTTCTGCTTCTGCTACGATCCCAATGGCC 1020  
Db 961 CTGCCCCGACAGATCCCAACCTTCTGCTTCTGCTACGATCCCAATGGCC 1020  
Qy 1021 TGGCTTCTGGCCAAATGCTGGGTGCGAGCTCTGACTTCCAGCTCCCATGAGCTGCAGTCT 1080  
Db 1021 TGGCTTCTGGCCAAATGCTGGGTGCGAGCTCTGACTTCCAGCTCCCATGAGCTGCAGTCT 1080  
Qy 1081 CATCTTCTGAGGGGACACTTGAATGGCTGAGGTCAATGTTGTGGCCACCATGAGGTGCTG 1140  
Db 1081 CATCTTCTGAGGGGACACTTGAATGGCTGAGGTCAATGTTGTGGCCACCATGAGGTGCTG 1140

Qy 1141 CGGTGATACATCTTATCTTCAAGCTTATAATTTCCCACTCGGATACACCTTGGAATTT 1200  
Db 1141 CGGTGATACATCTTATCTTCAAGCTTATAATTTCCCACTCGGATACACCTTGGAATTT 1200  
Qy 1201 AAGCTCCGGGCCAGGACTGGGCTGGTCTCTGATGGGAATTTTCGACCAGATTAATGACC 1260  
Db 1201 AAGCTCCGGGCCAGGACTGGGCTGGTCTCTGATGGGAATTTTCGACCAGATTAATGACC 1260  
Qy 1261 ACTGGTGGGGGAGGCCACGTGACGTGCTCAAGCAAGCTGGAGCCCTTCTTAACCTACAGC 1320  
Db 1261 ACTGGTGGGGGAGGCCACGTGACGTGCTCAAGCAAGCTGGAGCCCTTCTTAACCTACAGC 1320  
Qy 1321 TCCCTTCTGTCCTTCAATGACTTGGCCGACCGGGGGCTCCTGGGAGTGAAGTCTTCTCTTC 1380  
Db 1321 TCCCTTCTGTCCTTCAATGACTTGGCCGACCGGGGGCTCCTGGGAGTGAAGTCTTCTCTTC 1380  
Qy 1381 TATGCCAAGATGCGCTGGGCTCTGGGAAATCATCTATCGGTATGTGGAAGGAATCGTG 1440  
Db 1381 TATGCCAAGATGCGCTGGGCTCTGGGAAATCATCTATCGGTATGTGGAAGGAATCGTG 1440  
Qy 1441 AGTCTCCACTATAAGACAGACGTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGT 1500  
Db 1441 AGTCTCCACTATAAGACAGACGTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGT 1500  
Qy 1501 CGAGAGATCACTGAATTCGGGCTGCAAGGGGCCCAAGGACCGAGGGTTTCTGTCTTTTA 1560  
Db 1501 CGAGAGATCACTGAATTCGGGCTGCAAGGGGCCCAAGGACCGAGGGTTTCTGTCTTTTA 1560  
Qy 1561 CAGGCTCGGGACAGGTTTGCCACTTTGTTCACCATGTGTATCTTCACTGACCCGCCAA 1620  
Db 1561 CAGGCTCGGGACAGGTTTGCCACTTTGTTCACCATGTGTATCTTCACTGACCCGCCAA 1620  
Qy 1621 CAGCCTCTGTCACCTGGGCGAGCTGGACTGTACTCTTTGGGTGCTTAATGACCCCTGC 1680  
Db 1621 CAGCCTCTGTCACCTGGGCGAGCTGGACTGTACTCTTTGGGTGCTTAATGACCCCTGC 1680  
Qy 1681 ACGATGCGGCTGCCCCCGCCAAACCAAGGATGCAACGCTGGAGACAGTGAATGGCGACA 1740  
Db 1681 ACGATGCGGCTGCCCCCGCCAAACCAAGGATGCAACGCTGGAGACAGTGAATGGCGACA 1740  
Qy 1741 CTGCCCCAATTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGACAGCG 1800  
Db 1741 CTGCCCCAATTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGACAGCG 1800  
Qy 1801 CAGCCGTTATGCTGGCTGGGCGCAGCATGAGGAGGATATTTTCGGGCGCTGAGCCT 1860  
Db 1801 CAGCCGTTATGCTGGCTGGGCGCAGCATGAGGAGGATATTTTCGGGCGCTGAGCCT 1860  
Qy 1861 AAGGCTGTGCTGAAGAAGTTCAAGGGAGGAGCTGGCTGCCCTGGATGAAGAAATTTGAGATC 1920  
Db 1861 AAGGCTGTGCTGAAGAAGTTCAAGGGAGGAGCTGGCTGCCCTGGATGAAGAAATTTGAGATC 1920  
Qy 1921 CGGAATGCAAGCTGGACATGCTTACAGATGCTTGGGCGCCAGCGTGTGGAAGACAGT 1980  
Db 1921 CGGAATGCAAGCTGGACATGCTTACAGATGCTTGGGCGCCAGCGTGTGGAAGACAGT 1980  
Qy 1981 GTGGCCATCTAAGCGTCGCCACCTTTGGTATTTTCAGCGCCCATCACCAAGCCACAAG 2040  
Db 1981 GTGGCCATCTAAGCGTCGCCACCTTTGGTATTTTCAGCGCCCATCACCAAGCCACAAG 2040  
Qy 2041 CTGACCCCTTCTGGTGTATAGCCCTGCCCTCCCAAGTCCACCTCTTCCCATGTCCCAC 2100  
Db 2041 CTGACCCCTTCTGGTGTATAGCCCTGCCCTCCCAAGTCCACCTCTTCCCATGTCCCAC 2100  
Qy 2101 CTTCCCTTAGAGGGGACCTTTTCATGGTCTCTGACCCAGTGAAACATTTTACTCTAGA 2160  
Db 2101 CTTCCCTTAGAGGGGACCTTTTCATGGTCTCTGACCCAGTGAAACATTTTACTCTAGA 2160  
Qy 2161 GGCATCACTGGGACCTTACTCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220  
Db 2161 GGCATCACTGGGACCTTACTCTCTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2220



Db	1272	CTGCTGATGGGATCAAGGCCAAGCTCATTTCTCTGTATCCAGCAGACACCTGGCTGCCCTT	1331
Qy	901	CTAGTCACTGCTGAAATTCAGACCTGTATGGGAAATCTTTGGCCCATGGTCACTCCAGCTCCAG	960
Db	1332	CTAGTCACTGCTGAAATTCGAGCCTGTATGGGAAACTCTTGGCCATGGTCACTCCAGCTCCAG	1391
Qy	961	CTGCCCCGCAACGAGATCCCCACAACCTCCCTTTTCTGTGCTTACGGAATCCCCCAATGGCC	1020
Db	1392	CTGCCCCGCAACGAGATCCCCACAACCTCCCTTTTCTGTGCTTACGGAATCCCCCAATGGCC	1451
Qy	1021	TGGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTTCAGCTTCCATGAGCTCCATGAGCTGCA	1080
Db	1452	TGGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTTCAGCTTCCATGAGCTGCA	1511
Qy	1081	CATCTTCTGAGGGGACACTTGAATGGCTGAGGTCA-TTGTGTGGGCCACCAATGAGGTGCC	1139
Db	1512	CATCTTCTGAGGGGACACTTGAATGGCTGAGGTCA-TTGTGTGGGCCACCAATGAGGTGCC	1571
Qy	1140	GCGGTGAGTATCATCTTATCTTCAAGCTTATAATTTCCCAACTCTCGATACACCTTGGAAT	1199
Db	1572	GCGGTGAGTATCATCTTATCTTCAAGCTTATAATTTCCCAACTCTCGATACACCTTGGAAT	1631
Qy	1200	TAAAGTCCGGGCCAGGACTGGGTGCTCTGATGATGAGGAATTTTCGACAGATATAG	1259
Db	1632	TAAAGTCCGGGCCAGGACTGGGTGCTCTGATGATGAGGAATTTTCGACAGATATAG	1691
Qy	1260	CACGTGTGGGGAGGCCACGTGACAGCTGCTCAAGCAAGCTGAGACCTTCTCAACCTACAG	1319
Db	1692	CACGTGTGGGGAGGCCACGTGACAGCTGCTCAAGCAAGCTGAGACCTTCTCAACCTACAG	1751
Qy	1320	CTCCTTCTGTCCCCCTGATGACTTTGGCCGACCGGGGCTCTCTGGGAGTGAAGTCTTCTCTT	1379
Db	1752	CTCCTTCTGTCCCCCTGATGACTTTGGCCGACCGGGGCTCTCTGGGAGTGAAGTCTTCTCTT	1811
Qy	1380	CTATGCCCAAGATGCGCTGCGCTCTGGGAAATCATCTATCCGTATGTGGAAGGAATCGT	1439
Db	1812	CTATGCCCAAGATGCGCTGCGGCTCTGGGAAATCATCTATCCGTATGTGGAAGGAATCGT	1871
Qy	1440	GAGTCTCCACTATAAGACACAGCTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTG	1499
Db	1872	GAGTCTCCACTATAAGACACAGCTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTG	1931
Qy	1500	TCGAGAGATCACTGAAATTCGGGCTGCAAGGGGGCCAGGACCCGAGGGTTTCTGTCTCTTT	1559
Db	1932	TCGAGAGATCACTGAAATTCGGGCTGCAAGGGGGCCAGGACCCGAGGGTTTCTGTCTCTTT	1991
Qy	1560	ACAGGCTCGGGAACAGGTTTGCACCTTTTGTACCATGTGTATCTTCACTGACACCGGCCA	1619
Db	1992	ACAGGCTCGGGAACAGGTTTGCACCTTTTGTACCATGTGTATCTTCACTGACACCGGCCA	2051
Qy	1620	ACACGCTCTGTGACCTCGGCGCAGCTGGAATCTGTACTCTTGGGTGGCTTAATGCACCCCTG	1679
Db	2052	ACACGCTCTGTGACCTCGGCGCAGCTGGAATCTGTACTCTTGGGTGGCTTAATGCACCCCTG	2111
Qy	1680	CACGATGCGGCTGCCCCCGCCAAACCAACGAGGATGCAACGCTCGGAGACAGTGAATGGCGAC	1739
Db	2112	CACGATGCGGCTGCCCCCGCCAAACCAACGAGGATGCAACGCTCGGAGACAGTGAATGGCGAC	2171
Qy	1740	ACTGCCCAAATTCACACAGGCTTCTCTCCAGATGTCCATCATCTTGGCAGCTGGGCGAGCG	1799
Db	2172	ACTGCCCAAATTCACACAGGCTTCTCTCCAGATGTCCATCATCTTGGCAGCTGGGCGAGCG	2231
Qy	1800	CCAGCCCGTTATGGTGGCTGTGGGCCAGCATGAGGAGGATATTTTTTCGGGGCCCTGAGCC	1859
Db	2232	CCAGCCCGTTATGGTGGCTGTGGGCCAGCATGAGGAGGATATTTTTTCGGGGCCCTGAGCC	2291
Qy	1860	TAAGGCTGTGCTGAAGAAGTTTCAGGAGGAGCTGGCTGCCCTGGATAAGGAAATTCAGAT	1919
Db	2292	TAAGGCTGTGCTGAAGAAGTTTCAGGAGGAGCTGGCTGCCCTGGATAAGGAAATTCAGAT	2351
Qy	1920	CCGGAATGCAAGCTGACATGCCCCTACGATCTCGCGGCCACGCGTGTGGAAACACAG	1979
Db	2352	CCGGAATGCAAGCTGACATGCCCCTACGATCTCGCGGCCACGCGTGTGGAAACACAG	2411

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RESULT 3
US/10-398-663-13
, Sequence 13, Application US/10398663
, Publication No. US20040053281A1
,
, GENERAL INFORMATION:
, APPLICANT: INCYTE, CORPORATION; HARLAND, Lee;
, APPLICANT: ARVIZU, Chandra S.; DAS, Debopriya;
, APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah
, APPLICANT: DING, Li; CHAWLA, Narinder K.;
, APPLICANT: YAO, Monique G.; LU, Yan;
, APPLICANT: ELLIOTT, Vicki S.; THANGAVEJUU, Kavita
, APPLICANT: RAMKUMAR, Jayalaxmi; LAL, Preeti G.;
, APPLICANT: TRIBOULEY, Catherine M.
,
, TITLE OF INVENTION: LIPID METABOLISM ENZYMES
,
, FILE REFERENCE: FI-0250 USN
,
, CURRENT APPLICATION NUMBER: US/10/398,663
,
, CURRENT FILING DATE: 2003-03-04
,
, PRIOR APPLICATION NUMBER: PCT/US01/31302
,
, PRIOR FILING DATE: 2001-10-05
,
, PRIOR APPLICATION NUMBER: US 60/238,388
,
, PRIOR FILING DATE: 2000-10-06
,
, PRIOR APPLICATION NUMBER: US 60/240,616
,
, PRIOR FILING DATE: 2000-10-13

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; PRIOR APPLICATION NUMBER: US 60/245,719
; PRIOR FILING DATE: 2000-11-02
; PRIOR APPLICATION NUMBER: US 60/247,503
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/249,503
; PRIOR FILING DATE: 2000-11-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PERL Program
; SEQ ID NO 13
; LENGTH: 2844
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; OTHER INFORMATION: Incyte ID No. US20040053281A1 7484270CBI
US-10-3398-663-13

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Query Match	99.0%;	Score 2644.2;	DB 18;	Length 2844;
Best Local Similarity	99.5%;	Mismat. No. 0;		
Matches 2652;	Conservative	0;	PredMatches 13;	Indels 0; Gaps 0;
QY	1	AAGATGGGTCTCTACCGCATCGCGTGTCCACTGGGGCTCGCTCTATGSCGGTTTCCCAAC	60	
Db	170	AAGATGGGTCTCTACCGCATCGCGTGTCCACTGGGGCTCGCTCTATGSCGGTTTCCCAAC	229	
QY	61	AACAGGTGCAAGCTGTGTGCTCGGCCAGCACGGGGAGGGCGCTCGGGAAGGCACTG	120	
Db	230	AACAGGTGCAAGCTGTGTGCTCGGCCAGCACGGGGAGGGCGCTCGGGAAGGCACTG	289	
QY	121	TGGCCCGCAGGGGCAAGGAGACAGAACTCAAGTGTGAAGTACCCGAGTATCTGGGGCGG	180	
Db	290	TGGCCCGCAGGGGCAAGGAGACAGAACTCAAGTGTGAAGTACCCGAGTATCTGGGGCGG	349	
QY	181	CTGCTGTTTGTGAACCTGCGCAACCGCACCTCTTAAGGACGACCGCTGGTTCTGCAAC	240	
Db	350	CTGCTGTTTGTGAACCTGCGCAACCGCACCTCTCTTAAGGACGACCGCTGGTTCTGCAAC	409	
QY	241	TGGATCTCTGTGCAGGGCCCCGGAGCCGGGACGAGGTCAGGTTCCCTTGTTCACCGCTGG	300	
Db	410	TGGATCTCTGTGCAGGGCCCCGGAGCCGGGACGAGGTCAGGTTCCCTTGTTCACCGCTGG	469	
QY	301	GTGCAGGGCAACGGCGTCTCAGCCCTGCTGAAGCACCGGCGGACCTGTGGCGCAGGAC	360	
Db	470	GTGCAGGGCAACGGCGTCTCAGCCCTGCTGAAGCACCGGCGGACCTGTGGCGCAGGAC	529	
QY	361	CCTCAGGSCCTGTTCCAGAAAACCCGGGAAGAAGCTGGAGAGAGAAGGAAGTTGTAC	420	
Db	530	CCTCAGGSCCTGTTCCAGAAAACCCGGGAAGAAGCTGGAGAGAGAAGGAAGTTGTAC	589	
QY	421	CGGTGGGGAAACTGGAGGAAGGAGGTTCTGAATATGCTGGGGGCCAACTATATGAC	480	
Db	590	CGGTGGGGAAACTGGAGGAAGGAGGTTCTGAATATGCTGGGGGCCAACTATATGAC	649	
QY	481	CTCCCTGTGGATGACCGATTCTTGGAGAACAAGAGAGTTGACTTTGAGGTTTCGCTGGCC	540	
Db	650	CTCCCTGTGGATGACCGATTCTTGGAGAACAAGAGAGTTGACTTTGAGGTTTCGCTGGCC	709	
QY	541	AAGGGCTGGCCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTGTCTGGAAGGAT	600	
Db	710	AAGGGCTGGCCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTGTCTGGAAGGAT	769	
QY	601	CTAGATGACTTCAACCGGATTTCTGGTGTGGTCAGACGACCTGGCTGAGCGCTGGGG	660	
Db	770	CTAGATGACTTCAACCGGATTTCTGGTGTGGTCAGACGACCTGGCTGAGCGCTGGGG	829	
QY	661	GACTTCCTGGAAAGGAGATGCTTATTTGGGTACCAAGTTTCTTAATGCGGCCAACCCCGTG	720	
Db	830	GACTTCCTGGAAAGGAGATGCTTATTTGGGTACCAAGTTTCTTAATGCGGCCAACCCCGTG	889	
QY	721	GTGCTGAGCGCTCTGTCTCACTTCTCGTCCCTAGTGTTCCTCTCAGGCAATGAGGAA	780	
Db	890	GTGCTGAGCGCTCTGTCTCACTTCTCGTCCCTAGTGTTCCTCTCAGGCAATGAGGAA	949	

Qy	781	CTGAGGCCACAGCTGGAGAAAGAGAGCTGGAGGGAGGCACACTGTTTCGAAGCTGACTTCTCC	840
Db	950	CTCAGGCCACAGCTGGAGAAAGAGAGCTGGAGGGAGGCACACTGTTTCGAAGCTGACTTCTCC	1009
Qy	841	CTGCTGATGGGATCAAGGCCAAACGTCATTCTCTGTAGCCAGCAGCACCTCTGGCTGCGCCCT	900
Db	1010	CTGCTGATGGGATCAAGGCCAAACGTCATTCTCTGTAGCCAGCAGCACCTCTGGCTGCGCCCT	1069
Qy	901	CTAGTCAATGCTGAAATTTGCAGCCTGATGGGAAACTCTTTGCCCATGTGTCATCCAGCTCCAG	960
Db	1070	CTAGTCAATGCTGAAATTTGCAGCCTGATGGGAAACTCTTTGCCCATGTGTCATCCAGCTCCAG	1129
Qy	961	CTGCCCGGCACAGGATCCCAACACCTCCGCCCTTTCTTTGGCTACGATCCCCCAATGGCC	1020
Db	1130	CTGCCCGGCACAGGATCCCAACACCTCCGCCCTTTCTTTGGCTACGATCCCCCAATGGCC	1189
Qy	1021	TGCGTTCTGGCCAAAATGCTGGGTGGCAGCTCTGCACTTCCAGCTCCAATGAGCTGCAGTCT	1080
Db	1190	TGCGTTCTGGCCAAAATGCTGGGTGGCAGCTCTGCACTTCCAGCTCCAATGAGCTGCAGTCT	1249
Qy	1081	CATCTTTCTGAGGGGACACTTGATGGCTGAGGTCATTGTTGTGGCCCAATGAGGTCGCTG	1140
Db	1250	CATCTTTCTGAGGGGACACTTGATGGCTGAGGTCATTGTTGTGGCCCAATGAGGTCGCTG	1309
Qy	1141	CCGTGATATACCTCTATCTTCAAGCTTATAATTTCCCACTCTGGGATACACCTTGGAAATT	1200
Db	1310	CCGTGATATACCTCTATCTTCAAGCTTATAATTTCCCACTCTGGGATACACCTTGGAAATT	1369
Qy	1201	AAGCTCCGGGCCAGGACTCGGCTGTCTCTGACATCGGGAATTTTCGACCAAGATAATGAGC	1260
Db	1370	AAGCTCCGGGCCAGGACTCGGCTGTCTCTGACATCGGGAATTTTCGACCAAGATAATGAGC	1429
Qy	1261	ACTGTTGGGGAGGCCACCTGCAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACTACAGC	1320
Db	1430	ACTGTTGGGGAGGCCACCTGCAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACTACAGC	1489
Qy	1321	TCCTTCTGTCCTTCAATGACTTTGGCCGACCGGGGCTCTCTGGGATGAAAGTCTTCTCTTC	1380
Db	1490	TCCTTCTGTCCTTCAATGACTTTGGCCGACCGGGGCTCTCTGGGATGAAAGTCTTCTCTTC	1549
Qy	1381	TATGCCCAAGATCGGCTCGGGCTCTGGGAAATCATCTATCGGTATCTGGGAAGAAATCGTG	1440
Db	1550	TATGCCCAAGATCGGCTCGGGCTCTGGGAAATCATCTATCGGTATCTGGGAAGAAATCGTG	1509
Qy	1441	AGTCTCCACTATAAGACAGACGTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGT	1500
Db	1610	AGTCTCCACTATAAGACAGACGTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGT	1669
Qy	1501	CGAGAGATCACTGAAATTCGGCTGCAAGGGGCCACGAGCCGAGGGTTTCTGTCTCTTTA	1560
Db	1670	CGAGAGATCACTGAAATTCGGCTGCAAGGGGCCACGAGCCGAGGGTTTCTGTCTCTTTA	1729
Qy	1561	CAGGCTCGGACACAGGTTTGCACATTTGTTCACCATGTGTATCTTCACTGTGCACCGGCCAA	1620
Db	1730	CAGGCTCGGCTCAGGTTTGTCCAATTTGTTCACCATGTGTATCTTCACTGTGCACCGGCCAA	1789
Qy	1621	CAGCCTCTGTGCACCTGGGCCAGCTGGACTGTGTACTCTTTGGTGTCTAATGCACCTGTC	1680
Db	1790	CAGCCTCTGTGCACCTGGGCCAGCTGGACTGTGTACTCTTTGGTGTCTAATGCACCTGTC	1849
Qy	1681	ACGATCGGCTGCCCGGCCAACCAACCAAGGATGCAACGCTGGAGACAGTGTATGGCGACA	1740
Db	1850	ACGATCGGCTGCCCGGCCAACCAACCAAGGATGCAACGCTGGAGACAGTGTATGGCGACA	1909
Qy	1741	CTGCCAACTTCCACACAGGTTCTCTCCAGATGTTCATCACTTGGAGCTGGGACAGCGC	1800
Db	1910	CTGCCAACTTCCACACAGGTTCTCTCCAGATGTTCATCACTTGGAGCTGGGACAGCGC	1969
Qy	1801	CAGCCGTTATGGTGCTGTGGCCAGCATGAGGAGGATTTATTTTTCGGGCCCTGAGCCT	1860
Db	1970	CAGCCGTTATGGTGCTGTGGCCAGCATGAGGAGGATTTATTTTTCGGGCCCTGAGCCT	2029
Qy	1861	AAGGCTGTGCTGAAGAAATTTACGGGAGGAGCTGGCTGCCCTCGATTAAGGAAATTTGAGATC	1920

[illegible]

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RESULT 4
US-10-191-803-178
: Sequence 178, Application US/10191803
: Publication No. US20040014040A1
: GENERAL INFORMATION:
: APPLICANT: MENDRICK, Donna
: APPLICANT: PORTER, Mark
: APPLICANT: JOHNSON, Kory
: APPLICANT: HIGGS, Brandon
: APPLICANT: CASTLE, Arthur
: APPLICANT: ELASHOFF, Michael
: TITLE OF INVENTION: Cardiotoxin Mole
: FILE REFERENCE: 4921-5090US
: CURRENT APPLICATION NUMBER: US/10/19
: CURRENT FILING DATE: 2002-07-10
: PRIOR APPLICATION NUMBER: US 60/303,
: PRIOR FILING DATE: 2001-07-10

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; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 178
; LENGTH: 2048
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
;   OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031010
US-10-191-803-178

Query Match      48.9%; Score 1306; DB 17; Length 2048;
Best Local Similarity 78.3%; Pred. No. 0;
Matches 1580; Conservative 0; Mismatches 435; Indels 3; Gaps 1;

Qy 1 AAGATGGGTCTCTACCGCATCCGCGTGTCCACATGGGGCCCTCGCTCTATGTCGGTTCACAAC 60
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Qy 17 AAGATGGGTCTCTACCGCATCCGCGTGTCCACCGAGACTCCAAGTACGCGGCTCCAAC 76
Db |||||
Qy 61 AACAGGTGAGCTGTGGCTGTGGCCACACGCGGAGCGCGGTCTCGGGAAGCACTG 120
Db |||||
Qy 77 AACGAGTCTACCTGTGGTTGGTGGACAGCATGGAGAGGCATCTCTCGGGAAGCTGCTA 136
Db |||||
Qy 121 TGGCCCGCAGCGGCAAGAGACAGAACTCAAGGTGGAGTACCGGAGTATCTTGGGGCCG 180
Db |||||
Qy 137 CGAACCTGTCTCGGACTCGGAAGCAGAAATTCAAAGTGGATGTGTCAAGTAACCTTGGGCCA 196
Db |||||
Qy 181 CTGCTGTTCTGTAAGTGCAGAAATGGCATATCTACCGATGACGCTCGTCTTGCAC 240
Db |||||
Qy 197 CTGCTGTTCTGTAAGTGCAGAAATGGCATATCTACCGATGACGCTCGTCTTGCAC 256
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Qy 241 TGGATCTCTGTGAGGCCCCCGAGCC-- --GGGGAAGAGTCAAGTTCCTTGTATTACCGC 297
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Qy 257 TGGATTTCTGTGAAGGGCCCCGGAGACCAAGGATCAAGATACATGTTCCCTGTATTACCGA 316
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Qy 298 TGGGTGGAAGGCAACGGCGTCTTGAGCCTCGCTGAGGCAACCGGCGCATCTGTGGGGGAG 357
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Qy 317 TGGGTTTCAGGGCAGAAAGCATCTTGAGCCTCCCTGAGGGGCACTGGCTGCAACGCTGTTGAA 376
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Qy 358 GACCTCAGGGCCTGTTTCAGAAACACCGGGAAGAGAGCTTGAAGAGAGAAAGAAAGTTG 417
Db |||||
Qy 377 GATTCTCAAGACTGTTTCAGAAACATAGGGAAGAGAGCTTGAAGAGAGAGAGAGTCTG 436
Db |||||
Qy 418 TACCGTGGGGAACCTGGAAGGACGGGTAAATCTGAATATGCTGGGGCCAAACTATAT 477
Db |||||
Qy 437 TACAGTGGGGCACTGGAAGGATGGCTCAATCTTGAATGTGGCGGGCCAGTATATCT 496
Db |||||
Qy 478 GACCTCCCTGTGGATGAGCAATTTCTGGAAGACAGAGAGTTGACTTTGAGGTTTCGCTG 537
Db |||||
Qy 497 GACCTCCCTGTAGACCAACGATTTTCGAGAGGACAAAAGAAATTGAATTTGAAGCTTCAAG 556
Db |||||
Qy 538 GCCAAGGGGCTGGCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAG 597
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Qy 557 GTTATAGGGGTAAATGGATACATGTTGTCACTTCCCTATAAACACTGTGACTGCTGGAAG 616
Db |||||
Qy 598 GATCTAGATGACTTCAACCGGATTTTCTGGTGTGGTCAGAGCAAGCTGGCTGAGCGCGTG 657
Db |||||
Qy 617 AGCTAGATGACTTCAACTGGTGTTCAGAGTGGCCATACCAAAATGGCTGAGCGGGTT 676
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Qy 658 CGGACTCTCTGGAAGGAAGATGCGTTATTTGGGTACCAAGTTCTTAATGCGGCCAACCCC 717
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Qy 677 CGAAACTCTCTGGAAGGAAGATGCGTTCTTTGGGTACCAATTCCTCAATGTGTCTAAACCCC 736
Db |||||
Qy 718 GTGGTGTGAGGGCCTCTGCTCACCTTCTCTGCTCGCCTAGTGTGTTCCCTCTCAGGCAATGGAG 777
Db |||||
Qy 737 ATGGTGTCTGAAGCGCTCTACTTGTCTTCTCGCCGCTGGTATTTCCCTCTCAGGAAATGGAG 796
Db |||||
Qy 778 GAACCTGAGGCCACAGCTGGAAGAGGAGCTGGAGGGAGGCACTGTGTCGAAGCTGACTTC 837
Db |||||

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Db 797 AGCTACAGCCGACGCTGAAAGAGAGCTCCAGAAAGGCACCTCTGTTTGAAGCGGATTTTC 856  
Qy 838 TCCCTGCTGGATGGGATCAAGGCCAACGCTCATTTCTGTAGCAGCAGCACCTGGCTGCC 897  
Db 857 TTCCCTTCTGGATGGGATCAAGGCCAACGCTCATTTCTGTAGCAGCAGTACCTGGCTGCC 916  
Qy 898 CTTCTAGTCATCTGAAATGAGCCTGATGGGAACTCTTGGCCCATGTCATCAGCTTC 957  
Db 917 CTTCTGCTCATGCTGAAGCTGATGCTGATGACAACTCTTGGCCCATGTCATCAGCTTC 976  
Qy 958 CAGCTGCCCGCACAGGATCCACACACCTCCCTTTCTTCTGCTACGGATCCCCCAATG 1017  
Db 977 GAACTGCCCAAACTGGGTCTACTCCACCACTATTTTACGCCCTCGGATCCCCCAATG 1036  
Qy 1018 GCTGGCTTTCTGGCCAAATGCTGGGTGGCGACCTCTGACTTCCAGCTCCATGAGCTGCAG 1077  
Db 1037 GACTGGCTCTAGCCAAATGCTGGGTGGCGAGCTCGGAGCTCGACTTACAGCTCCATGAGCTGCAG 1096  
Qy 1078 TCTCATCTCTGAGGGGACACTGTATGGCTGAGGTCAATTTGTGGCCACCATGAGGTGC 1137  
Db 1097 GCTCATCTCTGAGGGGACACTGTATGGCTGAGCTCTTGTCTGTGGCCACCATGAGGTGC 1156  
Qy 1138 CTGGCTGATACATCTCTTCAAGCTTATAATTTCCCACTCGGATACACCTCGGAA 1197  
Db 1157 CTGGCTTCCGTGCACCTCTTTTAAAGCTTCTAGTTCTCTCATCTGCTTTACACCATGAA 1216  
Qy 1198 ATTAACGTCGGGGCAGGACCTGGGTGCTCTGACATGGGAATTTTCACACAGATAATG 1257  
Db 1217 ATTAATGTCGGGGCAGGAGTCACTGATCTCAGAGAGAGGCTTTTTCAGAAAGCAATG 1276  
Qy 1258 AGCACTGTGGGGAGGACCTGAGCTGCTCAAGCAAGCTGGAGCTTCTCAACCTAC 1317  
Db 1277 AGCAAGTGGGGAGGACCTGAGCTTCTCAAGCAAGCTGGAGCTTCTCAACCTAT 1336  
Qy 1318 AGCTCTTCTGTCCTGATGATGCTTGGCCGACGGGGCTCTGGGAGTGAAGTCTTCC 1377  
Db 1337 TGCTCATTTGTCCTGATGATGCTTGGCTGAGCAGGACTCTTGGATATCAGAGCTTGC 1396  
Qy 1378 TTCTATGTCGCAAGATGCTGCGGCTCTGGGAAATCATCTATCGGTATGTGGAAGAAATC 1437  
Db 1397 TTCTATGTCGCAAGATGCTGCGGCTCTGGGAAATCATCTATCGGTATGTGGAAGAAATC 1456  
Qy 1438 GTGAGTCTCCACTATAGACAGATGCTGTGAAAGACGACCCAGAGCTGCAGACCTGG 1497  
Db 1457 TTCAATCTCCACTAAGACAGCAGAAAGCTGTGCAAGACGACTATGAATGTCAGAGCTGG 1516  
Qy 1498 TGTGAGAGATCACTGAAATCGGCTGCAAGGGGCCAGGAGCTTCTGCTCTCT 1557  
Db 1517 TGTGAGAGATCACTGAAATCGGCTGCAAGGGGCCAGGAGCTTCTGCTCTCT 1576  
Qy 1558 TTACAGGCTCGGGACAGCTTGGCCACTTTGTCAACATGTGTATCTTCACTTGCACCGGC 1617  
Db 1577 CTTGAGTCCGGGCTCAGGCTTGTCTACTTCAACATGTGCAATCTTCACTGCAACCGCA 1636  
Qy 1618 CAACAGCTCTGTGACCTTGGCCAGCTGGATCTGTACTTCTTGGGTGCTTAATGCAACCC 1677  
Db 1637 CAGCACTCTTCCGTCCATCTTGGCCAGCTGGATTTGTTCTTACTTGGGTCTTAAATGCAACCC 1696  
Qy 1678 TGCAGATGCGGCTGCGCCCGCAACCAAGGATGCAACGCTGAGACAGTATGAGGG 1737  
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Qy 1738 ACACCTGCCCAACTTCCACAGGCTTCTCTCCAGATGTCTCATCTTGGCAGCTGGGAGCA 1797  
Db 1757 ACACCTGCCCAACTTCTACTCTACTCTTCCAGATTAATGTCTTGGCTCTGGGAGCA 1816  
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Db 1817 CGCCAGGCTGTTATGCTGTGGGCCAGCATGAGGAGGATATTTTTCGGGGCCCTGAG 1876  
Qy 1858 CCTAAGGCTGTCTGAAAGATTTCAAGGAGGAGCTGGCTGCTGCTGATTAAGGAATTTGAG 1917

Db 1877 GCCAAGGCTGTCTGAAGAGTTTCAGAGAGGACTGGCTGCTTGGATTAAGAAATTGAG 1936  
Qy 1918 ATCCGAATGCAAGCTGGACATGCCCTACGAGTACCTTGCGCCCCAGCGTGGTGGAAAC 1977  
Db 1937 ATTCGTAATAAGAGCTTGGACATACCTTTATGATACCTTGCGCCCCAGCATGCTGGAAAC 1996  
Qy 1978 AGTGTGGCATCTAAGCGTCCGCCACCTTTGGTTATTT 2015  
Db 1997 AGCGTGGCATATGAGCATCCCGAGACTCCTGCTTTGT 2034

## RESULT 5

US-10-152-319A-1857  
; Sequence 1857, Application US/10152319A  
; Publication No. US20040072160A1  
; GENERAL INFORMATION:  
; APPLICANT: Mendrick, Donna  
; APPLICANT: Porter, Mark  
; APPLICANT: Johnson, Kory  
; APPLICANT: Higgins, Brandon  
; APPLICANT: Castle, Arthur  
; APPLICANT: Elashoff, Michael  
; TITLE OF INVENTION: Molecular Toxicology Modeling  
; FILE REFERENCE: 44921-5089-US  
; CURRENT APPLICATION NUMBER: US/10/152,319A  
; CURRENT FILING DATE: 2002-05-22  
; PRIOR APPLICATION NUMBER: US 60/292,335  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/297,523  
; PRIOR FILING DATE: 2001-06-13  
; PRIOR APPLICATION NUMBER: US 60/298,925  
; PRIOR FILING DATE: 2001-06-19  
; PRIOR APPLICATION NUMBER: US 60/303,810  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,807  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/303,808  
; PRIOR FILING DATE: 2001-07-10  
; PRIOR APPLICATION NUMBER: US 60/315,047  
; PRIOR FILING DATE: 2001-08-28  
; PRIOR APPLICATION NUMBER: US 60/324,928  
; PRIOR FILING DATE: 2001-09-27  
; PRIOR APPLICATION NUMBER: US 60/330,867  
; PRIOR FILING DATE: 2001-11-01  
; PRIOR APPLICATION NUMBER: US 60/330,462  
; PRIOR FILING DATE: 2001-10-22  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 2221  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 1857  
; LENGTH: 2048  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. NM\_031010  
US-10-152-319A-1857

Query Match 48.9%; Score 1306; DB 18; Length 2048;  
Best Local Similarity 78.3%; Pred. No. 0;  
Matches 1580; Conservative 0; Mismatches 435; Indels 3; Gaps 1;  
Qy 1 AAGATGGGTCTTACCCGATCCCGGTGTCCACTGGGGCTCGCTCTATGCGGTTCCAAAC 60  
Db 17 AAGATGGGTCTTACCCGATCCCGGTGTCCACTGGGGCTCGCTCTATGCGGTTCCAAAC 76  
Qy 61 AACAGGTGACGTGTGGCTGGCCAGCAGCAGGGAGGGCGCTCGGGAAGGAGTGT 120  
Db 77 AACAGGTGACGTGTGGCTGGCCAGCAGCAGGGAGGATCTCTCGGGAAGGAGTGT 136  
Qy 121 TGGCCCGCAGGGGCAAGAGACAGAACTCAAGGTGGAGTACCGGAGTATCTGGGGCG 180  
Db 137 CGACCCCTGTCTGGGACTCGGAAGAGAAATTCAGATGGATGTTCAGAAATACCTTGGGCA 196

181 CTGCTGTTGTGAAACTGCGCAACGGCACCTCTTAAGGACGACGCTGTTCTGCAAC 240  
197 CTGCTGTTGTAAGAGTGAGAAATGGCATATATCAACGATGACGCTGTTCTGCAAC 256  
241 TGGATCTCTGTGAGGCGCCCGAGGCC---GGGAGAGAGGTGAGGTTCCTTGTACCGC 297  
257 TGGATTTCTGTGAAGGGCCCGGAGACCAAGGATCAGAGTACATGTTCCTCCCTGTTACCGA 316  
298 TGGGTGGAGGCAACGGCCCTCTGAGCCTGCTGAGGACGACGCGGACATGTGGGCGAG 357  
317 TGGGTTTCAGGCGAGAGCATCTGAGCCTCCCTGAGGCGACCTGGCTGCAACCGTGTGAA 376  
358 GACCCCTCAGGCGCTGTTCCAGAAACACCGGGAAGAGCTGGAAGAGAGAAAGGTTG 417  
377 GATTCTCAGGACTGTTACAGGAACATACGGGAAGAGACTTTGAAGAGAGGAGTCTG 436  
418 TACCGGTGGGAAACCTGGAAGAGCGGTTAATCTGGAATATGCTGGGCGCCAAACTATAT 477  
437 TACAGGTGGGCAACTGGAAGGATGGCTCAATCTGAAATGTGGCGCGCCAGTATATCT 496  
478 GACCTCCCTGTGATGAGCGATTTCTGGAAGACAGAGAGTTGACTTTGAGGTTTCGCTG 537  
497 GACCTCCCTGTGATGAGCAAGATTTGAGAGGACAAAGAAATTTGAACTTCAACAG 556  
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658 CGGACTCTCGGAGGAGAGTCCCTTATTTGGGTACCACTTTCTTAATGGCGCCAAACCC 717  
677 CGAAACTCTCGAAGGAGATGGTCTTTGGGTACCAATCTCAATGGTCTAACCC 736  
718 GTGGTCTGAGGCGCTCTGCTCACTTCCTGCTCGCTAGTGTTCCTCCAGGCATGGAG 777  
737 ATGGTCTGAGGCGCTCTACTTGTCTTCCTGGCGGCTGGTATTCCTCCAGGAATGGAG 796  
778 GAACTCGAGGCCAGCTGGAAGAGAGCTGGAGGAGGACACTGTTTGAAGTGAATCTTC 837  
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857 TCCCTTCTGATGGGATCAAGGCCAATGTCTCTTTGTAGCAGCGTACCTGGCTGCC 916  
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958 CAGCTGCGCGGACAGGATCCCAACCACTCTCCCTTTTCTGCTACGATCCGCAATG 1017  
977 GAACTGCCCAAACTGGGCTACTCCACCACTATTTTCAAGGCTCGGATCCCAATG 1036  
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1637 CAGCACTCTTCCGTCCATCTTGGCCAGCTGGATTGGTTCTACTGGGTTCTTAATGCACCC 1696  
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1858 CTTAAGGCTGTCTCAAGAGTTTCAAGGAGGAGCTGGCTGCCCTGATGAAGAAATGAG 1917  
1877 GCGAAGGCTGTCTGAAGAGTTTCAAGAGGAGTGGCTTGGCTTGGATGAAGAAATGAG 1936  
1918 ATCCGGAATGCAAGCTGACATGCGCTTACAGTACCTGCGGCCAGCGTGGTGGAAAC 1977  
1937 ATTCGTAATAGAGCTTGGACATACCTTATGATGATCTGCGGCCAGCATGGTGGAAAC 1996  
1978 AGTGTGGCATCTAAGCTGCGCACCTTTGGTTATTT 2015  
1997 AGCGTGGCCATATGAGCATCCCGAGACTCTCTTTGT 2034

## RESULT 6

US-10-240-425-1325  
; Sequence 1325, Application US/10240425  
; Publication No. US20040033502A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1325

; LENGTH: 2348

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION: Genbank Accession No. US20040033502A1 M62982

US-10-240-425-1325

Query Match 38.2%; Score 1021.2; DB 18; Length 2348;

Best Local Similarity 69.9%; Pred. No. 7,8e-295;

Matches 1393; Conservative 0; Mismatches 598; Indels 3; Gaps 1;

QY	4	ATGGGTCTCTACCGCATCCGGTGTCACCTGGGGCTCTCGCTCTATGCGGTTCCAAAC	63
DB	54	ATGGGCGGCTACCGCATCCGGTGTCACCTGGGGCTCTCGCTCTATGCGGTTCCAAAC	113
QY	64	CAGGTGACGTGTGGCTGGCCAGCACCGGGAGGGCGGCTCGGGAAGCATGTGG	123
DB	114	CGGTGACGTGTGGCTGGCCAGCACCGGGAGGGCGGCTCGGGAAGCATGTGG	173
QY	124	CCCGCACGGGCAAGGACACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCCGCTG	183
DB	174	CGGGCTGGGGCGAGGAGGAGTTTGATCATGACGTTCAGAGGACTTGGGGCTCTG	233
QY	184	CTGTTTGTGAACCTCGGCAACCGGCACTCTCTTAAGGACGACGCTGTCTGCAACTGG	243
DB	234	CAGTTCTGTGAGCTCGGCAAGCACCACTCGGTGTGTGGACGACGCTGTCTGCGACCGC	293
QY	244	ATCTCTGTGCAAGGCGGCGGAGCGGGGACGAGGTTCAGGTTCCCTTTGTTACCGTGGGTG	303
DB	294	ATCAGGTCGCAAGGCGGCGGAGCGGCTGCGCGGAGTGGGCTTCCCGTGTACCGTGGGTG	353
QY	304	GAGGCAACGGGCTCTGAGCTGCTGCAAGGACCGCGGCACTGTGGGGGAGGACCT	363
DB	354	CAGGCGGAGGACATCTGAGCTGCTCCGAGGGCACCGCGGCTGCCAGGAGACATGCT	413
QY	364	CAGGCGCTGTTCCAGAAACACCGGGAAGAAGCTGTGAAGAGAGAAAGTTGTACCGG	423
DB	414	TTGACATGTTCCAGAAAGCATCGAGAGAAGAACTGAAAGACAGACAGACAGATCTACTGC	473
QY	424	TGGGAAGCTGGAGGACGGGTTAATCTGATATGGCTGGGGCCAAACTATATGACCTC	483
DB	474	TGGGCACTGGGAAGGAGGTTTACCCCTGACCATGCTGCGAGACCGTAAGAGATGATCTA	533
QY	484	CTGTGGATGACGCAATTTCTGGAACAGAGAGTTGACTTTGAGGTTTCGCTGCGCCAA	543
DB	534	CCTCCAAATATGAGATTCATGAGAGAGAGGCTGGACTTTGAATGACACATGAGGCA	593
QY	544	GGGCTGGCCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGACTA	603
DB	594	GGGCTCTGGAGATGGCCCTCAACCGGTGTTTACACCTCTCTGAGCTCTGGAACTGCTTA	653
QY	604	GATGACTTCAACCGGATTTCTGGTGTGGTCAGACCAAGCTGGCTGAGCGGTGGGGAC	663
DB	654	GAAGACTTTGATCAGATCTTCTGGGGCCAGAGAGTGGCCCTGGCTGAGAAGGTTTGGCAG	713
QY	664	TCCTGGAAGGAGATGCTTATTTGGGTACAGTTTCTTAATGGGCCAAACCCGCTGGTG	723
DB	714	TGCTGGCAGGATGATGAGTTGTTAGCTACCAAGTTCTCAATGGTGGCCAAACCCCATGCTG	773
QY	724	CTGAGGCGCTCTGCTCACCTTCTGCTGCTCTGCTGCTGCTTCCCTCCAGGATGAGGAACTG	783
DB	774	TTGAGAGCTCGACCTCTCTGCGCTCCAGGCTAGTGTGCTGCGCTCGGGATGGAGAGCTT	833
QY	784	CAGGCGGAGCTGGAGAGGAGCTGGAGGGAGGCACACTGTTGCAAGCTGACTTCTCCCTG	843
DB	834	CAGGCTCAACTGGAGAAAGAACTTCAGAAATGTTTCCCTGTTTGAAGCTGACTTCACTCT	893
QY	844	CTGGATGGGATCAAGGCCAAAGCTTCTCTGTAGCAGGACGACCTGGCTGCCCTCTA	903
DB	894	CTGGATGGAAATCCAGGCCAAAGCTGATCCAGAGAGGAAGCAATACCTGGCTGCCCTCTC	953

QY	904	GTGATGCTGAATTTGCAGCCCTGATGGGAAACTCTTGGCCATGGTCTATCCAGCTCAGCTG	963
DB	954	GTTATGCTGAAGATGGAGCCCAATGGGAAAGCTGCAGCCCATGGTCTATCCAGATTGAGCT	1013
QY	964	CCCGCACAGGATCCCGACACCTCCCTCTTTTCTTGTCTACGATCCCGATCCCGATCCCTGG	1023
DB	1014	CCGAGCCCGAGCTCTCCAAACCCCAACTGTTCTCTGCTCAGACCCCGCTGCTGCTGG	1073
QY	1024	CTTCTGCGCCAAATGCTGGTGGCGAGCTGGAATTCAGAGTCTCCATGAGCTCAGTCTCAT	1083
DB	1074	CTCTGCGCCAAATGCTGGTGGCGGAAATTCAGATTTCCAACTGCAGAGATCCAGTATCAC	1133
QY	1084	CTTCTGAGGGAGACATTTGATGGCTGAGTCAATTTGTGGGCCACCATGAGTGGCTGGCG	1143
DB	1134	TTGCTGAACACTCACTACCTGGTGGCTGAGGTTCATCGCTGTGCGCACCATGCGGTGCCA	1193
QY	1144	TCGATACATCTATCTTCAAGCTTATAATTCGCCACCTGCGATACACCTCGGAAATTAAC	1203
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QY	1204	GTCCGGGCCAGGACTGGGCTGGTCTCTGACATGGAATTTTCGACAGATTAATGAGCACT	1263
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QY	1264	GGTGGGGAGGCGACGTCAGCTGCTCAAGCAAGCTGAGGCTTCTTAACCTACAGCTCC	1323
DB	1314	GGTGGAGGGGGCCATGTACAGTTGCTCGTGGGGCGGAGCTCAGCTGACCTACTGCTCC	1373
QY	1324	TTCTGTCCCTGATGACTTTGGCGGACCGGGGGCTCTTGGGAGTGAAGTCTTCTTCTAT	1383
DB	1374	CTCTGTCTCTGACGACTGGCTGACCGGGGCTCTGTTGGGACTCCCGAGTGTCTCTAT	1433
QY	1384	GCCCAAGATGCGTGGGCTCTGGGAAATCATCTATCGGTAATGTGAAGGAATCGTGTAGT	1443
DB	1434	GCCCATGATGCTTTACGGCTCTGGGAGATCATTCGCCAGTATGTGGAGGGATCGTCCAC	1493
QY	1444	CTCCACTATTAAGACAGAGTGGCTGTGAAGAAGACGACCCAGAGCTGCAGACCTGTGTGCA	1503
DB	1494	CTCTTCTACCAAGGGATGACATAGTGAAGGGGAGCCCTGAGCTGCAGGCTGGTGTGCG	1553
QY	1504	GAGATCACTGAAATCGGGCTGCAAGGGGCCCGAGGACGAGGGTTTCTGTCTCTTTACAG	1563
DB	1554	GAGATCAGGAGTGGGGCTGTGCGAGGCCAGAGACCGAGGTTTCCCTGTCTCTTCAG	1613
QY	1564	GCTCGGACACAGGTTTGCACATTTGTCAATGTGTATCTTCACTGACCGCGCCAAAC	1623
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QY	1624	GCCTCTGTGACCTGGGCGAGCTGGACTGTGTACTCTTGGGTGCTTAATGACCCCTGCA	1683
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QY	1684	ATGGGCTGCCCCCGCCCAACACCAAG--GATGCAACGCTGGAGACAGATGATGCGACA	1740
DB	1734	ATGGGATGCCCCCGCCCAACACCAAGAGATGTGACATGAGCCACAGTATGGGTGCA	1793
QY	1741	CTGCCCCAATTTCCACAGGCTTCTCTCCAGATGTCCATCACTTGGCAGCTGGGAGAGC	1800
DB	1794	CTACTGATGTCCGGCAGGCTGTCTTCAATGGCCATCTCATGCGATCTGAGTGGCGCG	1853
QY	1801	CAGCCGTTATGTTGGCTGTGGGCGAGCATGAGGAGGATATTTTTCGGGCGCTGAGCCT	1860
DB	1854	CAGCAGACATGTGTGCTCTGGGCGACCAAAAGAAAAATAATTTCTCAGGCCCCCAAGCC	1913
QY	1861	AAGCTGTGTGAAGATTTTCAGGAGGAGTGTGCTGCTCCCTGGATAGGAATTTGAGATC	1920
DB	1914	AAAGCTGTGTAAACCAATTTCCGAAACAGATTTGGAAGAGCTAGAAAAGGAGATTACGCC	1973
QY	1921	CGGAATGCAAGCTGGAATGCTCCCTTACAGTACCTGCGGGCCCGCTGGTGGTGAAGAA	1980
DB	1974	CGGAATGAGCACTTGTACTGGCTCTATGAAATATCTGAAGCCAGCTGCATAGAGACAGT	2033
QY	1981	GTGCCCATCTAAGC	1994

Db	2034	GTCCACCTGTGAGC	2047	Db	716	TGCTGGCAGGATGATGAGTTGTTGAGCTACCAAGTTCCTCAATGGTGCCAAACCCCAATGCTG	775
RESULT 7							
US-10-741-600-671							
; Sequence 671, Application US/10741600							
; Publication No. US20050026169A1							
; GENERAL INFORMATION:							
; APPLICANT: CARGILL, Michele et al.							
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH							
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF							
; FILE REFERENCE: CL001499							
; CURRENT APPLICATION NUMBER: US/10/741,600							
; CURRENT FILING DATE: 2003-12-22							
; NUMBER OF SEQ ID NOS: 73997							
; SOFTWARE: FastSeq for Windows Version 4.0							
; SEQ ID NO 671							
; LENGTH: 2368							
; TYPE: DNA							
; ORGANISM: Homo sapiens							
US-10-741-600-671							
Query Match							
Best Local Similarity 69.4%; Pred. No. 2.2e-293;							
Matches 1384; Conservative 8; Mismatches 599; Indels 3; Gaps 1;							
QY	4	ATGGGTCTCTACCGCATCCGCGTGTCCACTTGGGCGCTCGCTCTATGCGCGTTCCCAACAC	63	QY	1264	GTGGGGGAGGCCAGCTGCAGCTGCTCAAGCAAGCTGGAGCCTTCTAACTTACAGCTCC	1323
Db	56	ATGGGCGGCTACCGCATCCGCGTGGCCACCGGGCGCTGGCTCTTCTCCGGGTGCTACAAAC	115	Db	1316	GGTGGAGGGGGCCATGTACAGTTGCTCGTGGGGGGCAGCTCAGTCACTTCTCTCT	1375
QY	64	CAGGTGCAGCTGTGGCTGTGCGGCCAGCACGGGGAGGCGCGCTCGGGGAAGCACTGTGG	123	QY	1384	GCCCAAGATGCGCTGGGCTCTGGGAATCATCTATCGGTATGTGGAGGATCGTGAGT	1443
Db	116	CGGTGCAGCTTGGCTGTGCGGACGCGCGGGAGCGGAGCTGGAGCTGCGCTGGCG	175	Db	1436	GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGGAGGGGATCGTCCAC	1495
QY	124	CCGCGACGGGGCAAGAGACAGAACTCAAGGTGGAAAGTACCGGAGTATCTGGGGCGCGTG	183	QY	1444	CTCCACTATAAGACAGACGTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGTGGA	1503
Db	176	CSGCGCGGGCGGAGGAGGAGGAGTTGATCATGACGTTGCAGAGACTTGGGGCTCTCTG	235	Db	1496	CTCTTCTACBARAGGGATGACATAGTGAAGGGGGACCTTGAGCTGCAGGCCCTGGTGTGG	1555
QY	184	CTGTTTGTGAACCTGCGCAACCGCACCTCTTAAAGGACGAGCGCTGTTCTGCAACTGG	243	QY	1504	GAGATCACTGAAAATCGGGCTGCAAGGGCCGAGGACCCAGGAGGTTTCCTGTCTCTTTAAG	1563
Db	236	CAGTTCTGAGGCTGCGCAAGCAACCACTGGCTGTGGTGGAGCAGCGGTGTTCTGCAACCG	295	Db	1556	GAGATCACGGAGGTGGGGCTGTGCCAGGCCGAGGACCCAGGAGTTTCCCTGTCTCTTCCAG	1615
QY	244	ATCTCTGTGAGGGCCCGGAGCGGGGACGAGGTTCCTTTGTTTACCGCTGGGTG	303	QY	1564	GCTCGGAGACGAGTTTGGCACTTTGTCAACATGTGTATCTTCACTGCACCGGCCCAAC	1623
Db	296	ATCACGTTGACGGCCCTGGAGCCTCGCGGAGGTGGCTTCCGCTGTCTACCGCTGGGTG	355	Db	1616	TCCAGAGTCAACTCTGCCATTTTCTCCATGTGCGCTCTTCACTGCACCTGCCAGCAT	1675
QY	304	GAGGCAACGGCGCTCTGAGCTTGCCTGAAAGCACCGCGCGCACTGTGGCGAGGACCT	363	QY	1624	GCCTGTGCACTCGGGCAGCTGGACTGGTACTCTTGGGTGCTTAATGACCTTGCACG	1683
Db	356	CAGGGCGAGGACATCTGAGCCTGCCCGAGGCGACCGCGCGCTGCCAGGACAAATGCT	415	Db	1676	GCCGCATCAACGAGGGCCAGCTGGACTGGTATGTGCTGGGTCCCTTAATGCTCCATGCA	1735
QY	364	CAGGGCGCTGTTCCAGAAACACCGGGAAGAGAGCTCGAAGAGAGGAGTTGTACCGG	423	QY	1684	ATGCGGCTGCCCGCCCAACCAAG--GATGCAACGCTGGAGACAGTATGATGCGGACA	1740
Db	416	TTGGACATGTTCCAGAAAGCATCGAGAGAGGAACTGAAAGACAGACAGCAGATCTACTGC	475	Db	1736	ATGCGGATGCCCGCCACCCACCAAGGAGATGTGACGATGGCCACAGTATGATGGGTCA	1795
QY	424	TGGGAAAATGGAAGACCGGTTAAATCTGAAATATGGCTGGGGCCAAACTATATGACCTC	483	QY	1741	CTGCCCACTTCCACAGGCTTCTTCCAGATGTCCATCACTTGGCAGCTGGCAGAGC	1800
Db	476	TGGGCCACTGGGAAGAGGGTTACCCCTGACCATCGCTGCAGACCGTAAGGATGATCTA	535	Db	1796	CTACCTGATGTCCCGCAGGCGCTGTCTTCAATGGCCATCTCATGGCATTTGATGTCGCGC	1855
QY	484	CTGTGGATGAGCGATTTCTGGAAGACAAGAGATTTGACTTTTGTAGGTTTGGCTGGCCAG	543				
Db	536	CTTCCAAATATGAGATTTCATGAGGAGAAGAGGCTGGAATTTGATGAGACACTGAAGGCA	595				
QY	544	GCGCTGGCGCACTCGCTATCAAGACTCTTAATATGTTCTGACTTGTCTGGAGGATCTA	603				
Db	596	GCGGCTCTGGAGATGCCCTTCAACRTGTTTACACCTCTTCTGAGCTCTTGGAACTGCTTA	655				
QY	604	GATGACTTCAACCGGATTTTCTGGTGTGGTTCAGAGCAAGCTGGCTGAGCGCGTGGGGAC	663				
Db	656	GAAGACTTTCATCAGATCTTCTGGGCGCAGAGAGTGCCCTGGCTGAGAAGGTTGCGCAG	715				
QY	664	TCCTGGAAGAGATGCTTATTTGGGTACCAAGTTTCTTAATGGCGCCAAACCCCGTGGTG	723				

Db	716	TGCTGGCAGGATGATGAGTTGTTGAGCTACCAAGTTCCTCAATGGTGCCAAACCCCAATGCTG	775
QY	724	CTGAGGCGCTCTGCTTCACCTTCTGCTCGCTAGTGTTCCTCCAGGATGAGGAACTG	783
Db	776	TTGAGACGCTCGACCTCTCTGCCCTCCAGGCTAGTGTGCTCGCTCRGGATGGAAGGCTT	835
QY	784	CAGGCCACAGCTGGAGAGGAGCTGGAGGGAGGACACATGTTTGAAGCTGACTTCTCCCTG	843
Db	836	CRGGCTCAACTGGAGAAAGAACTTCAGAATGTTTCCCTGTTTGAAGCTGACTTCTATCCTT	895
QY	844	CTGATGGGATCAAGGCCAAAGTCAATCTCTGTAGCAGCAGCAGCCTGGCTGCCCTCTA	903
Db	896	CTGGATGAAATTCAGCCAAAGCTGATCCGAGGAGAGAACTACTTGGCTGCCCTCTC	955
QY	904	GTCACTGCTGAAATTCAGCCTGATGGGAAATCTTTCGCCCATGGTTCATCAGCTCCAGCTG	963
Db	956	GTTATGCTGAAGATGGAGCCCAATGGGAAGCTGAGCCCATGGTTCATCCAGATTGAGCT	1015
QY	964	CCCGCACAGGATCCCAACCACTCTCCCTTTTCTTTCCTACGGATCCGCCAATAGCCCTGG	1023
Db	1016	CCCARCCCGAGCTCTCCAAACCCCAACACTGTTCTCTGCTCAGACCCGCCCACTTGCCTGG	1075
QY	1024	CTTCTGGCCAAATGCTGGTGGGAGCTCTGACTTCCAGCTCCATGAGCTGAGTCTCAT	1083
Db	1076	CTCCTGGCAAAAGTCTCTGGGTCCGAAATTCAGATTTCCAACTGCACGAGATCCAGTATCAC	1135
QY	1084	CTTCTGAGGGGACACTTGTGAGTGTGAGTCAATGTTGTGGCCACCACATGAGGTGCTGCGG	1143
Db	1136	TGCTGAACACACACTCTGGTGGTGGTGTGCTGCTGCGCCACCATGGGTGCTCCCA	1195
QY	1144	TGATATACATCTTCAAGCTTATAATTCCTCCACCTGCGATACACCTCGGAAATTAAC	1203
Db	1196	GGACTGCACCCCATCTTCAAGTTCCTGATCCCCCATATCCGCTACACCATGGAATCAAC	1255
QY	1204	GTCGGGGCAGGACTGGGCTGCTCTGACATGGGAATTTTCGACAGACATATAGGACT	1263
Db	1256	ACCCGGGCGGAGCCAACTCATCTCAGATGGAGGAATTTTGTGTAAGGCAATGAGCACA	1315
QY	1264	GTGGGGGAGGCCAGCTGCAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACTTACAGCTCC	1323
Db	1316	GGTGGAGGGGGCCATGTACAGTTGCTCGTGGGGGGCAGCTCAGTCACTTCTCTCT	1375
QY	1384	TTCCTGCTCCCTGTATGACTTGGCCGACCGGGGGCTCTGGGAGTGAAGTCTTCTTCTAT	1383
Db	1376	CTCTGCTCTCTGACGACTGCTGACCGGGGCTGCTGGGACTCCAGGCTGCTCTCTAT	1435
QY	1384	GCCCAAGATGCGCTGGGCTCTGGGAATCATCTATCGGTATGTGGAGGATCGTGAGT	1443
Db	1436	GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGGAGGGGATCGTCCAC	1495
QY	1444	CTCCACTATAAGACAGACGTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGTGGA	1503
Db	1496	CTCTTCTACBARAGGGATGACATAGTGAAGGGGGACCTTGAGCTGCAGGCCCTGGTGTGG	1555
QY	1504	GAGATCACTGAAAATCGGGCTGCAAGGGCCGAGGACCCAGGAGGTTTCCTGTCTTTAAG	1563
Db	1556	GAGATCACGGAGGTGGGGCTGTGCCAGGCCGAGGACCCAGGAGTTTCCCTGTCTCTTCCAG	1615
QY	1564	GCTCGGAGACGAGTTTGGCACTTTGTCAACATGTGTATCTTCACTGCACCGGCCCAAC	1623
Db	1616	TCCAGAGTCAACTCTGCCATTTTCTCCATGTGCGCTCTTCACTGCACCTGCCAGCAT	1675
QY	1624	GCCTGTGCACTCGGGCAGCTGGACTGGTACTCTTGGGTGCTTAATGACCTTGCACG	1683
Db	1676	GCCGCATCAACGAGGGCCAGCTGGACTGGTATGTGCTGGGTCCCTTAATGCTCCATGCA	1735
QY	1684	ATGCGGCTGCCCGCCCAACCAAG--GATGCAACGCTGGAGACAGTATGATGCGGACA	1740
Db	1736	ATGCGGATGCCCGCCACCCACCAAGGAGATGTGACGATGGCCACAGTATGATGGGTCA	1795
QY	1741	CTGCCCACTTCCACAGGCTTCTTCCAGATGTCCATCACTTGGCAGCTGGCAGAGC	1800
Db	1796	CTACCTGATGTCCCGCAGGCGCTGTCTTCAATGGCCATCTCATGGCATTTGATGTCGCGC	1855



Qy	1801	CAGCCCGTTATGTGGCTGTGGGC	CAGCATGAGGAGGAGTATTTTTCGGGCCCTTGAGCCT	1860
Db	1856	CAGCCAGACATGGTGCTCTGGGGC	CACCAAGAAAATATTTCTCAGGCCCAAGCCC	1915
Qy	1861	AAGSCTGTGCTGAAGATTCAGGGAGGAGCTGCCTCCCTGGATTAAGGAAATTGAGATC	1920	
Db	1916	AAAGCTGTGCTTAACCAATTCCGAACAGATTTGGAAAAGCTRGAANAAGGAGATTTACAGCC	1975	
Qy	1921	CGGAATGCAAGCTGGACATGCCCTACAGAGTACTCGCGGCCAGCTGGTGGGAAAAACAGT	1980	
Db	1976	CGGAATGAGCAACTTGACTGSCCTTATGAACTATCTGAAGCCCACTGATGAGAGAACAGT	2035	
Qy	1981	GTGCCCATCTTAAGC	1994	
Db	2016	GTCACCATCTGAGC	2049	

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RESULT 8
US-10-741-600-672
; Sequence 672, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 672
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-600-672

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Query Match	38.1%	Score 1016.4	DB 21	Length 2867
Best Local Similarity	69.4%	Pred. No. 2.4e-293		
Matches 1384	Conservative	8	Mismatches 599	Indels 3
			Gaps	1
Qy	4	ATGGGTCTCTACCGCATCCGGTGTCCACTGGGGCCTCGCTCTATGCGGGTTCACAAAC	63	
Db	555	ATGGGCGCGCTACCGCATCCGGTGTGGCCACCGGGCCCTGGCTCTCTCCGGTGGTACAA	614	
Qy	64	CAGGTGCAGCTGTGGCTGGTCCGCCAGCACGGGAGCGCGCTCGCGAAGCGACTGTGG	123	
Db	615	CGCGTGACACTTTGGCTGTGTCGGACGGCGGGAGCGGAGCTGAGACTGCAGCTCGG	674	
Qy	124	CCGCGACGGGCAAGGAGACAGAACTCAAGGTGGAAGTACCGGAGTATCTGGGGCCGCTG	183	
Db	675	CCSGCGGGGCGAGGAGGAGGATTTGATCATGACGTTGCAGAGGACTTGGGGCTCCTG	734	
Qy	184	CTGTTTGTGAACCTGCGCAAAACGGCACTCTCTTAAGGACGACGCTGGTCTCTGCAACTG	243	
Db	735	CAGTTCTGTAGGCTGTGCGAAGCACCACTGGCTGTGTGGACGACGCGTGTTCTTCGACCGC	794	
Qy	244	ATCTCTGTGAGGGCCCGGACCGGGGACGAGGTCAGGTTCCCTTGTACCGCTGGGTG	303	
Db	795	ATCACGCTGACGGGCCCTGGAGCGCTGCGCGAGGTGGCTTCCCGTCTACCGCTGGGTG	854	
Qy	304	GAGGGCAACGCGCTCTGAGGCTCCCTGAAGGCACCGCGCGCACTGTGGGGGAGGACCT	363	
Db	855	CAGGCGAGGACATCTTGAGCCTGCCCGAGGACCCGCCCTGCCAGGAGACAATGCT	914	
Qy	364	CAGGGCCTGTTCCAGAAACACCGGGGAAGAGGCTGGAAGAGAGAAAGTGTGTACCGG	423	
Db	915	TTGGACATGTTCCAGAGACATCGAGAGNAGGAACTGAAGACACACAGCAGATCTACTGC	974	
Qy	424	TGGGGAACTGGAAGGACGGGTTTAATCTGTAATATGGCTGGGGCCAAACTATATGACCTC	483	
Db	975	TGGGCCACCTTGAAGGAGGGTTACCCCTGCACATCGCTGAGACCGTGAAGGATGACTA	1034	

Qy	484	CCTGTGGATGAGCGCATTTCTTGGNAGACAAGAGAGTTGACTTTTGAGGTTTTCGTGGCGCAAG	543
Db	1035	CCTCCAAATATGAGATTCCATGAGGAGNAGAGCGCTGGATCTTTGAATTGGACACTGGAAGGCA	1094
Qy	544	GGGCTGGCGGACCTCGCTATCAAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGGATCTA	603
Db	1095	GGGGCTCTGGAGATGGCCCTCAAACTGTGTTTACACCTCTGAGCTCTTGGAACTGCCTA	1154
Qy	604	GATGACTTCAACCGGATTTTCTGGTGTGTGTCAGAGCAAGCTGGCTGAGCGCTGCGGGAC	663
Db	1155	GAAGACTTTGATCAGATCTTCTGGGGCCAGAAGAGTGCCCTGGCTCAGAAGGTTTCCCGAG	1214
Qy	664	TCTTGGNAGGAAGATGCTTATTTTGGGTACAGTTTCTTAAATGGCGCCAAACCCGTGGTG	723
Db	1215	TGCTGGCAGGATGATGAGTTGTTTCAGTACCACTTCTCAATGGTGGCCAAACCCCATGCTG	1274
Qy	724	CTGAGGGCTCTGCTCACCTTCTGCTCGCTTGTCTTCCCTCAGGCAATGGAAGAACTG	783
Db	1275	TTGAGAGCTCTGACCTCTCTGCCCCTCAGGCTAGTGTGCTTCCCTCTCGGGATGGAAGACTT	1334
Qy	784	CAGGCCACAGCTGAGAGGAGCTGGAGGGAGGCACACTGTTTGGAACTGACTTCTTCCCTG	843
Db	1335	CRGGCTCACTTGGAGAAAGAACTTTCAGATGTTTCCCTGTTTGAAGCTGACTTTCATCCTT	1394
Qy	844	CTGGATGGGATCAAGGCGCAACGTCATCTCTGTAGCCAGCAGACACCTGGCTGCCCTCTA	903
Db	1395	CTGGATGGAATTCAGCCAAACGTGATCCGAGGAGAGAAGCAATACCTGGCTGCCGCCCTC	1454
Qy	904	GTCACTGCTGAAATTCAGCCTGATGAGGAAACTCTTGGCCATGCTCATCCAGCTCCAGCTG	963
Db	1455	GTATGCTGAAGATGAGAGCCCAATGGGAAGCTGCAGCCCATGTCATCCAGATTCAGCCT	1514
Qy	964	CCCGCACAGGATCCCAACCACTCCCTTTTCTTGCTACGGATCCCCCAATGGGCTGG	1023
Db	1515	CCARCCCAGCTCTCCNACCCCAACACTGTTCTTGCCCTCAGACCCCACTTGGCTGG	1574
Qy	1024	CTTCTGGCCAAATGCTGGTGGCCAGCTCTGACTTTCAGCTCCATGAGCTGCACTCAT	1083
Db	1575	CTCTGGCAAGTCTCTGGTCCGAAATTCAGATTTCCAACTGCACGAGATCCAGTATCAC	1634
Qy	1084	CTTCTGAGGGGAACATTGATGGCTGAGGTCATTGTTGTGGCCACCATGAGTGCCTGCCG	1143
Db	1635	TTGCTGAACAACKACCTGGTGGCTGAGGTCATCGCTGTGGCCACCATGCGGTGCCCTCCA	1694
Qy	1144	TCGATACATCTATCTTCAAGCTTTAATTTCCCACTTCGGATACACCTTGGAAATTAAC	1203
Db	1695	GGACTGCACCCATCTTCAAGTTCCTGNTCCCCCATATCGGCTACACCATGGAAATCAAC	1754
Qy	1204	GTCCGGCCAGGACTGGGCTGTCTCTGACATGGGAATTTTGCACAGATAATGAGCACT	1263
Db	1755	ACCGGGCCCGGACCCAACTCATCTCAGATGGAGGAATTTTGTAAAGCAGTGAGCACA	1814
Qy	1264	GGTGGGGAGGCCACGTGCACTGTCTCAAGCAAGCTTGGAGCCTTCTTAACCTACAGTCC	1323
Db	1815	GGTGGAGGGGGCCATGTACAGTTGTCCTCGTGGCGCGCAGCTCAGCTGACCTACTGCTCC	1874
Qy	1324	TTCTGTCCCTCTCATGACTTGGCCGACCGGGGCTCTCTGGAGTGAAAGTCTTCTTCTCTAT	1383
Db	1875	CTCTGTCTCTCTGACGACCTGGCTGACCGGGGCTCTCTGGACTCCAGGTTGCTCTCTAT	1934
Qy	1384	GCCCAAGATCGCTGGGCTCTGGGAAATCATCTATCGGTATGTGGAAGAAATCGTGAGT	1443
Db	1935	GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGATATGTTGGAGGGATCGTCCAC	1994
Qy	1444	CTCCACTATAAGACAGACGTGGCTGTGAAAGACGACCCAGCTGACAGCTTGGTGTGGA	1503
Db	1995	CTCTTCTACCARAGGATGACATAGTGAAGGGGGACCTGAGCTGCAGGCTGGTGTGCG	2054
Qy	1504	GAGATCACTGAAATCGGGCTGCAAGGGGCCCGAGCCGAGGGTTTCTGTCTCTTTACAG	1563
Db	2055	GAGATACGAGAGTGGGGCTGTGCCAGGCCACGAGCGAGGTTTCCCTGTCTCTTCCAG	2114
Qy	1564	GCTCGGACACAGGTTTGGCCACTTTGTTCACCATGTGATCTTTCACCTCGCACCGGCCAACAC	1623



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QY 1384 GCCAAGATGCGCTGCGCTCTGGGAAATCATCTATCGGTATGTGGAAAGAAATCGTGAGT 1443
DB 1436 GCCCATGATGCTTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGGAGGGATCGTCCAC 1495
QY 1444 CTCACATATAGACAGAGTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGTGGA 1503
DB 1496 CTCCTTACCARAGGATGACATAGTGAAGGGGACCTGTAGCTGCGAGGCTGGTGTGCG 1555
QY 1504 GAGATCACTGAAATCGGCTGCAAGGGCCCGAGGACCGAGGGTTTCTGTCTCTTTACAG 1563
DB 1556 GAGATCAGGAGGTGGGCTGTGCCAGGCCCGAGGACCGAGGTTTCCCTGTCTCTTCCAG 1615
QY 1564 GCTCGGACCAAGGTTGTCACCTTTGTACCAATGTATCTTCACTGCAACCGGCCAACAC 1623
DB 1616 TCCAGAGTCAACTCTGCGCAATTTCTCAACCATGTGCGTCTTCACTGCACTGCCAGCAT 1675
QY 1624 GCCTGTGCACTTGGGCGAGCTGGAATGTTACTCTTGGGTGCTTAATGCACTTGCACG 1683
DB 1676 GCCGCCATCAACAGGGCCAGCTGGACTGGTATGCTTGGGTCCCTTAATGCTTCCATGCA 1735
QY 1684 ATGCGGCTGCCCGCCCAACACCAAG--GATGCAACGCTGGAGACAGTATGCGGACA 1740
DB 1736 ATGCGGATGCCCGCCCAACCAAGGAAGATGTGACGATGGCCACAGTATGGGTCA 1795
QY 1741 CTGCCCACTTCCACAGGCTTCTCTCCAGATGTCCATCATCTGGCAGCTGGGCGAGCGC 1800
DB 1796 CTACCTGATGTCGGCGAGGCTGTCTTCAATGGCCATCTCATGGCATYTGAGTGGCCGC 1855
QY 1801 -CAGCCCGTTATGTTGGCTGTGGCCAGCATGAGGAGGATATTTTCGGGCGCTGAGCCT 1860
DB 1856 CAGCGACAGATGTTGGCTCTGGGCGACCAAGAAAAATATTTCTCAGGCCCGCCAGGCC 1915
QY 1861 AAGGCTGTGCTGAAGAGTTTCAGGGAGGAGCTGGCTGCCCTGGATAAGGAAATGAGATC 1920
DB 1916 AAAGCTGTGCTAAACCAATTCGAACAGATTTGGAAAGCTTGAAGAGATTAACGCC 1975
QY 1921 CGGAATGCAAGCTGGACATGCCCTTACGAGTACCTTGGCGGCCAGCGTGGTGGAAACAGT 1980
DB 1976 CGGAATGAGCACTTGTGCGCCCTATGAATATCTGAAGCCCGCAGCTGTATAGAGAACAGT 2035
QY 1981 GTGCCCATCTAAGC 1994
DB 2036 GTCACCATCTGAGC 2049

RESULT 10
US-10-741-601-233
; Sequence 233, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS; METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 233
; LENGTH: 2867
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-741-601-233

Query Match 38.0%; Score 1015.2; DB 19; Length 2867;
Best Local Similarity 69.4%; Pred. No. 5.6e-293;
Matches 1384; Conservative 7; Mismatches 600; Indels 3; Gaps 1;

QY 4 ATGGGTCTCTACCGCATCCGCTGTCTCCACTTGGGGCTCGCTCTATGCGCGTTCCCAACAC 63
DB 555 ATGGGCGGCTACCGCATCCGCTGTGGCCACCGGGGCGCTGGCTCTTCTCCGGGCTGTGACAC 614
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QY 64 CAGGTGAGCTGTGGCTGTGGTCCAGCACGGGGAGGGGGCTCGGGAGAGCACTGTGG 123
DB 615 CGGCTGAGCTTTGGCTGTGGTCCGAGACGCGGGGGAGCGGAGCTGGAGCTGCAGCTCGG 674
QY 124 CCGCACGGGGCAAGAGACAGACAACTCAAGGTGGAAGTACCGAGTATCTGGGGCCGCTG 183
DB 675 CCGGCGGGGGCGAGGAGGAGGATTTGATCATGACCTTGCAGAGGACTTTGGGGCTCCTG 734
QY 184 CTGTTGTGAAACTTGCAGAAACCGGCACTCTTAAAGGACGACGCTGTGTTCTGCAATGG 243
DB 735 CAGTTCTGAGGCTGCGCAAGCACTGCTGTGTGGACGACGCGTGTCTTGGGACCGC 794
QY 244 ATCTCTGTGAGGGCCCGGAGCGGGAGCGAGTCAAGTTCCCTTGTACTCCGTGGGTG 303
DB 795 ATCAGGTGAGGGCCCTGAGGCTGCGCGAGGTGGCTTCCCGTGTCTACCGTGGGTG 854
QY 304 GAGGGCAACGGCGTCTGAGCTGCTGAAAGGACACCGGCGGCACTGTGGGGAGGACCT 363
DB 855 CAGGGCGAGACATCTCTGAGCTTCCCGAGGGACACCGCCGCTGCCAGGAGACATGCT 914
QY 364 CAGGGCTGTTCAGAAACACCGGGAAAGAGAGCTGGAAGAGAGAGAAAGTTGTACCGG 423
DB 915 TTGACATGTTCCAGAAAGCATCGAGAGAAAGAACTGAAAGACAGACAGACATCTACTGC 974
QY 424 TGGGAACTGGAAGAGCGGTTAATTTCTGAATATGCTGGGCGCAAACTATATGACCTC 483
DB 975 TGGGCCACCTGGAAGGAGGTTTACCCCTGACCATCTGCGAGACCGTAAGAGATGATCTA 1034
QY 484 CTTGTGATGAGCGATTTCTGGAAGACAGAGAGTTGACTTTGAGGTTTCCTCTGCCCAAG 543
DB 1035 CTTCCAATATGATTTCCATGAGGAGAGAGGCTGACCTTTGATGGACACTGAAGGCA 1094
QY 544 GGGCTGCGCAGCTCGCTATCAAAGACTCTCTAAATGTTCTGACTTGTCTGGAAGATCTA 603
DB 1095 GGGCTCTGAGAGATGGCCCTCAAACTGTTTACACCTCTCTGAGCTCTCTGGAATGCTCCTA 1154
QY 604 GATGACTTCAACCGGATTTCTGTGTGTGTCAGAGCAAGCTGGCTGAGCGGTGGGAC 663
DB 1155 GAAGACTTTGATCAGATCTTCTGGGGCCAGAGAGTGGCTGGGTGGAAGGTTTCGCCAG 1214
QY 664 TCTTGAAGGAAGATGCTTATTTGGGTACCAGTTCTTAAATGGCGCCAAACCCGCTGGT 723
DB 1215 TGCTGGCAGGATGATGATGTTTCACTACAGTTCTTCAATGTGTCACACCCCATGCTG 1274
QY 724 CTGAGGCGCTCTGCTCACTTCTGCTGCGCTAGTGTTCCTCCAGGCATGAGGAACTG 783
DB 1275 TTGAGACGCTCGACCTCTCTGCGCTCAGCGCTAGTGTGCTCTCGGATGGAAGGCTT 1334
QY 784 CAGGCCAGCTGGAGAGAGAGCTGGAGGGAGGACACATGTTGGAAGCTGACTTCTCCCTG 843
DB 1335 CRGGCTCAACTGGAGAAAGAACTTCAGAAATGGTTTCCCTGTTTGAAGCTGACTTTCATCCTT 1394
QY 844 CTGATGGATCAAGGCCAAGCTCATTTCTGTAGCCAGCAGACCTGGCTGCCCTCTA 903
DB 1395 CTGATGGAATTCAGCCCAAGCTGATCCGAGGAGAGAACTACCTGGCTGCCCTCTC 1454
QY 904 GTCATGCTGAAATTCAGCCTGTGAGGAAACTCTTGGCCATGGTCACTCAGCTCCAGCTG 963
DB 1455 GTTATGCTGAAGTGGAGGCCAATGGGAGAGCTGCGAGCCCATGGTTCATCCAGATTCAGCT 1514
QY 964 CCCGCGACAGGATCCCAACACCTCCCTTTTCTTGTGCTACGGATCCCGCAATGGCTGG 1023
DB 1515 CCCACCCCGAGCTCTCCAAACCCCAACACTGTTCTCTGCTCCAGACCCCGCCCACTTGGCTGG 1574
QY 1024 CTTCTGGCCAAATGCTGGGTGCGAGCTCTGACTTCCAGCTCCATGAGCTCAGTCTCAT 1083
DB 1575 CTCCTGGCAAGTCTCGGTCCGAAATTCAGATTTCCAATTCAGAGATCCAGTATCCAT 1634
QY 1084 CTTCTGAGGGGACACTTGTGATGGCTGAGGTCAATTTGTGGCCACCATGAGTGGCTCGCG 1143
DB 1635 TTGCTGAACACKACCTGGTGGCTGAGGTCACTCGTGTGCGCAACCATGCGGTGCTCCCA 1694
QY 1144 TCGATACATCTATCTTCAAGCTTATAATTTCCCACTCTGGGATACACCCCTGGAAATTAAC 1203
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Db 1695 GGAATGACCCATCTTCAAGTTCTTGATCCCCCATATCCGCTACACCATGGAATCAAC 1754  
QY 1204 GTCCGGCAGAGCTGGCTGCTCTGACATGGGAATTTGACAGATATGAGCACT 1263  
Db 1755 ACCGGGCCGGACCCAACTCATCTCAGATGAGGAATTTTGTAAAGCATGAGCACA 1814  
QY 1264 GGTGGGGAGGCCACGCTGACAGCTGCTCAAGCAAGCTGGAGCCTTCTTAACCTACAGCTCC 1323  
Db 1815 GGTGAGGGGGCCATGATACAGTTGCTCCGTGGGGCGGACGCTCAGCTGACCTACTGCTCC 1874  
QY 1324 TTCTGTCCCTTGATGACTTGGCCGACCGGGGCTCTCGGAGTGAAAGTCTTCTTCTAT 1383  
Db 1875 CTCTGTCTCTGACGACCTGCTGACCGGGCTCTCGGAGCTCCAGGTGCTCTCTAT 1934  
QY 1384 GCCAAGATGCGTGGGCTCTGGGAATCATCTATCGGTATGTGGAAGGATCGTGAGT 1443  
Db 1935 GCCCATGATGCTTTACGGCTCTGGGAGATCATTCGACGATATGTGAGGGGATCGTCCAC 1994  
QY 1444 CTCCTACTAAGACAGACGCTGGCTGTGAAAGACGACCCAGAGCTGCAGACCTGGTGTGCA 1503  
Db 1995 CTCTTCTACARAGGATGACATAGTAGAGGGGACCTGAGCTGCAGGCTGTGTGG 2054  
QY 1504 GAGATCAGTAATCGGGCTGCAAGGGGCCAGGACCGAGGGTTTCTCTCTCTTTACAG 1563  
Db 2055 GAGATCAGGAGGTGGGGCTGTGCCAGGCCAGGACCGAGGTTTCCCTGTCTCTTCCAG 2114  
QY 1564 GCTCGGGAACGAGTTGGCACTTGTGACCATGTGTATCTTCCCTGCACCGCCCAACAC 1623  
Db 2115 TCCAGAGTCAACTCTGCCATTCTCCATCCATGTGGCTTTCACGTGCACTGCCAGCAT 2174  
QY 1624 GCCTCTGTGACCTGGGGCAGCTGGAGTGTACTCTTGGGTGCTTAATGCACCTGCAGC 1683  
Db 2175 GCGCCATCAACAGGGCCAGCTGGAGTGTGATGCTGGTCCCTPATGCTCCATGCACA 2234  
QY 1684 ATGCGCTGCCCCGCCCAACCAACAG---GATGCAACGCTGGAGACAGTATGGCGACA 1740  
Db 2235 ATGCGGATGCCCCACCCACCAAGGAAGATGTGACGATGGCCACAGTATGGGTCA 2294  
QY 1741 CTGCCCAACTTCAACGAGCTTCTCCAGATGTCCATCACTTGGCAGCTGGCAGACGC 1800  
Db 2295 CTACCTGATGTGCGGAGGCTGTCTTCAATGGCCATCATGGCCATGTAGTGGCCGC 2354  
QY 1801 CAGCCCGTTATGTGGCTGTGGGCCAGCATGAGGAGGATTTTTCGGGCCCTGAGCCT 1860  
Db 2355 CAGCCAGATGTGTGCTCTGGGGCACCAAGAAATATTTCTCAGGCCCCAGGCC 2414  
QY 1861 AAGGCTGTCTGAAGAGTTTCAGGGAGGAGCTGGCTGCCCTGGATGAAGAAATTTGAGATC 1920  
Db 2415 AAAGCTGTCTAAACCAATTCGAAACAGATTTGAAAGCTGAAAGAGATTACAGCC 2474  
QY 1921 CGGAATGCAAGCTGACATGCCCTACGAGTACCTGGGCCAGCGTGTGGAACAGT 1980  
Db 2475 CGGAATGACCACTTGAAGCTGGCCCTATGAATATCTGAAGCCAGCTGYATAGAACAGT 2534  
QY 1981 GTGGCCATCTAAGC 1994  
Db 2535 GTCACCATCTGAGC 2548

RESULT 11  
US-10-170-097-652  
; Sequence 652, Application US/10170097  
; Publication No. US20030228582A1  
; GENERAL INFORMATION:  
; APPLICANT: Blumenfeld, Marta  
; APPLICANT: Bougueleret, Lydie  
; APPLICANT: Chumakov, Ilya  
; APPLICANT: Cohen, Annick  
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING  
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
; FILE REFERENCE: GEN-T114XC2D1  
; CURRENT APPLICATION NUMBER: US/10/170,097

; CURRENT FILING DATE: 2002-06-10  
; PRIOR APPLICATION NUMBER: US 09/641,638  
; PRIOR FILING DATE: 2000-08-16  
; PRIOR APPLICATION NUMBER: US 09/502,330  
; PRIOR FILING DATE: 2000-02-11  
; PRIOR APPLICATION NUMBER: US 60/133,200  
; PRIOR FILING DATE: 1999-05-07  
; PRIOR APPLICATION NUMBER: US 09/275,267  
; PRIOR FILING DATE: 1999-03-23  
; PRIOR APPLICATION NUMBER: US 60/119,917  
; PRIOR FILING DATE: 1999-02-12  
; NUMBER OF SEQ ID NOS: 1304  
; SOFTWARE: Patent.pm  
; SEQ ID NO 652  
; LENGTH: 2343  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: 5' UTR  
; LOCATION: 1..39  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 40..2031  
; FEATURE:  
; NAME/KEY: 3' UTR  
; LOCATION: 2032..2343  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 366  
; OTHER INFORMATION: 10-343-231 : deletion of C  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 605  
; OTHER INFORMATION: 10-346-141 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 712  
; OTHER INFORMATION: 10-347-111 : polymorphic base G or C  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 766  
; OTHER INFORMATION: 10-347-165 : polymorphic base C or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 804  
; OTHER INFORMATION: 10-347-203 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 821  
; OTHER INFORMATION: 10-347-220 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1004  
; OTHER INFORMATION: 10-349-97 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1049  
; OTHER INFORMATION: 10-349-142 : polymorphic base G or C  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1123  
; OTHER INFORMATION: 10-349-216 : deletion of CTG  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1131  
; OTHER INFORMATION: 10-349-224 : polymorphic base G or T  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1491  
; OTHER INFORMATION: 10-507-170 : polymorphic base A or G  
; FEATURE:  
; NAME/KEY: allele  
; LOCATION: 1742

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: : OTHER INFORMATION: 10-340-112 : polymorphic base A or C
: : FEATURE:
: : NAME/KEY: allele
: : LOCATION: 1760
: : OTHER INFORMATION: 10-340-130 : polymorphic base A or T
: : FEATURE:
: : NAME/KEY: allele
: : LOCATION: 1941
: : OTHER INFORMATION: 10-341-116 : polymorphic base A or G
: : FEATURE:
: : NAME/KEY: allele
: : LOCATION: 2144
: : OTHER INFORMATION: 10-341-319 : polymorphic base C or T
US-10-170-097-652

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Query Match 37.9%; Score 1013.6; DB 17; Length 2343;  
Best Local Similarity 69.2%; Pred. No. 1.5e-292;  
Matches 1380; Conservative 11; Mismatches 600; Indels 3; Gaps 1;

Qy	4	ATGGGTCTCTACCGCATCCGGTGTCCACTTGGGGCTCGCTCTATGCGGGTTCACAAAC	63
Db	40	ATGGGCGGCTTACCGCATCCGGTGTGCCACCGGGGCTGGCTCTTCTCCGGGTCTGTAAC	99
Qy	64	CAGGTGCACGTGTGGCTGGTCCGCAGACACGGGAGAGGGGCGCTCGGGAAGCAGCTGTGG	123
Db	100	CGCGTGCAGCTTTTGGCTGTGTCGGACGCGCGGGAGCGCAGCTGTGAGCTGCAGCTCCG	159
Qy	124	CCGCGACGGGGCAAGSAGACAGAACTCAAGTGTGGAAGTACCGGAGTATCTTGGGGCCGCTG	183
Db	160	CCGGCGGGGGCGAGAGAGAGTGTGATCATGACGTTGCAGAGCACTTGGGGCTCTCTG	219
Qy	184	CTGTTTGTGAACCTGCGCAAAACGGCACCTCTCTTAAGGACGACGCTGCTTCTGCAACTGG	243
Db	220	CAGTTCGTGAGCTGCGCAAGCACCACTGGCTGGTGTGACGACGCGTGTCTCGGACCGC	279
Qy	244	ATCTCTGTGCGAGGGCCCGGAGCCGGGGAACAGGTCAAGTTTCCCTTGTTAACGCTGGGTG	303
Db	280	ATCACGGTTCAGGGGCTTGGAGCTTCGCGAGGTGGCTTCCCGTACTACCGCTGGGTG	339
Qy	304	GAGGGCAAACGGCGTCTGAGCTGCTGAAAGGCAACGGCCGCACTGTGGGCGAGGACCT	363
Db	340	CAGGGCGAGGAATCTGAGCGTCCCGAGGGCACCGCCGCTGCCAGGAGACAATGCT	399
Qy	364	CAGGGCCTCTTCAGAAACACCGGGAAGAGAGCTGGAAGAGAGAGAAAGTTGTACCGG	423
Db	400	TTTGACATGTTCCAGAGCATCGAGAGAAGAACTGAAAACAGACAGCAGATCTACTGC	459
Qy	424	TGGGAAACTGGAAGGACGGGTTAATCTGTAATATGGCTGGGGCCAAACTATATGACCTC	483
Db	460	TGGGCCACCTGGAAGGAAGGGTTACCCCTGACCATCGCTGCAGACCGTAAGGATGATCTA	519
Qy	484	CCGTGTGGATGACGATTTCTGGAGACAGAGAGTTGACTTTGAGGTTTGCCTGGCCAG	543
Db	520	CCTCCAAATATAGAGATTCATGAGGAGAAGGCTGGACTTTGAAATGGAACACTGAAGCA	579
Qy	544	GGGCTGGCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTGCTGCGAAGGATCTA	603
Db	580	GGGGCTCTGGAATGGCCCTCAACRPTGTTTACACCTCTCTGAGCTCTGTGAACTGCCTA	639
Qy	604	GATGACTTCAACCGGATTTTCTGGTGTGGTCAGAGCAAGCTGGCTGACGCGCTGCGGGAC	663
Db	640	GAAGACTTTGATCAGATCTCTTGGGGCCAGAAGAGTGCCCTGGCTGAGAAAGTTTCCAG	699
Qy	664	TCTTGGAGGAAGATGCCTTATTTGGGTGACAGTTTCTTAATGGCGCCCAACCCGTGGTG	723
Db	700	TGCTGGCAGGATATAGTGTGTTTCAGCTTACAGTTTCCATGCTGATGCTGATGCTGCTG	759
Qy	724	CTGAGGCGCTCTGCTCACCTTCTGCTCGCTAGTGTTCCTCCAGSCATGAGGAACTG	783
Db	760	TTGAGAYGCTCGACCTCTCTGCCCCTCAGGGCTAGTGTGCTTCRGGGATGGGAAGCTT	819
Qy	784	CAGGCCCACTGGAGAAGGAGCTGGAGGGGCACTGTTCGAAGCTGACTTCTCCCTG	843

820	CRGCTCAA	CTGGAGAAAGAACTT	CAGAA	TGGTTCCCTGTTTGAAGCTGA	CTTCATCTTT	879
844	CTGGATGGGAT	CAAGGCCAAACGTCAT	TCTCTGTAGCCACAGCAGCA	CTCTGGCTGCCCTCTA	903	
880	CTGGATGGAA	TTCCAGCCAAAGTGA	TCCGAGGAGAGAAGCAA	TACTTGGCTGCCCTC	939	
904	GTCATGCTGAAA	TTTGCAGCTGTATGGGAA	AACTCTTTGCCCATGGTCA	TCTCAGCTCAGCTG	963	
940	GTTATGTGAAGAT	TGGAGCCCAATGGGAAGCTG	CAGCCCATGGTCA	TCCAGATTCAGCCT	999	
964	CCCGCACAGAT	TCCCAACCACTCCCTCTTTCTT	TGCTACGGATCCCCAATGCCCTGG	1023		
1000	CCCACTCCAGCT	CTCCAAACCAACTGTCTCTG	CCCTCAGACCCCCCTTGGCTGG	1059		
1024	CTTCTGCCAAA	TGCTGGTGCAGCTCTGCACT	TTCAGCTTCCAGCTC	CAATGAGCTGCTCAT	1083	
1060	CTCTGSCAA	AGTCTGGTCCGAAATTCAGAT	TTTCCAACTGCACGAGAT	CCAGTATCAC	1119	
1084	CTTCTGAGGG	GAACATTTGATGGCTGAGGTCA	TTGTTGTGGCCACCATGAGTGGCTG	CGCG	1149	
1120	TTGCTGAACA	CKACACCTGTGGTGTAGGTCA	TGCTGTGCGCAACATGCGGTG	CTCCCA	1179	
1144	TGCATACAT	CTATCTTCAAGCTTATAATTTCC	CACTGGATACACCTTGGAAATTAAC	1203		
1180	GGACTGCAC	CCCCATCTTCAAGTCTCCGAT	CCCCCATATCCGCTACA	CAATGGAAATCAAC	1239	
1204	GTCCGGCC	CAGGACTGGGCTGGTCTCTG	ACATGGGAATTTTCGACCA	CAGATAATGAGCACT	1263	
1240	ACCGGGCC	CGGACCACTCATCTCAGAT	GGAGGAATTTTGTATAGGCAGT	GTGAGACA	1299	
1264	GGTGGGG	AGGCCACGTGCAGCTGTCTA	AGCAAGCTGGAGCTTCTTAA	CACTACAGTCTC	1323	
1300	GGTGGAG	GGGCCCATGTGACAGTTGCT	CCGTGCGGCGGCACTCAGCTGA	CCATACTGTCTC	1359	
1324	TTCTGTCC	CCCTCATGACTTGGCCGAC	CCGGGGCTCTCTGGAGTGAAGT	CTTCTCTTCTAT	1383	
1360	CTCTGTCT	CTCTGA	CGACCTGGCTGACCGGGGGCT	TGCTGGGACCTCCAGGTGTCTCTAT	1419	
1384	GCCCAAGAT	CGCTGCGGCTCTGGGAA	TCACTATCGGTATGTGGAAGAA	TGCTGAGT	1443	
1420	GCCCATGAT	GCTTTACGCTCTGGGAGAT	CAATTTGCCAGGTATGTGGAGGGAT	CGTCCAC	1479	
1444	CTCCA	CTATAAGACAGACGTGGCTGT	GAAGAAGCAACCAGAGCTG	CACAGCTTGGTGTGCGA	1503	
1480	CTCTTCT	ACCARAGGATGACATAGT	GAAGGGGACCTCAGCTGC	AGGCTGGTGTGCG	1539	
1504	GAGATCA	CTGAAA	TCCGGCTGCAAGGGGCCAGACA	CCGAGGGTTTCTGTCTCTTTACAG	1563	
1540	GAGATCA	CGAGGTGGGGCTGTGCC	AGGCCCAAGACCGAGGTTTCC	CTGTCTCTCTCCAG	1599	
1564	GCTCGG	ACAGGTTTGCCACTTTTGC	ACCATGTATCTTCACTCCAGCGGCA	CAACAC	1623	
1600	TCCAGAGT	CAACTGTGCCATTTCTC	ACCATGTGGCTCTTACGTGC	ATGCCACAGT	1659	
1624	GCCTCTGT	GCACTGGGCCAGCTGGACT	TGTGTA	CTCTTTGGTGGCTAATGCA	CCCTGCACG	1683
1660	GCGCCAT	CAACAGGGCCAGCTGGACT	GGTATGCTCTGGGTCCCTA	TGCTCCATG	CACA	1719
1684	ATGGGGT	GTCCCGCCCAACCA	CAAG---GATGCAACGCTGGAGACA	CAGTGTATGGCGACA	1740	
1720	ATCGGAT	GTCCCGCCCAACCA	CAAGAGAGATGTGAC	GAAGGCCACAGTGTATGGGGTCA	1779	
1741	CTCGCC	CAACTTCCACAGGCTTCTCT	CCAGATCCATCACTTGGCAGCTGGG	CAGACGC	1800	
1780	CTACCT	TGATGTCGGCAGGGCTGTCT	TTCAAATGGCCATCTCAT	GGGCATCTGAGTGTGGCCG	1839	
1801	CAGCCG	CTTATGTTGGCTGTGGGCCAGCA	TGAGGAGGATTAATTTT	CGGGCCCTGAGCCT	1860	
1840	CAGCCAGA	CATGTTGGCTCTGGGGCC	CAACAAAGAAATATTTT	CTCAGGCCCCCAAGCCC	1899	
1861	AAGGCT	GTGCTGAAGAAGTT	CAGGGAGGAGCTGGCTGCC	CTGGATTAAGGAAA	TTGAGATC	1920
1900	AAAGCT	GTGCTAAACCAATTC	CGAAACAGATTTGGAAAAGCT	TCGAAAAGGAGATTA	CAGCC	1959

	1921	1960	1981	2020	1980
Qy	CGGATCCAAAGCTGGACATGCCCTACAGCTACTCGCGGCCACAGCTGTGTGGAAACAGT		GTGGCCATCTAAGC		
Db	CGGAATGAGCAACTTGACTGGCCCTATGAATATCTGAAGCCCACTGCATAGAGAACAGT		GTCAACATCTGAGC		

RESULT 12  
US-10-926-684-652  
Sequence 652, Application US/10926684  
Publication No. US20050014190A1  
GENERAL INFORMATION:  
APPLICANT: Blumenfeld, Marta  
APPLICANT: Bougueleret, Lydie  
APPLICANT: Chumakov, Ilya  
APPLICANT: Cohen, Annick  
TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS  
TITLE OF INVENTION: CARRYING  
TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM  
FILE REFERENCE: GEN-T114XC2D1  
CURRENT APPLICATION NUMBER: US/10/926,684  
CURRENT FILING DATE: 2004-08-25  
PRIOR APPLICATION NUMBER: US/10/170,097  
PRIOR FILING DATE: 2002-06-10  
PRIOR APPLICATION NUMBER: US 09/641,638  
PRIOR FILING DATE: 2000-08-16  
PRIOR APPLICATION NUMBER: US 09/502,330  
PRIOR FILING DATE: 2000-02-11  
PRIOR APPLICATION NUMBER: US 60/133,200  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/275,267  
PRIOR FILING DATE: 1999-03-23  
PRIOR APPLICATION NUMBER: US 60/119,917  
PRIOR FILING DATE: 1999-02-12  
NUMBER OF SEQ ID NOS: 1304  
SOFTWARE: Patent.pm  
SEQ ID NO 652

[illegible]

Query Match	37.9%	Score 1013.6	DB 21	Length 2343
Best Local Similarity	69.2%	Pred. No. 1.5e-292		
Matches 1380	Conservative 11	Mismatches 600	Indels 3	Gaps 1
Qy	4	ATGGGTCTCTACCGCATCCGGCTGTCACATGGGGCGCTCGCTCTATGCGGTTTCCAAACAAC	63	
Db	40	ATGGCGCGCTACCGCATCCGGGTGGCACCGGGCGCTGGCTCTTCTCCGGTCTGTACAAAC	99	
Qy	64	CAGGTGCAGCTGTGGCTGGTCCGGCCAGCACGGGGAGGCGGCTCGGGAAAGCACTGTGG	123	
Db	100	CGCGTCAGCTTTGGCTGGTCCGGACGCGCGGGAGCGGAGCTGGAGCTCGAGCTGGG	159	
Qy	124	CCGCGACGGGGCAAGGAGACAGAACTCAAGGTGGAAGTAACGGAGTATCTGGGGCCGCTG	183	
Db	160	CCGGCGGGGCGAGGAGGAGGAGTTGATCATACGTTGCAGAGGAACTTGGGGCTCCTG	219	
Qy	184	CTGTTTGTGAACTGCCCAACGGCACTCTCTTAAGGACGAGCGCTGCTTCTGCAACTGG	243	
Db	220	CAGTTCGTGAGGCTGCGCAAGCACACTCTGGCTGTGTGACGACGGCTGTCTTCGCACCGC	279	
Qy	244	ATCTCTGTGAGGGCCCGGAGCCGGGACCGAGGTCAGGTTCCCTTGTATTACCGCTGGGTG	303	
Db	280	ATCACGGTGCAGGGCCCTGGAGCTTCGCGGAGGTGGCCCTTCCCGTGTACCGCTGGGTG	339	
Qy	304	GAGGGCAACCGCGTCTCTGAGCCTGCCTGAAGCCACCGGCCCGCACTGTGGCGAGGACCTT	363	
Db	340	CAGGGCGAGGACATCTCTGAGCTGCCGAGGGCCACCGCCCGCTGCCAGGAGCAATGCT	399	
Qy	364	CAGGGCTGTTCCAGAAACACCGGGAGAGAGCTGGAGAGAGAGGAAGTGTGTACCGG	423	
Db	400	TTTGACATGTTCCAGTAGCATCTCGAGAGGAAGGAACTGAAGAAGACAGACGACATCTACTGC	459	



QY 424 TGGGAAACTGGAAGACGGTTAATCTGAATATGGCTGGGGCCAAACTATATACCTC 483  
DB 460 TGGGCACTTGGAGGAAGGGTTACCCCTGACCATCGCTCGTCAGACCGTAAGGATGATCTA 519  
QY 484 CTTGTGGATGAGCGATTTCTGGAACACAAGAGATTGACTTTGAGGTTTCGCTGCCCAAG 543  
DB 520 CTTCCAAATATGAGATTCATGAGGAGAGAGCGCTGGACTTTGATGTGACACTGGAAGCA 579  
QY 544 GGGCTGGCGACCTCGCTATCAAGACTCTCTAAATGTTCTGACTTGTGGAAGGATCTA 603  
DB 580 GGGGCTCTGGAGATGGCCCTCAAACTGTGTTTACACCTCTCTGAGCTCTCTGGAATCGCTA 639  
QY 604 GATGACTTCAACCGGATTTCTGGTGTGGTCAGAGCAAGCTGGCTGAGGGGTGGGGAC 663  
DB 640 GAAGACTTTGATCAGATCTTCTGGGGCCAGAGAGTGGCTGGCTGGAAGGTTTCGCCAG 699  
QY 664 TCCTGGAAGGAAGATGCTTATTTGGGTACCAAGTTTCTTAATGGGCCCAACCCCGTGGT 723  
DB 700 TGCTGGCAGGATATGAGTTGTTGAGCTACCAAGTTCTCAATGGTGCCAAACCCCATGGCT 759  
QY 724 CTGAGGCGCTCTGCTCACCTTCTGCTCGCCCTAGTGTTCCTTCCAGGATGGAAGAACTG 783  
DB 760 TTGAGAYGCTCGACCTCTCTGCGCTCCAGGCTAGTGTGCTCGCCCTCRGGATGGAAGGCTT 819  
QY 784 CAGGCCAGCTGGAGAGAGCTGGAGGAGGACACATGTTTCAAGAGCTGACTTCTCCCTG 843  
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DB 940 GTTATGCTGAGATGGAGCCCAATCGGAAGCTGCAGCCCATGGTTCATCCAGATTGAGCT 999  
QY 964 CCCGCGACAGGATCCCAACCACTCCCTTTTCTGGCTCAAGATCCCAATGAGCGCTGG 1023  
DB 1000 CCCARCCCGAGCTCTCAACCCCAACACTGTTCTGCGCTCAGACCCCSACTTGGCTGG 1059  
QY 1024 CTTCTGGCCAAATGCTGGTGGCAGCTGACTTCCAGCTCCAGCTCCAGCTCAGTCTCAT 1083  
DB 1060 CTCCTGGCAAAAGCTCGGGTCGAAATTCAGATTTCCAACTGCAGAGATCCAGTATCAC 1119  
QY 1084 CTTCTGAGGAGACATGATGCTGAGCTGATGTTGTGGCCACCACATGAGTGCTCGCG 1143  
DB 1120 TTGCTGAACACKACCTGGTGGCTGAGTCTGCTGTGCGCACCATGGGTGCTCCCA 1179  
QY 1144 TCGATACATCTTATCTTCAAGCTTAAATTCGCCACCTGGGATACACCTGGAAATTAAC 1203  
DB 1180 GGACTGCAACCCCATCTTCAAGTTCTGATCCGCCATATCCGCTACACCATGGAATCAAC 1239  
QY 1204 GTCCGGGCGAGCTGGGCTGGTCTGACATGGGAATTTTCGACAGATAATGAGCACT 1263  
DB 1240 ACCCGGGCCGAGCCCAACTCATCTCAGATGAGGAATTTTGAATAGGCGAGTGAACCA 1299  
QY 1264 GGTGGGGGAGGCCAGCTGCTGAGCTGCTCAAGAAAGCTGGAGCTTCTTAACCTTACAGCTCC 1323  
DB 1300 GGTGGAGGGGCCATGATGATGTTCTCGTGGGGGGGAGCTCAGCTACCTACTGCTCC 1359  
QY 1324 TTCTGTCCCTGTATGATGCTTGGCCGACCGGGGGCTCTGGGAGTGAAGTCTTCTTCTAT 1383  
DB 1360 CTCTGTCTCTGACGACCTGGCTGACCGGGGCTGCTGGGACTCCAGGCTCTCTCTAT 1419  
QY 1384 GCCCAAGATCGGCTCGGCTCTGGGAATCATCTATCGGTATGTGGAAGGATCGTGAAT 1443  
DB 1420 GCCCATGATGCTTACGGCTCTGGGAGATCATTTGCCAGGTATGTGGAGGGGATCGTCCAC 1479  
QY 1444 CTCACATTAAGACAGAGCTGGCTGTGAAGACGACCCAGAGCTGCAGACCTGGTGTGGA 1503  
DB 1480 CTCCTTACCAAGAGGATGACATAGTGAAGGGGACCTCAGCTGACGCGCTGTGTGCG 1539  
QY 1504 GAGATCACTGAAATCGGGCTGCAAGGGGGCCAGGACCGAGGGTTTCTCTCTTTACAG 1563

DB 1540 GAGATCAGGAGGTGGGGCTGTGCCAGGCCCAGGACCGAGGTTTCCCTGTCTCTTCACG 1599  
QY 1564 GCTCGGACACAGGTTTGGCACTTTGTGTCACCATGTGTATCTTTCACCTGACCGCGCAACAC 1623  
DB 1600 TCCAGAGTCAACTCTGCCATTTCTCACCATGTGGTCTTTCAGCTGCACTGCCAGCAT 1659  
QY 1624 GCCTGTGTGCACTGGGCGAGCTGGAATGCTGTTGGGTGCTTAATGCAACCTGCAAG 1683  
DB 1660 GCCGCCATCAACACAGGCGAGCTGGAATGCTGCTGGGTCCCTTAATGCTCATGCA 1719  
QY 1684 ATGGGGCTGCCCCCGCCCAACCAACCAAG--CATCAACGCTGGAGACAGTATGSCGACA 1740  
DB 1720 ATGGGATGCCCCCACCACCACCAAGAAATGTGAGWGGGCCACAGTATGGGGTCA 1779  
QY 1741 CTGCCCCAACTTCCACCAGGCTTCTCTCCAGATGTCATCTTGGCAGCTGGGCAAGCGC 1800  
DB 1780 CTACTGATGTCCGCGAGGCTGCTTCAATGSCCATCTCATGGCATCTGAGTCGCCGC 1839  
QY 1801 CAGCCCGTATGTTGGTGTGGGCGAGCATGAGGAGGATATTTTTCGGGCGCTGAGCT 1860  
DB 1840 CAGCCAGACATGTTGCTCTGGGCGACCCACAAAGAAATATTTCTCAGGCGCCCAAGGCC 1899  
QY 1861 AAGCTGTGCTGAAGAAATTCAGGAGGAGCTGCTGCCCTGGATAAGGAAATTCAGATC 1920  
DB 1900 AAGCTGTGCTAAACCAATTCGAAACAGATTTGGAAAGCTTGAAGAGGATTCAGGCC 1959  
QY 1921 CGGAATGCAAGCTGCGACATGCCCTCAAGTACCTTGGCGCCAGCGTGTGGAAACAGT 1980  
DB 1960 CGGAATGAGCAACTGACTGGCCCTATGAATATCTGAAGCCAGCTGCATAGAGAACAGT 2019  
QY 1981 GTGGCCATCTAAGC 1994  
DB 2020 GTCACCATCTGAGC 2033

## RESULT 13

US-10-681-818-13  
; Sequence 13, Application US/10681818  
; Publication No. US20040157240A1  
; GENERAL INFORMATION:  
; APPLICANT: Weiss, Scott  
; APPLICANT: Tantleira, Kelan  
; TITLE OF INVENTION: Diagnostic Assay and Related Products  
; FILE REFERENCE: B0801.70290US00  
; CURRENT APPLICATION NUMBER: US/10/681,818  
; CURRENT FILING DATE: 2003-10-08  
; PRIOR APPLICATION NUMBER: US 60/416,969  
; PRIOR FILING DATE: 2002-10-08  
; NUMBER OF SEQ ID NOS: 374  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 13  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-681-818-13

Query Match 19.3%; Score 515.6; DB 19; Length 584;

Best Local Similarity 99.8%; Pred. No. 1.8e-143;

Matches 515; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1812 GGTGGCTGTGGGCCAGCATGAGGAGGAGTATTTTTCGGGCGCTCAGCTTAAGGCTGTCT 1871

DB 69 GGTGGCTGTGGGCCAGCATGAGGAGGAGTATTTTTCGGGCGCTCAGCTTAAGGCTGTCT 128

QY 1872 GAAAGATTCAGGAGGAGCTGGCTGCCCTGGATAAGGAAATTCAGATCCGGAATGCAAA 1931

DB 129 GAAGAGTTCAGGAGGAGCTGGCTGCCCTGGATAAGGAAATTCAGATCCGGAATGCAAA 188

QY 1932 GCTGCACATGCCCTACAGTACCTGCGGCCAGCGTGTGGAAACAGTGTGGCCATCTA 1991

DB 189 GCTGCACATGCCCTACAGTACCTGCGGCCAGCGTGTGGAAACAGTGTGGCCATCTA 248

QY 1992 AGCGTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCAACCCAGCCCAAGCTGACCCCTTC 2051  
DB 249 AGCGTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCAACCCAGCCCAAGCTGACCCCTTC 308  
QY 2052 GTGGTTATAGCCCTGCCCTCCCAAGTCCACCCCTCTTCCCATGTGCCACCCCTCCCTAGAG 2111  
DB 309 GTGGTTATAGCCCTGCCCTCCCAAGTCCACCCCTCTTCCCATGTGCCACCCCTCCCTAGAG 368  
QY 2112 GGGCACCTTTTCATGTCTCTGTCGACCCAGTGAACACATTTTACTCTAGAGGCATCACCTG 2171  
DB 369 GGGCACCTTTTCATGTCTCTGTCGACCCAGTGAACACATTTTACTCTAGAGGCATCACCTG 428  
QY 2172 GGACCTTACT 2231  
DB 429 GGACCTTACT 488  
QY 2232 CTTTCTTCATCAGATCTATATGCGCAATAGCCACAATATATATATATATATATATATATAT 2291  
DB 489 CTTTCTTCATCAGATCTATATGCGCAATAGCCACAATATATATATATATATATATATATAT 548  
QY 2292 GAATAGGGGGAT 2327  
DB 549 GAATAGGGGGAT 584

## RESULT 14

US-10-681-818-12

; Sequence 12, Application US/10681818

; Publication No. US20040157240A1

; GENERAL INFORMATION:

; APPLICANT: Weiss, Scott

; APPLICANT: Tantisira, Kelan

; TITLE OF INVENTION: Diagnostic Assay and Related Products

; FILE REFERENCE: B0801.70290US00

; CURRENT APPLICATION NUMBER: US/10/681,818

; CURRENT FILING DATE: 2003-10-08

; PRIOR APPLICATION NUMBER: US 60/416,969

; PRIOR FILING DATE: 2002-10-08

; NUMBER OF SEQ ID NOS: 374

; SOFTWARE: Patentin version 3.2

; SEQ ID NO 12

; LENGTH: 584

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-681-818-12

Query Match 19.2%; Score 514; DB 19; Length 584;

Best Local Similarity 99.6%; Pred. No. 5.6e-143;

Matches 514; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1812 GTGGCTGTGGGCCAGCATGAGGAGGATATTTTCGGGCCCTGAGCCTTAAGCGTGTGCT 1871  
DB 69 GTGGCTGTGGGCCAGCATGAGGAGGATATTTTCGGGCCCTGAGCCTTAAGCGTGTGCT 128  
QY 1872 GAAGAAGTTTCAGGAGGAGCTGCTCCCTCGATAGGAAATTTGAGATCCGGAATGCAAA 1931  
DB 129 GAAGAAGTTTCAGGAGGAGCTGCTCCCTCGATAGGAAATTTGAGATCCGGAATGCAAA 188  
QY 1932 GCTGGACATGCTCAGATACCTGGGCCACGCTGGTGGAAAACAGTGTGGCCATCTA 1991  
DB 189 GCTGGACATGCTCAGATACCTGGGCCACGCTGGTGGAAAACAGTGTGGCCATCTA 248  
QY 1992 AGCGTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCAACCCAGCCCAAGCTGACCCCTTC 2051  
DB 249 AGCGTCGCCACCCCTTTGGTTATTTTCAGCCCCCATCAACCCAGCCCAAGCTGACCCCTTC 308  
QY 2052 GTGGTTATAGCCCTGCCCTCCCAAGTCCACCCCTCTTCCCATGTGCCACCCCTCCCTAGAG 2111  
DB 309 GTGGTTATAGCCCTGCCCTCCCAAGTCCACCCCTCTTCCCATGTGCCACCCCTCCCTAGAG 368  
QY 2112 GGGCACCTTTTCATGTCTCTGACCCAGTGAACACATTTTACTCTAGAGGCATCACCTG 2171  
DB 369 GGGCACCTTTTCATGTCTCTGACCCAGTGAACACATTTTACTCTAGAGGCATCACCTG 428

QY 2172 GGACCTTACT 2231  
DB 429 GGACCTTACT 488  
QY 2232 CTTTCTTCATCAGATCTATATGCGCAATAGCCACAATATATATATATATATATATATAT 2291  
DB 489 CTTTCTTCATCAGATCTATATGCGCAATAGCCACAATATATATATATATATATATATATAT 548  
QY 2292 GAATAGGGGGAT 2327  
DB 549 GAATAGGGGGAT 584

## RESULT 15

US-10-240-305-15

; Sequence 15, Application US/10240305

; Publication No. US20030162193A1

; GENERAL INFORMATION:

; APPLICANT: GLAXO GROUP LIMITED

; APPLICANT: ANDERSON, WAYNE H.

; APPLICANT: EDWARDS, Lisa D.

; APPLICANT: EMMETT, Amanda H.

; APPLICANT: FILIAI, Sreekumar

; APPLICANT: SPRANKEL, Catherine S.

; TITLE OF INVENTION: Medicine Response Assay in Respiratory Disease

; FILE REFERENCE: PU3958 &amp; PU4254

; CURRENT APPLICATION NUMBER: US/10/240,305

; CURRENT FILING DATE: 2001-04-17

; NUMBER OF SEQ ID NOS: 16

; SOFTWARE: Patentin version 3.0

; SEQ ID NO 15

; LENGTH: 2420

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (3)..(1994)

US-10-240-305-15

Query Match

14.3%; Score 382.6; DB 16; Length 2420;

Best Local Similarity 52.5%; Pred. No. 3.5e-103;

Matches 1022; Conservative 0; Mismatches 884; Indels 39; Gaps 7;

QY 126 CGCAGCGGCGGAGAGACAGAACTCAAGGTGGAAGTACGGAGTATCTGGGCGCGTGTCT 185  
DB 107 CGAGGTGCGCGGTGGATTCTATACAGTGAATCTGTGAGAGGAACTGGGCGAGATCCA 166  
QY 186 GTTGTGAAACTGCGCAACCGCACCTCTTAAGGACGACGCGCTGGTCTGCAACTGGAT 245  
DB 167 GCTGTCTAGAACTCGAAGAGCGCAAGTACTGGCTGAATGACGACTGCTGTAAGTACAT 226  
QY 246 CTCGTGTGAGGCGCCGAGGAGCGGGGACGAGGTCAAGTTCCTTGTACCGGTGGGTGA 305  
DB 227 CACGCTGAAGACGCGCC---CACGGGAGCTACATCAGTTCCTCCCTGCTACCGCTGGATCAC 283  
QY 306 GGGCAACCGCGCTCTGAGCCTCCCTGAAGGACACCGCGCACCTGTGGGCGAGGACCCCTCA 365  
DB 284 CGGCGATGTGCGAGGTGTCTGAGGATGGACCGCCCAAGATTGGCCCGAGATGACCAAT 343  
QY 366 GGGCCTGTTTCCAGAAACACCGGGAGAGAGCTGGAAGAGAGAGAAAGTGTACCGGTG 425  
DB 344 TCACATTTCTAAGCAACACCGAGCTGAAGAACTGGAAAACACGCAAAAACAATATCGATG 403  
QY 426 GGGAACTCGGAGGACGGGTTAATTTCTGAATGCTGGGGCCAAACTATATGACCTCCC 485  
DB 404 GATGAGTGGAAACCTTGGCTTCCCTTGAGCATCATGCGCAATGCGCAACAGGATTTACC 463  
QY 486 TGTGATCAGCGGATTTCTGGAAGACAGAGAGTTCGATTTTGAGGTTTCGCTGGCCAAAGG 545  
DB 464 CGGTATATCCAGTTTGTATGTGAAAAGAGAGTGGACTTTGTTCTGAATTAATCTCCAAGC 523  
QY 546 GCTGGCGGACCTCGCTATCAAGAAGCT---CTCTAAATGTTCTGACTTGTGCGGAAGGATCT 602

Db 524 GATGAGAACTGTTTCATCAACCGCTTCATGCACATGTTTCAGTCTTCTTGGAAATGACTT 583  
Qy 603 AGATGACTTCAACCGAATTTCTGTGTGGTGCAGAGCAAGCTGGCTGAGCGCGTGCAGGGA 662  
Db 584 GCGGACTTTGAGAAAATCTTTGTCAAGATCAGCAACACTATTTCTGAGCGGGTCATGAA 643  
Qy 663 CTCCTGGAAGNAGATGCTTATTTGGGTACAGTTTCTTAATGGCGGCAACCCCGTGT 722  
Db 644 TCACTGGCAGGAGAACCTGATGTTTTGGCTACAGTTCTCTGAATGGCTGCAACCCCTGTGTT 703  
Qy 723 GCTGAGGCGCTGCTGCTCACTTCTGCTCGCTAGTCTTCCCTCCAGGCATGGA----- 776  
Db 704 GATCCGGGCTGCACAGAGCTGCCGAGAAAGCTCCGGTGACACGGAGATGGTAGATG 763  
Qy 777 -----GGAACCTGCAAGGCCAGCTGGAGAAGAGCTGGAGGAGGCACACTGTTTCGAAGC 830  
Db 764 CAGCCTGGAGCGGCAGCTCAGCTTGGAGCAGAGGTCAGCAAGGGAACATTTTCATGCT 823  
Qy 831 TGAATTTCTCTGCTGGATGGATCAAGGCCAAAGCTCA---TTCTCTGTAGCCAGCAGCA 887  
Db 824 GGACTTTGAGCTGCTGGATGGATCGATGCCAAACAAACAGACCCCTGCACACTCCAGTT 883  
Qy 898 CTTGGCTGCCCTCTAGTCATGCTGAATTCAGCCTGATGGGAACCTTTGGCCATGCT 947  
Db 884 CTTGGCCGCTCCCATCTGCTGTCTGTATGAAGAACCTGGCCAAAGATTTGCCCATTCG 943  
Qy 948 CATCCAGCTCCAGCTGCCCGGCACAGGATCCCCACACTCCCTTTCTTCTGCTTACCGGA 1007  
Db 944 CATCCAGCTCAACCAATCCCGGAG-----ATGAGAACCTTATTTCTCCCTTCGGA 997  
Qy 1008 TCCCCCAATGGCTGGCTTCTGGCCAAATGCTGGGTGGCAGCTCTGACTTTCAGCTCCA 1067  
Db 998 TCGAAAATACGACTGGCTTTTGGCCAAAATCTGGGTGGCTTCCAGTGACTTTCACAGTCCA 1057  
Qy 1068 TGAGTGCAGTCTCATCTTCTGAGGGGACACTTGATGCTGAGGTCAATTTGTTGGCCAC 1127  
Db 1058 CCAGACCATCACCCACCTTCTGCGAACACATCTGTGTCTGAGGTTTTTGGCAITGGCAAT 1117  
Qy 1128 CATGAGTGCTTCCGCTCGATACATCTTATTTCAAGCTTATAATTCGCCACCTCGGATA 1187  
Db 1118 GTACGCCAGCTGCTGCTGTGCACCCCATTTTCAAGCTGTGGTGGCACACGAGAT 1177  
Qy 1188 CACCTTGAATTAAGCTCCGGGCAGGACTGGGTCTGTCTGACATGGGAATTTTCGA 1247  
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Qy 1248 CCAGATATGAGCACTGTTGGGGAGGCCACGTGCAAGCTGCTCAAGCAAGCTGGAGCCTT 1307  
Db 1238 CAAGGCCAACGCCACAGGGGGCGGTGGGCAAGTGCAGATGGTGCAGAGGGGCCATGAAGGA 1297  
Qy 1308 CTTAACTTACAGCTCCTTCTGTCCCTGTGATGACTTGGCCGACCGGGGCTCCTG----- 1362  
Db 1298 CTTGACCTATGCTCTCTGTGCTTTCAGAGGCCATCAAGGCCCGGGGCGTGGAGGAA 1357  
Qy 1363 -----GGAGTGAAGTCTTCTTCTATGCCCAAGATGCGCTCGGGCTCTGGGAAATCATCTA 1418  
Db 1358 AGAAGACATCCCTACTACTTCTACCGGAGCAGCGGCTCCTGGTGTGGGAAGCCATCAG 1417  
Qy 1419 TCGGTATGTGAGAGAAATCGTGAGTCTCCATATTAAGACAGAGCTGGCTGTGAAAGAGGA 1478  
Db 1418 GACGTTTACCGCCGAGGTGGTAGACATCTACTACAGGGCGCACCAAGGTTGGTGGAGGAGGA 1477  
Qy 1479 CCCAGAGCTGCAGACTGGTGTGAGAGATCACTGAATCGGGCTGCAAGGGGCCAGGA 1538  
Db 1478 CCCGAGCTGCAGGACTTGTGTGAACGATGTCTACGTGTACGGCATCGGGGCCGCAAGTC 1537  
Qy 1539 CCGAGGGTTTCTGTCTCTTTACAGGCTCGGACAGAGTTTGCACATTTGTACCATGTG 1598  
Db 1538 CTCAGGCTTCCCAAGTCCGTCAGAGCCGGGAGCAGCTGTCCGAGTACCTGACCGTGT 1597  
Qy 1599 TATCTTACCTGCACCGGCCAAACAGCCTCTGTGACCTGGGCCAGCTGGAGTGTACTC 1658

Db 1598 GATCTTCAACCGCTCCGCCAGCAGCCGCGGTCAACTTTCGGCCAGTACGACTGTTGCTC 1657  
Qy 1659 TTGGTGCCTTAATGCAACCTTGCAAGTGGCTGCCCGCCGCAACCCACCAAG---GATGC 1715  
Db 1658 CTGGATCCCAATCGGCCCCCAACCATGTCGAGCCCGCCACCGACTGCCAAGGGCGTGT 1717  
Qy 1716 AACGCTGGAGACAGTGTATGGCGACACTGCCCAACTTCCACAGGCTTCTCTCCAGATGTC 1775  
Db 1718 GACCAITGAGCAGATCGTGGACACGCTGCCCGACCCGGCGCGCTCTGCTGGCATCTGGG 1777  
Qy 1776 CATCACTTGGCAGCTGGGCGAGACGCCAGCCCGCTTATGTTGGCTGTGGGCCAGCATGAGGA 1835  
Db 1778 TGCACTGTGGCGCTGAGCCAGTTCCAGGAAACAGAGCTGTTCTTGGCATGTACCCAGA 1837  
Qy 1836 GGAGTATTTTTTCGGGCCCTGAGCCCTAAGGCTGTGCTGAAGAAGTTTCAGGGAGGAGCTGGC 1895  
Db 1838 AGAGCATTTTATCGAAGAGCCTGTGAAGGAAGCCATGGCCCGATTCCGCAAGAACTCGA 1897  
Qy 1896 TGCCCTGGATAAGGAATTGAGATCCGGAATGCAAGCTGGACATGCCCTACGAGTACCT 1955  
Db 1898 GGCCATTTGTCAAGCTGATTTGCTGAGCGCAACAAAGAAGCAGCTGCCATATTACTATT 1957  
Qy 1956 GCGGCCAGCGTGTGGAATAACAGTGTGGCCATCTAAGCGTGGCCACCTTTGGTTATTT 2015  
Db 1958 GTCCCCAGACCGGATTCGGAACAGTGTGGCCATCTGAGCACAACCTGCTCACTGTGG 2017  
Qy 2016 CAGCCCCCATCACCCAAAGCCCAAG 2040  
Db 2018 GAAGGCCAGCTGCCCCAGCCAGATG 2042

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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:50:48 ; Search time 30.1353 Seconds  
(without alignment)  
1637.384 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

Sequence: 1 MGLYRIRVSTGASLYAGSNN.....KLDMPYELRBSVVNSVAI 661

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3503.5	99.7	662	3	US-09-061-768A-25
2	3503.5	99.7	662	4	US-09-764-246-25
3	2280	64.9	663	4	US-09-641-638-653
4	2280	64.9	663	4	US-10-170-097-653
5	1298.5	37.0	674	4	US-09-949-016-5980
6	1298.5	37.0	689	4	US-09-949-016-5980
7	1203.5	34.2	679	4	US-09-949-016-11692
8	1202.5	34.2	676	3	US-09-061-768A-2
9	1202.5	34.2	676	4	US-09-764-246-2
10	1202.5	34.2	676	4	US-09-949-016-6027
11	1184	33.7	677	3	US-09-061-768A-4
12	1184	33.7	677	4	US-09-764-246-4
13	1153	32.8	711	4	US-09-547-435-2
14	1153	32.8	867	4	US-09-547-435-24
15	1124	32.0	701	3	US-09-087-727-2
16	1124	32.0	701	4	US-09-853-053-2
17	1124	32.0	701	4	US-09-949-016-6026
18	954.5	27.2	556	4	US-09-547-435-6
19	946.5	26.9	615	4	US-09-547-435-10
20	946.5	26.9	771	4	US-09-547-435-28
21	761.5	21.7	675	4	US-09-902-540-12713
22	748	21.3	460	4	US-09-547-435-12
23	704.5	20.0	489	4	US-09-547-435-4
24	704.5	20.0	645	4	US-09-547-435-26
25	580.5	16.5	291	4	US-09-547-435-14
26	548.5	15.6	582	3	US-09-413-814-83
27	506	14.4	334	4	US-09-547-435-8

28 463 13.2 857 4 US-09-751-687-17 Sequence 17, Appl  
29 458.5 13.0 360 4 US-09-949-016-8911 Sequence 8911, Ap  
30 456 13.0 901 4 US-03-714-767A-4 Sequence 4, Appli  
31 451 12.8 864 4 US-09-810-268-3 Sequence 3, Appli  
32 448.5 12.8 862 4 US-09-751-687-9 Sequence 9, Appli  
33 445.5 12.7 864 4 US-09-751-687-18 Sequence 18, Appl  
34 442 12.6 865 4 US-09-751-687-16 Sequence 16, Appl  
35 441.5 12.6 862 4 US-09-751-687-12 Sequence 12, Appl  
36 441.5 12.6 862 4 US-09-978-522-1 Sequence 1, Appli  
37 439.5 12.5 859 4 US-09-978-522-3 Sequence 3, Appli  
38 418.5 11.9 839 4 US-09-751-687-7 Sequence 15, Appl  
39 396 11.3 692 4 US-09-252-991A-19668 Sequence 19668, A  
40 374 10.6 195 4 US-09-547-435-20 Sequence 20, Appl  
41 347.5 9.9 131 4 US-09-641-638-654 Sequence 654, App  
42 347.5 9.9 131 4 US-10-170-097-654 Sequence 654, App  
43 268.5 7.6 139 4 US-09-547-435-18 Sequence 18, Appl  
44 193.5 5.5 110 4 US-09-547-435-22 Sequence 22, Appl  
45 167 4.8 477 4 US-09-902-540-12721 Sequence 12721, A

## ALIGNMENTS

RESULT 1  
US-09-061-768A-25  
; Sequence 25, Application US/09061768A  
; Patent No. 6204037  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; APPLICANT: BOEGLIN, WILLIAM E.  
; APPLICANT: JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/061.768A  
; FILING DATE: APRIL 16, 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: NONE  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 662 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
US-09-061-768A-25

Query Match 99.7%; Score 3503.5; DB 3; Length 662;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MGLYRIRVSTGASLYAGSNNQVLWLVCQHGGAALGKRLNFPARG-ETELKVEVPYELGPL 59

Db 1 MGLYRIRVSTGASLYAGSNNQVQLMWVGQHGAAALGKRLWPARGKETELKVEVPEYLGPL 60  
QY 60 LFKLRKRHLKDDAWFCNWISVQPGAGDEVRFPFCYRWVEGNVLSLPEGTGRTVGEDP 119  
Db 61 LFKLRKRHLKDDAWFCNWISVQPGAGDEVRFPFCYRWVEGNVLSLPEGTGRTVGEDP 120  
QY 120 QGLFQKHREELERKLYRWGNWKGDLILNMGAKLYDLVDERFLEDKRVDFFVSLAK 179  
Db 121 QGLFQKHREELERKLYRWGNWKGDLILNMGAKLYDLVDERFLEDKRVDFFVSLAK 180  
QY 180 GLADLAIKDSLNLVTCWKDLDDFNRFWCQSKLAERVRDSWKEDALFGYQFLNGANPVV 239  
Db 181 GLADLAIKDSLNLVTCWKDLDDFNRFWCQSKLAERVRDSWKEDALFGYQFLNGANPVV 240  
QY 240 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGIKANVILCSQOHLAAPL 299  
Db 241 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGIKANVILCSQOHLAAPL 300  
QY 300 VMLKLPDQKLLPMVITQLQPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 359  
Db 301 VMLKLPDQKLLPMVITQLQPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 360  
QY 360 LLRGHLMAEVIVVATMRCPLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419  
Db 361 LLRGHLMAEVIVVATMRCPLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420  
QY 420 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 479  
Db 421 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 480  
QY 480 LHYKTDAVKDDPELOTWCREITEIGLOAQDQGFVPSIQARDQVCHFTVMCI FCTGOH 539  
Db 481 LHYKTDAVKDDPELOTWCREITEIGLOAQDQGFVPSIQARDQVCHFTVMCI FCTGOH 540  
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRQ 599  
Db 541 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRQ 600  
QY 600 PVMVAVGQHEEYFSGPEPKAVLKKFRELAALDKKEIERNAKLDMPEYLRPSVVVENS 659  
Db 601 PVMVAVGQHEEYFSGPEPKAVLKKFRELAALDKKEIERNAKLDMPEYLRPSVVVENS 660  
QY 660 AI 661  
Db 661 AI 662

RESULT 2

US-09-764-246-25  
; Sequence 25, Application US/09764246  
; Patent No. 6649355  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; BOEGLIN, WILLIAM E.  
; JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESSES:  
; ADDRESS: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/764,246  
; FILING DATE: 17-Jan-2001

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 25:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 662 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-764-246-25  
Query Match 99.7%; Score 3503.5; DB 4; Length 662;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 MGLYRIRVSTGASLYAGSNNQVQLMWVGQHGAAALGKRLWPARGKETELKVEVPEYLGPL 59  
Db 1 MGLYRIRVSTGASLYAGSNNQVQLMWVGQHGAAALGKRLWPARGKETELKVEVPEYLGPL 60  
QY 60 LFKLRKRHLKDDAWFCNWISVQPGAGDEVRFPFCYRWVEGNVLSLPEGTGRTVGEDP 119  
Db 61 LFKLRKRHLKDDAWFCNWISVQPGAGDEVRFPFCYRWVEGNVLSLPEGTGRTVGEDP 120  
QY 120 QGLFQKHREELERKLYRWGNWKGDLILNMGAKLYDLVDERFLEDKRVDFFVSLAK 179  
Db 121 QGLFQKHREELERKLYRWGNWKGDLILNMGAKLYDLVDERFLEDKRVDFFVSLAK 180  
QY 180 GLADLAIKDSLNLVTCWKDLDDFNRFWCQSKLAERVRDSWKEDALFGYQFLNGANPVV 239  
Db 181 GLADLAIKDSLNLVTCWKDLDDFNRFWCQSKLAERVRDSWKEDALFGYQFLNGANPVV 240  
QY 240 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGIKANVILCSQOHLAAPL 299  
Db 241 LRRSAHLPARLVFPFGMEELQALEKELEGGTLEADFSLLDGIKANVILCSQOHLAAPL 300  
QY 300 VMLKLPDQKLLPMVITQLQPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 359  
Db 301 VMLKLPDQKLLPMVITQLQPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHELQSH 360  
QY 360 LLRGHLMAEVIVVATMRCPLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419  
Db 361 LLRGHLMAEVIVVATMRCPLPSIHPFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420  
QY 420 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 479  
Db 421 GGGHVOLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAODALRLWEIYYRYVEGIVS 480  
QY 480 LHYKTDAVKDDPELOTWCREITEIGLOAQDQGFVPSIQARDQVCHFTVMCI FCTGOH 539  
Db 481 LHYKTDAVKDDPELOTWCREITEIGLOAQDQGFVPSIQARDQVCHFTVMCI FCTGOH 540  
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRQ 599  
Db 541 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATTLETVMATLPNFHQASLQMSITWOLGRQ 600  
QY 600 PVMVAVGQHEEYFSGPEPKAVLKKFRELAALDKKEIERNAKLDMPEYLRPSVVVENS 659  
Db 601 PVMVAVGQHEEYFSGPEPKAVLKKFRELAALDKKEIERNAKLDMPEYLRPSVVVENS 660  
QY 660 AI 661  
Db 661 AI 662







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Db 417 CECGLFDKANATGGGHHVQVORAMKOLTYASLCFPEAIKARGMESKEDIPIYFYRDDGL 476
Qy 465 RWELIYRYVEGIVSLHYKTDVAVKDDPELQWCREITEIGLOQAQDRGPPVLSQARQV 524
Db 477 LWELAIRTTAEVNDIYEGDQWVEDPELQDFVNDVYVYGMGRKSGSGFPKSVKSRQL 536
Qy 525 CHFVTCIFCTCGOASVHLGQDWSVWPNAPCTMRLLPPTTKD-ATLETVMATLPNFH 583
Db 537 SBYLTWVIFTASQAHAANFGQYDWCSPINAPPTMRAPPPTAKGVVITIEQIVDTLPDRG 596
Qy 584 QASLQMSITWOLGRQPPVMAVGOHEEYFSGPEKAVLKKFREELALADKIEIRNAKL 643
Db 597 RSCWHLGAVWALSQFQENELFLGMPPEHFIEKPVKEAMARFRKNLEAIVSVIAERNKKK 656
Qy 644 DMPYELRPSVENSVAI 661
Db 657 QLPYYLSPDRIPNSVAI 674

RESULT 6
US-09-949-016-11692
; Sequence 11692, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11692
; LENGTH: 689
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11692

Query Match 37.0%; Score 1298.5; DB 4; Length 689;
Best Local Similarity 39.7%; Pred. No. 4.5e-135;
Matches 269; Conservative 140; Mismatches 248; Indels 21; Gaps 11;

Qy 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHG---EALQKRLMP--ARGETE-LKVEVPE 54
Db 16 MBSYTVTVATGSGQWFAQTDDYIYLSVGSAGCEKHLDDKPFYNDPFRGAVDSDYDVTDE 75
Qy 55 YLGPLLFLVKLRKHLLKDDAWFCNWSVQGPAGDEVFPCCYRWVWEGVLSLPGTGRT 114
Db 76 ELGETQLVRIEKRKRWLNDWTLKYLITKTP-HGDIYIEFPCCYRWITGVGVVLRDGRAKL 134
Qy 115 VGEDPQGLFQKHREBELEERRKLYRWGNWKDGLILNAGAKLYDLFVDERFLEDRVDPE 174
Db 135 ARDDQIHLKHQRKELETRQYRWMEWNPFGPILSIDAKCHKDLPRDIQDFSEKGVDFV 194
Qy 175 VSLAGLADLAIKDSINVL-TCKDLDNPNRIFWCGQSKLAERVDSWKEDALFYQFQLN 233
Db 195 LNSYKAMENLFINRMFMHQSSWDFADPEKIFVKISNTISERVNMHWQEDLMFGYQFLN 254
Qy 234 GANPVVLSRAHLPARLVPPQMEEL---QAQLEKEGGTLFEADSLDGIKAN-VI 288
Db 255 GCNPVLIRCTELPEKLPVTTEMVSCSLERQSLSEQQVQGNIFIVDFELLDGIDANKTD 314
Qy 289 LCSQQHLAAPLVMLKLQDPKLLPMVQL-QLPRTGSGPPPLFLPTDPPMAMLLAKCWR 347
Db 315 PCTLOFLAAPICLLYKNLANKVIAIQLNQIP---GDNFIFLPSDAKYDWLLAKIWR 371
Qy 348 SSDFQLHELQSHLRGHLMAEVIVVATWTRCLPSIHPFKLIIPHILRYLTLEINVRARTGLV 407
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Db 372 SSDFHHVHTITHLRTHLVSEVFGIMYRQPAVHPFKLIVAHVRFIIANTKAREQLI 431
Qy 408 SDMGIFDQIMSTGGGHHVQLLKQAGAFITYSSFCPPDDDLADRGLLG---VKSSFYAQDAL 464
Db 432 CECGLFDKANATGGGHHVQVORAMKOLTYASLCFPEAIKARGMESKEDIPIYFYRDDGL 491
Qy 465 RWELIYRYVEGIVSLHYKTDVAVKDDPELQWCREITEIGLOQAQDRGPPVLSQARQV 524
Db 492 LWELAIRTTAEVNDIYEGDQWVEDPELQDFVNDVYVYGMGRKSGSGFPKSVKSRQL 551
Qy 525 CHFVTCIFCTCGOASVHLGQDWSVWPNAPCTMRLLPPTTKD-ATLETVMATLPNFH 583
Db 537 SBYLTWVIFTASQAHAANFGQYDWCSPINAPPTMRAPPPTAKGVVITIEQIVDTLPDRG 611
Qy 584 QASLQMSITWOLGRQPPVMAVGOHEEYFSGPEKAVLKKFREELALADKIEIRNAKL 643
Db 612 RSCWHLGAVWALSQFQENELFLGMPPEHFIEKPVKEAMARFRKNLEAIVSVIAERNKKK 671
Qy 644 DMPYELRPSVENSVAI 661
Db 672 QLPYYLSPDRIPNSVAI 689

RESULT 7
US-09-949-016-8912
; Sequence 8912, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8912
; LENGTH: 679
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8912

Query Match 34.2%; Score 1203.5; DB 4; Length 679;
Best Local Similarity 37.8%; Pred. No. 1.7e-124;
Matches 259; Conservative 126; Mismatches 267; Indels 33; Gaps 10;

Qy 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHGEEA-----LGKRLMPARGETELKVEVPE 54
Db 4 MAEFRRVSTGEAFGAGTGWKSVSIIVTGRGESSPLPLDNLGKB-FTAGASEDFQVTLPE 62
Qy 55 YLGPLLFLVKLRK-----HLLKDDAWFCNWSVQGPAGDEVFPCCYRWVWEGVLSL 107
Db 63 DVGRLVLLRVHKAHPVPLPLGLPADAWFCNWFOLT-PPRGHLLFPYQWLEGAGTLVL 121
Qy 108 PEGTGRVTEGDPQGLFQKHREBELEERRKLYRWGNWKDGLILNAGAKLYDLFVDERFLE 167
Db 122 QEGTAKVSWADHPVLQOQRESELOARQEMQYQWKAYNPGWPHCLDEKTVLELNLKYST 181
Qy 168 DKRVDFEVSILAGLADLAIKDSINVLTCWKDLDNPNRIFWCGQSKLAERVDSWKEDALF 227
Db 182 AKNAFVYLAGSAPFAEMKIKGLLDRKGLWRSLSNEKRIFFNRFPAPAAHAFEHMQEDAFF 241
Qy 228 GYQFLNGANPVVLSRAHLPARL-----VPPGMEELQAQLEKEGGTLFEADFS 278
Db 242 ASQFLNGLNPVLIIRCHYLPKNFPVTDAMVASVLGPG-TSLQALEK-----GSLFLVDHG 296
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COMPUTER: IBM PC/XT/AT compatible  
 OPERATING SYSTEM: Windows 3.1  
 SOFTWARE: WORD PERFECT 6.1 and ASCII  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/764,246  
 FILING DATE: 17-Jan-2001  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: <Unknown>  
 FILING DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: ARLES A. TAYLOR, JR.  
 REGISTRATION NUMBER: 39,395  
 REFERENCE/DOCKET NUMBER: 1242/5  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (919) 493-8000  
 TELEFAX: (919) 419-0383  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 676 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: unknown  
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
 US-09-764-246-2

Query Match 34.2%; Score 1202.5; DB 4; Length 676;  
 Best Local Similarity 37.8%; Pred. No. 2.2e-124;  
 Matches 260; Conservative 126; Mismatches 264; Indels 37; Gaps 11;

Qy 1 MGLYRVRVSTGASLYAGSNQVQLWLVQHGEEA-----LGKRLWPARGETELKVEVPE 54  
 Db 1 MAEPRVSTGAEAGTWDKVSIVGTRGESPLPLDNLGKE-FTAGAEEDFQVTLPE 59

Qy 55 YLGPELLFVKLRK-----HLKDDAFWFCNWSVQPGAGDEVPRPCVWRVWEGNGLSL 107  
 Db 60 DVGRVLLRVRHKAAPPVLLGLPLADPAWFCRWFQLT-PPRGHLLPCCQWLEGAGTLVL 118

Qy 108 PEGTGRVSGDPQGLFQKHREELERKLYRWGNKDGILLNMAKGLYDLPVDERFLE 167  
 Db 119 QEGTAKVSWADHPVLVQOQOELOARQEMQKAYNPGWPHCLDEKTVDELNLIKYST 178

Qy 168 DKRVDFEVSIAKGLADIATKOSLVNLTCKWDLDDFNRIFWCGQSKLAERVRDSWKEDALF 227  
 Db 179 AKNANFYLAQSAFAEMKIKGLDRKGLWRSINEMKRIENFRRTPAAEHAFEHQWQEDAF 238

Qy 228 GYQFLGANGPVLRSSAHLPARLVFP-----PGMEELQAOLEKELEGGTLFEAD 276  
 Db 239 ASQFLNGINPVLRCHYLPKN--FPVTDANVASLLGPG-TSLQAELK-----GSLFLVD 291

Qy 277 FSLLDGKANKVILCSQOHLAAPLVMKLQPD-GKLLPMVLIQLPRTGSPPPPLFLPTDP 335  
 Db 292 HGILSGIQTNVINGKQFSAAPMTLLYQSPGCGPLPLAIQLS--QTPGPNSPFLPTDD 349

Qy 336 PMAWLLAKCWRSSDFQLHQLSHLRHGLMAEIVVATWRCPLPSIHPFKLIIPLHRYT 395  
 Db 350 KWDMLLAKTWVRNAEFSFEALTHLLSHLLPEVFTLATRLQPHCHPLFKLIIPHTRY 409

Qy 396 LEINVRARTGLVSDMGIFDQIMSTGGGHVQLLKQAGAFITYSSFCPPDDLADRLGLGVK 455  
 Db 410 LHINTLARELLIVPGQVVDVSTGIGEGFSELIQRNNKQLNYSLLCLPEDIRTRGVEDIP 469

Qy 456 SSFAQDALRLWEIIYRYVEGIVSLHYKTDVAVKDDPELQTCREITEIGLOAQDGRGP 515  
 Db 470 GYYRDDGMQINGAVERFVSEIIGIYPSDESQDDRELQAWVREIFSGFLNQESSGIP 529

Qy 516 VSLQARDQVCHFTWCICTCTGQHASVHLQGLDWYSWVPNAPCTMLPPTTKD-ATLET 574  
 Db 530 SSLTEALVQYVTWVLTCSAKHAASVACQFDS CAMMNLPSMQLPPTSKGLATCEG 589

Qy 575 VMATLPNFHQASLQMSITWQGRQPVMAVAGQHEEYFSGPEKAVLKKFREELAADK 634  
 Db 574 VSLQARDQVCHFTWCICTCTGQHASVHLQGLDWYSWVPNAPCTMLPPTTKD-ATLET 574

Db	530	SSLETREALVQVTVVITFCSAKHAASAGQFDSACWPNLPPSMQLPPPTSKGLATCEG	589
Qy	575	VNATLPNPHOASLQWSITWOLGRRQPVVAVGOHEEYFSGSPKAVLKKFREELAALDK	634
Db	590	FATLPLPVNATCDVIALWLWSKSGDQRPUGTYPDHFHTEEAPRSIATFQSRLAQISR	649
Qy	635	EIEIRNAKLDMPYEYLRPSVVENSVAI	661
Db	650	GICERNRGLVLPYTYLDPPLIENSVSI	676
RESULT 11			
US-09-061-768A-4			
: Sequence 4, Application US/09061768A			
: Patent No. 6204037			
: GENERAL INFORMATION:			
: APPLICANT: BRASH, ALAN R.			
: APPLICANT: BOEGLIN, WILLIAM E.			
: APPLICANT: JISAKA, MITSUO			
: TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS			
: NUMBER OF SEQUENCES: 36			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: ARLES A. TAYLOR, JR.			
: STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD			
: CITY: DURHAM			
: STATE: NORTH CAROLINA			
: COUNTRY: USA			
: ZIP: 27707			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage			
: COMPUTER: IBM PC/XT/AT compatible			
: OPERATING SYSTEM: Windows 3.1			
: SOFTWARE: WORD PERFECT 6.1 and ASCII			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/09/061.768A			
: FILING DATE: APRIL 16, 1998			
: CLASSIFICATION: 435			
: PRIOR APPLICATION DATA: NONE			
: APPLICATION NUMBER:			
: FILING DATE:			
: ATTORNEY/AGENT INFORMATION:			
: NAME: ARLES A. TAYLOR, JR.			
: REGISTRATION NUMBER: 39,395			
: REFERENCE/DOCKET NUMBER: 1242/5			
: TELECOMMUNICATION INFORMATION:			
: TELEPHONE: (919) 493-8000			
: TELEFAX: (919) 419-0383			
: TELEX:			
: INFORMATION FOR SEQ ID NO: 4:			
: SEQUENCE CHARACTERISTICS:			
: LENGTH: 677 amino acids			
: TYPE: amino acid			
: STRANDEDNESS: single			
: TOPOLOGY: unknown			
US-09-061-768A-4			
Query Match 33.7%; Score 1184; DB 3; Length 677;			
Best Local Similarity 37.7%; Pred. No. 2.6e-122;			
Matches 259; Conservative 126; Mismatches 266; Indels 36; Gaps 12			
Qy	1	MGLYRIRVSTGASLYAGSNNOVLWLVCQHCEAA-----LGRKLMPARGETELKVEVE	54
Db	1	MAKCRVRVSTGACGAGKWDKVSIVTGHSPLVPLDLHLGKE--FSAGAEDEFVILPQ	59
Qy	55	YLGPILLFVKLRK-----HLKDDAWFCNWISVQG--PCAGDEVRFPCYRWVEGNGVL	105
Db	60	DVGTVLMLRVHKAPPEVSLPLMSFSDAWFCRFELEWLFGAA--LHFPCYQWLEGAGEL	117
Qy	106	SUPEGTGRTVGBDPGLFQKHREBLEERRKLYRWGNWKDG--LILNAGAKYLDLPVDE	163
Db	118	VLFRGAAKVSWDHHPTLQDORQKELESQRQKYSWKTYIEGWPRCLDHEFTVKOLDLNKY	177

164	QY	164	RELEKRVDFEVSIAKGLADLAIAKDSINVITCWKOLDDFNRIFWCGOSKLAERVRSWKE	232
178	Db	178	SAMKNAKFFFAHSA--YTELKVGKGLDRTGLWRSLEMERLEFNFAAEYVFAHWQE	235
224	QY	224	DALFCYQELNGANPVILRSAAHLPARLVFPFGMEELQA-----OLEKELEGSTLFEAD	276
236	Db	236	DAFFASQELNGINPVILIRRHCHSLNPF---PVTDEMVAIVLPGCTSLQAELEKGSFLVD	292
277	QY	277	FSLLDGIKXANVILCSQQHAAPIVWL-KLOPDGKLLPMVITQLPRTGSPPPFLFPTDP	335
293	Db	293	HGILSGVHTNILNGKPKQFSAAPMTLLHQSSGSGPLPIAQLK--QTPGPDNFIPLPSD	350
336	QY	336	PMAWLLAKCWRSSDFQHELOSHLHGLHMAEVIVVATWRCULPSHTPIKLIPIHLRYT	395
351	Db	351	TWMDLLAKTWRNSEFYTHEAVTLLHAHLIPEVFALATLQLPCHPLFKLLIPIHRYT	410
396	QY	396	LEINVRARTGLVSDGIFDQIMSTGGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVK	455
411	Db	411	LHINTLARELIVAPGKLIDKSTGLTGSGFSDLIKRNMEQNYSVLCLEFDIRARGVEDIP	470
456	QY	456	SSFYAQDALRLWEIIRYRVEGIVSLHYKTVAVKDDPELOQTWCREITEIGLQAGQDRGFP	515
471	Db	471	GYYYRDDGQWINGALKSFVSEIVSIYYPSTSVQDDQELQAWREIFSEFGFGRESSGWP	530
516	QY	516	VSLOARDQVCHFVTCICTCTGQHASVHLGQLDWYSVWPNAPCTMRLPPPTTK-DATLET	574
531	Db	531	SLLDTREALVOYITWVIFTCSAHAAVSSGQFSCVWMPNLPTTMQLPPTPSKGQARPS	590
575	QY	575	VMATLPNFHQSLQMSITWQIGRQPPVMAVGQHEEYFSGPPEKAVLKKFREELAAJDK	634
591	Db	591	FIATLPAVNSSSYHIALWLLSAEPGQRPGLGHPYDEHFTEDAPRRSVAAFORKLIQISK	650
635	QY	635	EIEIRNAKMDPYELRPSVVVENSVAI	661
651	Db	651	GIRERNRGALPYVLDPLIENSVI	677
RESULT 12				
US-09-764-246-4				
; Sequence 4, Application US/09764246				
; Patent No. 6649355				
; GENERAL INFORMATION:				
; APPLICANT: BRASH, ALAN R.				
; BOEGLIN, WILLIAM E.				
; JISAKA, MITSUO				
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS				
; NUMBER OF SEQUENCES: 36				
; CORRESPONDENCE ADDRESS:				
; ADDRESSEE: ARLES A. TAYLOR, JR.				
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD				
; CITY: DURHAM				
; STATE: NORTH CAROLINA				
; COUNTRY: USA				
; ZIP: 27707				
; COMPUTER READABLE FORM:				
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage				
; COMPUTER: IBM PC/XT/AT compatible				
; OPERATING SYSTEM: Windows 3.1				
; SOFTWARE: WORD PERFECT 6.1 and ASCII				
; CURRENT APPLICATION DATA:				
; APPLICATION NUMBER: US/09/764,246				
; FILING DATE: 17-Jan-2001				
; CLASSIFICATION: 435				
; PRIOR APPLICATION DATA:				
; APPLICATION NUMBER: <Unknown>				
; FILING DATE: <Unknown>				
; ATTORNEY/AGENT INFORMATION:				
; NAME: ARLES A. TAYLOR, JR.				
; REGISTRATION NUMBER: 39,395				
; REFERENCE/DOCKET NUMBER: 1242/5				
; TELECOMMUNICATION INFORMATION:				
; TELEPHONE: (919) 493-8000				
; TELEFAX: (919) 419-0383				

## RESULT 12

US-09-764-246-4

: Sequence 4, Application US/09764246

; Patent No. 6649355

**GENERAL INFORMATION:**

APPLICANT: BRASH, ALAN R.

BOEGLIN, WILLIAM E.

JISAKA, MITSUO

1. TITLE OF INVENTION: LIPOX

NUMBER OF SEQUENCES: 36

CORRESPONDENCE ADDRESS:

ADDRESSEE: ARLES A. TAYLOR, JR.

STREET: SUITE 1400, UNIVERSITY

; CITY: DURHAM

STATE: NORTH CAROLINA

; COUNTRY: USA

ZIP: 27707

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inc

COMPUTER: IBM PC/XT/AT compatible  
COMMUNICATING SYSTEM: windows 3.1

```

;
;
OPERATING SYSTEM: WINDOWS 3.1
COMPILED WORD PERFECT 6.1 and

```

; SOFTWARE: WORD PERFECT 6.1 and  
CURRENT APPLICATION DATA.

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: IIS/00/764 2

APPLICATION NUMBER: US/05/184,2  
FILING DATE: 17-Jan-2001

FILING DATE: 17-JUN-2001  
CLASSIFICATION: 435

CLASSIFICATION: 433  
PRIOR APPLICATION DATA:

ERROR REFLECTION DATA:  
APPLICATION NUMBER: <Unknown>

FILING DATE: &lt;Unknown&gt;

**ATTORNEY/AGENT INFORMATION:**

NAME: ARLES A. TAYLOR, JR.

REGISTRATION NUMBER: 39,395

REFERENCE/DOCKET NUMBER: 1242/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919) 493-8000

TELEFAX: (919) 419-0383





```
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547,435
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-547-435-24

Query Match      32.8%; Score 1153; DB 4; Length 867;
Best Local Similarity 35.5%; Pred. No. 1.1e-118;
Matches 255; Conservative 126; Mismatches 273; Indels 64; Gaps 12;

QY 1 MGLYRIRVSTGASLYAGSNNOVQLMWLVGQHGGEA-----ALGKRLMPARGETELKVEVPE 54
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 55 YLGPLLFVKLRKH--LLKDDAWFCNWIISVQGPAGDEVFPFCYRWVEGNGVLSLPEGTG 112
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 216 ELGELLRLVHKERYAFRRKDSWYCSRICVTBPD-GSVSHFPCYQWIEGYCTVELRPGTA 274
QY 113 RTVGEDPQGLFOKHREELERKLYRWGNKDGILLNAGAKLYDLPVDERFLEDK--- 169
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 275 RTICQBSLPLLDHRTRELRARQECYRWKIYAPGFCWVDVNSFOEMSDKKFATKTTT 334
QY 170 -----RVDF-----EVLAKGLADL--AIKDLNVLNLT----- 194
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 335 CVDQDSSGNRYLPGFPMKIDPLSMYMEPNVRYSATKISILFNPAISLGNKRLGLLD 394
QY 195 ---CWKDLDDFNRFWCGSKLAERVRDSWKEDALFGYQFLNGANPVVLRSAHLPARLV 251
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 395 RKGSKWKLDDMQNIFWCHTKFTTKYVTEHWCEDHFFGYQYLVGNVDMVLMHLCISSLPK 453
QY 252 FPGMELOAQ-----LEKEEGGTLFEADPSLLDGIKANVILCSQOHLAAPLVMLKL 304
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 454 --PVTNDMVAPLLGQDTCIQTELEGNIFLADYWIILAEAPTHCLNGRQOYVAAPLCILML 511
QY 305 QPDGKLLPMVIOQLPRTGSPPPPLPPTDPPMAWLLAKCWVRSSDFOLHELQSHLLRGH 364
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 512 SPOGALVPLAIQLS--QTGPDSPILPDTSEWDLAKTWYRNSEFLVHENTHFLCTH 569
QY 365 LMAEVIVATMRCLPSIHPFKLIIPHLYTLEINVRARTGLVSDMGIFDQIMSTGGGGH 424
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 570 LLCEAFAMATLRQLPCHPIYKLLPHTRYTLQVNTIARATLINPBLVDQVTSIGRQGL 629
QY 425 VOLLKAGAFITYSSFCPPDDADRLGLGVKSSFYAQDALRLWEIIRYRVEGIVSLHYKT 484
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 630 IYLMSTGLAHFTYTNFCLPDSLRAARGVLAIPNHYRDGLGKIMAAIESFVSEIVGYTPS 689
QY 485 DVAVKDDPELOTCREITEIGLQAGDGRGFPVSLQARDQVCHFTVTCICTGQHASVHL 544
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 690 DASVQDSELOQWGTGIFAQAFGRSGSPPLSLCTPGEWVPLTAIIFNCSAQHAHVNS 749
QY 545 GQLDWYSWVPNAPCTMRLPPPTTK-DATLETVMATLPNFHQASLOMSITWQLRGQPVNV 603
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 750 GQHDFGAWNPAPSSMRQPPQKGTTLTKYLDLTPVNISSCNLLFLWLSQEBKQOR 809
QY 604 AVQCHHEEYFSGPEKAVLKKFREELALDKIEIRNAKLDMPYELRFSVVENSVAI 661
DB |||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 810 PLGTYPDEHTEAPRRSIAAFQSRQAISRDIOERNQOGLAFLPYTLYDPLPLIENSVSI 867
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RESULT 15

US-09-087-727-2

; Sequence 2, Application US/09087727A

; Patent No. 6103496

```
; GENERAL INFORMATION:
; APPLICANT: Brash, Alan R
; APPLICANT: Boeglin, William E
; APPLICANT: Kim, Richard B
; TITLE OF INVENTION: Isolated and Purified 12R-Lipoxigenase Protein and
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE: Attorney Docket No. 6103496 1242-7
; CURRENT APPLICATION NUMBER: US/09/087,727A
; CURRENT FILING DATE: 1998-05-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-087-727-2
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Query Match      32.0%; Score 1124; DB 3; Length 701;
Best Local Similarity 34.0%; Pred. No. 1.3e-115;
Matches 243; Conservative 140; Mismatches 265; Indels 66; Gaps 12;

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QY 59 QDLGELIIRLHKERYAFFPKDPWYCNVQICAPN-GRYHFPAYQWMDGYETLALREAT 117
QY 112 GRTVGEDPQGLFOKHREELERKLYRWGNKDGIL----- 147
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QY 118 GKTADDLSPLVLELHKEEIRAKODFYHWRVFLPGLPSYVHIPSYRPPVRRHRNPNRPEW 177
QY 148 -----ILNMACAKLYDLPVDERFLEDKRVDPEVSLAKGLADLAIKDSLNLVLTCKWD 198
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QY 199 LDDFNRIFWCGSKLAERVRDSWKEDALFGYQFLNGANPVVLRSAHLPARLVFP----- 253
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QY 254 --PGHEE---LQAOLEKELEGTLFEADPSLLDGIKANVILCSQOHLAAPLVMLKLQPDG 308
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QY 489 KDDPELQWTCREITEIGLQAGDGRGFPVSLQARDQVCHFTVTCICTGQHASVHLQGLD 548
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QY 549 WYSWVPNAPCTMRLPPPTTKD-ATLETVMATLPNFHQASLOMSITWQLRGQPVNVAVQ 607
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QY 598 FTAWNPENFASMRNPPIQTKGLTILETFMDTLVDKTCITLLVLTWLSREDDRRPLGH 647
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Search completed: July 18, 2005, 22:03:20

JOB time : 33.1353 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2005, 21:53:28 ; Search time 102.756 Seconds  
(without alignments)  
2497.095 Million cell updates/sec

Title: US-10-688-676A-2

Perfect score: 3514

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1736639 seqs, 388188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	3514	100.0	661	16 US-10-688-676A-2	Sequence 2, Appli
2	3503.5	99.7	662	9 US-09-764-246-25	Sequence 25, Appl
3	3503.5	99.7	662	16 US-10-716-204-25	Sequence 25, Appl
4	3494.5	99.4	684	15 US-10-398-663-5	Sequence 5, Appli
5	2316	65.9	663	16 US-10-741-601-516	Sequence 516, App
6	2316	65.9	663	16 US-10-741-601-517	Sequence 517, App
7	2316	65.9	663	17 US-10-741-600-1499	Sequence 1499, App
8	2316	65.9	663	17 US-10-741-600-1500	Sequence 1500, App
9	2280	64.9	663	15 US-10-170-097-653	Sequence 653, App
10	2280	64.9	663	17 US-10-926-684-653	Sequence 653, App
11	1969	56.0	399	17 US-10-498-788-27	Sequence 27, Appl

12	1298.5	37.0	674	14	US-10-240-305-14	Sequence 14, Appl
13	1298.5	37.0	674	16	US-10-485-310-22	Sequence 22, Appl
14	1261.5	35.9	663	14	US-10-240-305-16	Sequence 16, Appl
15	1202.5	34.2	676	9	US-09-764-246-2	Sequence 2, Appli
16	1202.5	34.2	676	16	US-10-716-204-2	Sequence 4, Appli
17	1184	33.7	677	9	US-09-764-246-4	Sequence 4, Appli
18	1184	33.7	677	16	US-10-716-204-4	Sequence 4, Appli
19	1184	33.7	677	16	US-10-688-676A-4	Sequence 2, Appli
20	1153	32.8	711	9	US-09-862-658-2	Sequence 2, Appli
21	1153	32.8	711	14	US-10-175-696-23	Sequence 23, Appl
22	1153	32.8	711	14	US-10-422-264-2	Sequence 2, Appli
23	1153	32.8	711	16	US-10-776-871-23	Sequence 23, Appl
24	1153	32.8	867	14	US-10-422-264-24	Sequence 24, Appl
25	1148	32.7	711	15	US-10-275-998-3	Sequence 3, Appli
26	1124	32.0	701	9	US-09-853-053-2	Sequence 2, Appli
27	1124	32.0	701	15	US-10-445-484-2	Sequence 6, Appli
28	954.5	27.2	556	14	US-10-422-264-6	Sequence 10, Appl
29	946.5	26.9	615	14	US-10-422-264-10	Sequence 28, Appl
30	946.5	26.9	771	14	US-10-422-264-28	Sequence 19529, A
31	761.5	21.7	671	15	US-10-369-493-19529	Sequence 12, Appl
32	748	21.3	460	14	US-10-422-264-12	Sequence 4, Appli
33	704.5	20.0	489	14	US-10-422-264-4	Sequence 25, Appl
34	704.5	20.0	645	14	US-10-422-264-26	Sequence 14, Appl
35	686.5	19.5	389	16	US-10-485-310-3	Sequence 5694, Ap
36	593.5	16.9	491	9	US-09-862-658-4	Sequence 19963, A
37	593.5	16.9	491	14	US-10-175-696-25	Sequence 8, Appli
38	593.5	16.9	491	16	US-10-776-871-25	Sequence 19726, A
39	580.5	16.5	291	14	US-10-422-264-14	Sequence 51226, A
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44	494.5	14.1	814	15	US-10-425-114-51226	
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#### ALIGNMENTS

#### RESULT 1

US-10-688-676A-2  
; Sequence 2, Application US/10688676A  
; Publication No. US20040248794A1  
; GENERAL INFORMATION:  
; APPLICANT: Alcon, Inc.  
; APPLICANT: Yanni, John M.  
; APPLICANT: Ganache, Daniel A.  
; APPLICANT: Miller, Steven T.  
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo  
; TITLE OF INVENTION: Activity to Ocular Surface Cells  
; FILE REFERENCE: 2394 US  
; CURRENT APPLICATION NUMBER: US/10/688.676A  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: US 60/435,988  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 661  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-688-676A-2

Query Match	100.0%	Score 3514;	DB 16;	Length 661;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 661;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MGLYRIRVSTGASLYAGSNNQVQLWLVQHGEAALGKRLWPARGETELKVEVPEYLGPIIL	60	
Db	1	MGLYRIRVSTGASLYAGSNNQVQLWLVQHGEAALGKRLWPARGETELKVEVPEYLGPIIL	60	
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Db 121 GLFQKHREBELEBERRKLYRWGNWKGDLILNMAKAKLYDLPVDERFLEDKRVDFEYSLAG 180  
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Db 181 LADLAIKDSNLVLTWCWLDLDDFNRIFWCGSKLAERVRDSWKEDALFGYQFLNGANPVYL 240  
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Db 241 RRSAPHLPARLVFPFGMEELQAQLEKELEGGTLEADFSLLDGTKANVILCSQOHLAAPLV 300  
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Db 301 MLKLPQDGLLPMVIOQLPRTGSPPLFLPTDPPMAWLLAKCWRSSDFOLHELQSHL 360  
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QY 661 I 661  
Db 661 I 661

RESULT 2

US-09-764-246-25  
; Sequence 25, Application US/09764246  
; Patent No. US20010046672A1  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; BOEGLIN, WILLIAM E.  
; JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/764,246  
; FILING DATE: 17-Jan-2001  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:

NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 662 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-764-246-25  
Query Match 99.7%; Score 3503.5; DB 9; Length 662;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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; Sequence 25, Application US/10716204  
; Publication No. US20040137483A1

GENERAL INFORMATION:  
APPLICANT: BRASH, ALAN R.  
BOEGLIN, WILLIAM E.  
JISAKA, MITSUO  
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA: US/10/716, 204  
FILING DATE: 18-Nov-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 662 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-10-716-204-25  
Query Match 99.7%; Score 3503.5; DB 16; Length 662;  
Best Local Similarity 99.8%; Pred. No. 0;  
Matches 661; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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QY 360 LLRGLHMAEVIIVATWRCILPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419  
DB 361 LLRGLHMAEVIIVATWRCILPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 420

QY 420 GGGGHVOLLKQAGAFITYSSFCPPDDLADRLGLLVKSSFYAODALRLWEIIRYVVEGIVS 479  
DB 421 GGGGHVOLLKQAGAFITYSSFCPPDDLADRLGLLVKSSFYAODALRLWEIIRYVVEGIVS 480  
QY 480 LHYKTDVAVKDDPELOQWTCREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCIFTCTGQH 539  
DB 481 LHYKTDVAVKDDPELOQWTCREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCIFTCTGQH 540  
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDALTETVATLNFHQAOLMSITWOLGRRQ 599  
DB 541 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDALTETVATLNFHQAOLMSITWOLGRRQ 600  
QY 600 PMVAVGQHEEYFSGPEPKAVLKKFREELAAALDKEIEIRNAKLDMPYEYLRPSVVENS 659  
DB 601 PMVAVGQHEEYFSGPEPKAVLKKFREELAAALDKEIEIRNAKLDMPYEYLRPSVVENS 660  
QY 660 AI 661  
DB 661 AI 662  
RESULT 4  
US-10-398-663-5  
Sequence 5, Application US/10398663  
Publication No. US20040053281A1  
GENERAL INFORMATION:  
APPLICANT: INCYTE, CORPORATION; HARLAND, Lee;  
APPLICANT: ARVIZU, Chandra S.; DAS, Debopriya;  
APPLICANT: GRIFFIN, Jennifer A.; BAUGHN, Mariah R.;  
APPLICANT: DING, Li; CHAWLA, Narinder K.;  
APPLICANT: YAO, Montique G.; LU, Yan;  
APPLICANT: ELLIOTT, Vicki S.; THANGAVELU, Kavitha;  
APPLICANT: RAMKUMAR, Javalaxmi; LAL, Preeti G.;  
APPLICANT: TRIBOULEY, Catherine M.  
TITLE OF INVENTION: LIPID METABOLISM ENZYMES  
FILE REFERENCE: PI-0250 USN  
CURRENT APPLICATION NUMBER: US/10/398,663  
CURRENT FILING DATE: 2003-03-04  
PRIOR APPLICATION NUMBER: PCT/US01/31302  
PRIOR FILING DATE: 2001-10-05  
PRIOR APPLICATION NUMBER: US 60/238,388  
PRIOR FILING DATE: 2000-10-06  
PRIOR APPLICATION NUMBER: US 60/240,616  
PRIOR FILING DATE: 2000-10-13  
PRIOR APPLICATION NUMBER: US 60/245,719  
PRIOR FILING DATE: 2000-11-02  
PRIOR APPLICATION NUMBER: US 60/247,503  
PRIOR FILING DATE: 2000-11-08  
PRIOR APPLICATION NUMBER: US 60/249,503  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PERL Program  
SEQ ID NO 5  
LENGTH: 684  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc.feature  
OTHER INFORMATION: Incyte ID No. US20040053281A1 7484270CD1  
US-10-398-663-5

Query Match 99.4%; Score 3494.5; DB 15; Length 684;  
Best Local Similarity 99.7%; Pred. No. 0;  
Matches 660; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  
QY 1 MGLYRIRVSTGASLYAGSNNOVQLVQGHGAALGKRLWPARG-ETELKVEVPYLGPL 59  
DB 23 MGLYRIRVSTGASLYAGSNNOVQLVQGHGAALGKRLWPARGKETELKVEVPYLGPL 82  
QY 60 LFVKLRKRLKDDAWFCNWIISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 119  
DB 83 LFVKLRKRLKDDAWFCNWIISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGEDP 142

```
QY 120 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDPEVSLAK 179
Db 143 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDPEVSLAK 202
QY 180 GLADLAIKSLNVLTCWKDLDNFNRIFWCGSKLAERVDSWKEDALFGYQFLNGANPVV 239
Db 203 GLADLAIKSLNVLTCWKDLDNFNRIFWCGSKLAERVDSWKEDALFGYQFLNGANPVV 262
QY 240 LRRSAHLPARLVFPFGMBELQAQLEKELEGGTLEADFSLLDGIKANVILCSQQHAAAPL 299
Db 263 LRRSAHLPARLVFPFGMBELQAQLEKELEGGTLEADFSLLDGIKANVILCSQQHAAAPL 322
QY 300 VMLKLPQDGKLLPMVILQOLPRGTSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 359
Db 323 VMLKLPQDGKLLPMVILQOLPRGTSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 382
QY 360 LLRGHLMAEVIVVATWRCPLPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGI FDOIMST 419
Db 383 LLRGHLMAEVIVVATWRCPLPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGI FDOIMST 442
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db 443 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 502
QY 480 LHYKTDVAVKDDPELQTCWREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCI FCTGQH 539
Db 503 LHYKTDVAVKDDPELQTCWREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCI FCTGQH 562
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATTLETWATLPNFHQASLQMSITWOLGRQ 599
Db 563 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATTLETWATLPNFHQASLQMSITWOLGRQ 622
QY 600 PWMVAVGQHEEYFSGPEPKAVLKKFREELAAALDKEIERNAKLDMPEYLRPSVVENS 659
Db 623 PWMVAVGQHEEYFSGPEPKAVLKKFREELAAALDKEIERNAKLDMPEYLRPSVVENS 682
QY 660 AI 661
Db 683 AI 684
```

## RESULT 5

```
US-10-741-601-516
; Sequence 516, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 516
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-516
```

```
Query Match 65.9%; Score 2316; DB 16; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;
```

```
QY 1 MGLYRIRVSTGASLYAGSNQVQLMWVGQHGAEALGKRLWPARG-ETELKVEVPEYLGPL 59
Db 1 MGRYRIRVATGAWLFGSGYNRVQLMWVGTRGEAELEQLRPARGEEEFHDHVAEDLGL 60
QY 60 LFKVLKRHLKDDAWFCNWIISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRVTGEDP 119
Db 61 QFVLRKHHWLVDDAWFCDRITVQGPAGCAEVAFFPCYRWVQGEDILSLPEGTARLPGDNA 120
```

```
QY 120 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDPEVSLAK 179
Db 121 LDMFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDPEVSLAK 180
QY 180 GLADLAIKSLNVLTCWKDLDNFNRIFWCGSKLAERVDSWKEDALFGYQFLNGANPVV 239
Db 181 GALEMALKRVYTLSSWNCLEDFDQIFWQKSALAERQRCWQDDLEFSYQFLNGANPWL 240
QY 240 LRRSAHLPARLVFPFGMBELQAQLEKELEGGTLEADFSLLDGIKANVILCSQQHAAAPL 299
Db 241 LRRSTSLPSRLVLPFGMBELQAQLEKELEGGTLEADFSLLDGIKANVIRGEKQYLAAPL 300
QY 300 VMLKLPQDGKLLPMVILQOLPRGTSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 359
Db 301 VMLKMEPNKGLQPMVILQOLPRGTSPPPPLFLPTDPPMAWLLAKCWRSSDFQLHQLSH 360
QY 360 LLRGHLMAEVIVVATWRCPLPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGI FDOIMST 419
Db 361 LINTHLVAEIVATWRCPLPSIHPIFKLIIPHLRYTLEINVRARTGLVSDMGI FDOIMST 420
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db 421 GGGHVQLLKQAGAFITYSSFCPPDDLADRGLLGVKSSFYAODALRLWEIIVRYVEGIVS 480
QY 480 LHYKTDVAVKDDPELQTCWREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCI FCTGQH 539
Db 481 LHYKTDVAVKDDPELQTCWREITEIGLQGAQDRGFPVSLQARDQVCHFTVTCI FCTGQH 540
QY 540 ASVHLGQLDWYSWVPNAPCTMRLPPPTTKDATTLETWATLPNFHQASLQMSITWOLGR 598
Db 541 AAINGQGLDWYAWVPNAPCTMRLPPPTTKDATTLETWATLPNFHQASLQMSITWOLGR 600
QY 599 PWMVAVGQHEEYFSGPEPKAVLKKFREELAAALDKEIERNAKLDMPEYLRPSVVENS 658
Db 601 QDMVPLGHHKEKESGPKKAVLNQFRITDLEKLEKEITARNEQLDWPYELKPSCIENS 660
QY 659 VAI 661
Db 661 VTI 663
```

## RESULT 6

```
US-10-741-601-517
; Sequence 517, Application US/10741601
; Publication No. US20040166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 517
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-601-517
```

```
Query Match 65.9%; Score 2316; DB 16; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;
```

```
QY 1 MGLYRIRVSTGASLYAGSNQVQLMWVGQHGAEALGKRLWPARG-ETELKVEVPEYLGPL 59
Db 1 MGRYRIRVATGAWLFGSGYNRVQLMWVGTRGEAELEQLRPARGEEEFHDHVAEDLGL 60
QY 60 LFKVLKRHLKDDAWFCNWIISVQGPAGDEVRFPCYRWVEGNGVLSLPEGTGRVTGEDP 119
Db 61 QFVLRKHHWLVDDAWFCDRITVQGPAGCAEVAFFPCYRWVQGEDILSLPEGTARLPGDNA 120
QY 120 QGLFQKHREELERKLYRWGNWKGILLNAGAKLYDLPVDERFLEDKRVDPEVSLAK 179
```



```
Db 121 LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKODLPPNMRPFHEKRLDPFWTLKA 180
Qy 180 GLADLAIKDSNLVLTCKWDLDDFNRIFWCGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db 181 GALEMALKRVVYTLSSWNCLEDFOQIFWGQKSALAERKVRQWQDDDELFSYQFLNGANPML 240
Qy 240 LRRSAHLPARLVFPFGMBELQALKELEGGLTLEADSLDGIKANVILCSQQHAAAPL 299
Db 241 LRRSTSLPSRLVLPFGMBELQALKELEGGLTLEADSLDGIKANVILCSQQHAAAPL 300
Qy 300 VMLKLOPDGKLLPMVIOQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 359
Db 301 VMLKMEPNKGLQPMVIOQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 360
Qy 360 LLRGHLMAEVIVVATMRCLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LLNTHLVAEVIATMRCLPGLHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420
Qy 420 GGGHVQLLKQAGAFITYSSCPDDLDAGRLGLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db 421 GGGHVQLLRRAAQLTYCSLCPDDLDAGRLGLGVKSSFYAODALRLWEIIVRYVEGIVS 480
Qy 480 LHYKTDVAVKDDPELOTWCREITBGLQAGDRGPPVSLQARDQVCHVFTWCICTGQH 539
Db 481 LFYQRDDIVKGDPELOTWCREITBGLQAGDRGPPVSLQARDQVCHVFTWCICTGQH 540
Qy 540 ASVHLGQLDWYSWVNPACTMRLPPTTK-DATLETVMATLPNFHQASLQMSITWOLGRR 598
Db 541 AAINQGQLDWYAWVNPACTMRLPPTTK-DATLETVMATLPNFHQASLQMSITWOLGRR 600
Qy 599 QPMVAVGQHEEYFSGPEPKAVLKKFREELAAALKEIEIRNAKLDMPYELRPSVENS 658
Db 601 QPMVPLGHKHEKYFSGPKAVLNQFRTDLEKLEKEITARNEQDQWPEYELKPCSCIENS 660
Qy 659 VAI 661
Db 661 VTI 663
```

```
RESULT 7
US-10-741-600-1499
; Sequence 1499, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1499
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1499
```

```
Query Match 65.9%; Score 2316; DB 17; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;

Qy 1 MGLYRIRVSTGASLYAGSNNOVLVQGHGAALGKRLWPARG-ETELKRVPEYVLGPL 59
Db 1 MGRYIRVATGAWLFGSGYNRVQLWLVGTRGAELEQLRPARGEEEFDDHDAEDLGL 60
Qy 60 LFLVKLRKHLKDDAWFCNWIISVQGGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGDDP 119
Db 61 QFVRLKHHWLVDDAWFCDRITVQGGACAEVAFPCYRWVQGEDILSLPEGTARLPDGA 120
Qy 120 QGLFQKHREELERKRLYRWGNWKGILLNAGAKLYDLVDFRFLDKRVDPEVSLAK 179
Db 121 LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKODLPPNMRPFHEKRLDPFWTLKA 180
```

```
Db 121 LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKODLPPNMRPFHEKRLDPFWTLKA 180
Qy 180 GLADLAIKDSNLVLTCKWDLDDFNRIFWCGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db 181 GALEMALKRVVYTLSSWNCLEDFOQIFWGQKSALAERKVRQWQDDDELFSYQFLNGANPML 240
Qy 240 LRRSAHLPARLVFPFGMBELQALKELEGGLTLEADSLDGIKANVILCSQQHAAAPL 299
Db 241 LRRSTSLPSRLVLPFGMBELQALKELEGGLTLEADSLDGIKANVILCSQQHAAAPL 300
Qy 300 VMLKLOPDGKLLPMVIOQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 359
Db 301 VMLKMEPNKGLQPMVIOQLPRTGSPPLFLPTDPPMAWLLAKCWVRSSDFQLHELOSH 360
Qy 360 LLRGHLMAEVIVVATMRCLPSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LLNTHLVAEVIATMRCLPGLHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMST 420
Qy 420 GGGHVQLLKQAGAFITYSSCPDDLDAGRLGLGVKSSFYAODALRLWEIIVRYVEGIVS 479
Db 421 GGGHVQLLRRAAQLTYCSLCPDDLDAGRLGLGVKSSFYAODALRLWEIIVRYVEGIVS 480
Qy 480 LHYKTDVAVKDDPELOTWCREITBGLQAGDRGPPVSLQARDQVCHVFTWCICTGQH 539
Db 481 LFYQRDDIVKGDPELOTWCREITBGLQAGDRGPPVSLQARDQVCHVFTWCICTGQH 540
Qy 540 ASVHLGQLDWYSWVNPACTMRLPPTTK-DATLETVMATLPNFHQASLQMSITWOLGRR 598
Db 541 AAINQGQLDWYAWVNPACTMRLPPTTK-DATLETVMATLPNFHQASLQMSITWOLGRR 600
Qy 599 QPMVAVGQHEEYFSGPEPKAVLKKFREELAAALKEIEIRNAKLDMPYELRPSVENS 658
Db 601 QPMVPLGHKHEKYFSGPKAVLNQFRTDLEKLEKEITARNEQDQWPEYELKPCSCIENS 660
Qy 659 VAI 661
Db 661 VTI 663
```

```
RESULT 8
US-10-741-600-1500
; Sequence 1500, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1500
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1500
```

```
Query Match 65.9%; Score 2316; DB 17; Length 663;
Best Local Similarity 65.5%; Pred. No. 3.7e-220;
Matches 434; Conservative 93; Mismatches 134; Indels 2; Gaps 2;

Qy 1 MGLYRIRVSTGASLYAGSNNOVLVQGHGAALGKRLWPARG-ETELKRVPEYVLGPL 59
Db 1 MGRYIRVATGAWLFGSGYNRVQLWLVGTRGAELEQLRPARGEEEFDDHDAEDLGL 60
Qy 60 LFLVKLRKHLKDDAWFCNWIISVQGGAGDEVRFPCYRWVEGNGVLSLPEGTGRTVGDDP 119
Db 61 QFVRLKHHWLVDDAWFCDRITVQGGACAEVAFPCYRWVQGEDILSLPEGTARLPDGA 120
Qy 120 QGLFQKHREELERKRLYRWGNWKGILLNAGAKLYDLVDFRFLDKRVDPEVSLAK 179
Db 121 LDMFQKHREKELKDRQOIIYCWATWKEGLPLTIAADRKODLPPNMRPFHEKRLDPFWTLKA 180
```

Qy	180	GIADLAIKOSLNVLCWKDLDNFNRIFWCGSQSKUAERVRSWKEDALFGVQFLINGANPVV	239
Db	181	GALEWALKRVYVTLSSWNCLEDFOQIFWGQSKALAEKRVQCWDDELFSYQFLINGANPML	240
Qy	240	LRRSAHLPARLVFPFGMEELQAQLEKELEGTLFEADPSLLDGIKANVILCSOOHLAAPL	299
Db	241	LRRSTLSRLVPLSGMEELQAQLEKELQNGSLFEADFIILLDGPANVIRGEKQYLAAAPL	300
Qy	300	VMLKLPDQDKLLPMWIOQLPRTGSPPPPLFLPTDPPMAMLLAKCWRVRSDDFQHELQSH	359
Db	301	VMLKMEPNKGLQPMWIOQPNNPSSPTPTFLPSDPLLAWLLAKSWRNSDFQHEIQIYH	360
Qy	360	LLRGHLMAEVIIVATMRCULPSIHPIFKLIIPIHRYTLEINVRARTGLVSDMGIFDQIMST	419
Db	361	LLNTHLVAEVIIVATMRCULPGLHPHFKELIPIHRYTMEINTRARTQLISDGGIFDRAVST	420
Qy	420	GGSGHVOLLKQAGAFITYTSSFCPPDDLADRGLLGVKSSFYAODALRLWEIIYYVVGIVS	479
Db	421	GGSGHVOLLURRAAQUTYCSLCPDDLADRGLLGPGALYAHDLARLWEIIARYVGEIVH	480
Qy	480	LHYKTIDVAKDDPELQTCREITEITGLQAGDRGFPVSLQARDQVCHFTVMCIPTCTGOH	539
Db	481	LFYORDDIVKGPDELQAMCREITEITGLCQAGDRGFPVFSQSQSLCHFTLMCVFTCTAOH	540
Qy	540	ASVHLGOLDWYSWVNACTMRLBPPTTK-DATLETWATILPNPHOASLOMSITWOLGRR	598
Db	541	AAINQOLDWYAWVNAPECTMRMPPTTKEDVMTATVWGLSPFDVRQRCLOQALMSWLSRR	600
Qy	599	QPMWAVGQHEEYFSGPEPKAVLKFKFEALAAKDKIEIRNAKLDMPYEYLPRSPVENS	658
Db	601	QPMVPLGHKKKEKYSFGPKPAVLNQFTDLELKEKIEITARNEQOLDWPYEYLKSPSCIENS	660
Qy	659	VAI 661	
Db	661	VTI 663	

```

RESULT 9
US-10-170-097-653
; Sequence 653, Application US/10170097
; Publication No. US20030228582A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/170,097
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 653
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 189
; OTHER INFORMATION: Xaa=Arg or His
; FEATURE:

```

```
QY 540 ASVHLGOLDWYSWVPNAPCTMELPPTTK-DATLETVMATLPNFHOASIQMSITWOLGRR 598
Db 541 AAINQGQDWDYAWVPNAPCTMRMPPTTKBEDVTXATVMSLDPVQACIQMAISWHLGRR 600
QY 599 QPVMVAVGQHEEYFSGPEKAVLKKFREELAALDKIEIRNAKLDMPYELRPSWVENS 658
Db 601 QPDMVPLGHKKEKYFSGPKPAVLNQFRDLEKLEKEITARNEQLDWPYELKPSCIENS 660
QY 659 VAI 661
Db 661 VTI 663

RESULT 10
US-10-926-684-653
; Sequence 653, Application US/10926684
; Publication No. US20050014190A1
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Chumakov, Ilya
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGIONS
; TITLE OF INVENTION: CARRYING
; TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
; FILE REFERENCE: GEN-T114XC2D1
; CURRENT APPLICATION NUMBER: US/10/926,684
; CURRENT FILING DATE: 2004-08-25
; PRIOR APPLICATION NUMBER: US/10/170,097
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/641,638
; PRIOR FILING DATE: 2000-08-16
; PRIOR APPLICATION NUMBER: US 09/502,330
; PRIOR FILING DATE: 2000-02-11
; PRIOR APPLICATION NUMBER: US 60/133,200
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: US 09/275,267
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: US 60/119,917
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 1304
; SOFTWARE: Patent.pm
; SEQ ID NO 653
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 189
; OTHER INFORMATION: Xaa=Arg or His
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 225
; OTHER INFORMATION: Xaa=Asp or His
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 243
; OTHER INFORMATION: Xaa=Arg or Cys
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 261
; OTHER INFORMATION: Xaa=Gln or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 322
; OTHER INFORMATION: Xaa=Ser or Asn
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 337
; OTHER INFORMATION: Xaa=Pro or Arg
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 362
```

```
; OTHER INFORMATION: Deletion of Leu
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 568
; OTHER INFORMATION: Xaa=Asn or Thr
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 574
; OTHER INFORMATION: Xaa=Met or Lys
US-10-926-684-653
```

Query Match 64.9%; Score 2280; DB 17; Length 663;

Best Local Similarity 64.7%; Pred. No. 1.4e-216; Indels 2; Gaps 2;

Matches 429; Conservative 92; Mismatches 140; Indels 2; Gaps 2;

```
QY 1 MGLYRIRVSTGASLYAGSNNOVLVQGHGEAALGKRLWPARG-ETELKVEYFYLGPL 59
Db 1 MGRYRIRVATGAWLFSGSYNRVQLWLVGTRGEAELEQLRPARGEEREFDDVAEDLGLL 60
QY 60 LFVKLRKRLHLLKDDAWFCNWNISVQGPAGDVRPFCYRWVVEGNGVLSLPEGTGRTVGDDP 119
Db 61 QFVRLRKHHWLVDDAWFCDRITVQPGACAFAVFCYRWVQGEDILSLPEGTARLPGGNA 120
QY 120 QGLFQKHREELERRKLYRWGNWKGILNMACAKLYDLPVDRERFLEDKRVDPEVSLAK 179
Db 121 LDMFQKHREKELDKRQYCWATWKEGLPLTIAADRKDDLPNNRFFHEEKRLDFEWTLKA 180
QY 180 GLADLAIKDSLNVLTCWKDLDDFNRIFWCGGSKLAERVRDSWKEDALFGYQFLNGANPVV 239
Db 181 GALEWALKXVYVTLSSWNLCLEDFQIFWGQKSALAERKVCQWQXELFSYQFLNGANPML 240
QY 240 LRRSAHLPARLVFPFGMEELQAQLEKELEGGTLFEADPSLLDGKANVILCSQQHAAPL 299
Db 241 LRXSTSLPSRLVLPSPGMEELXAQLEKELQNGSLFEADPILLDGIPANVIRGEKQYLAAPL 300
QY 300 VMLKLPQDGLPMVIOQLPRTGSPPPPLFLPTDPPMAWLLAKCWVRSSDPQLHELQSH 359
Db 301 VMLKMEPGKLPQPMVIOIQPEXSSPTTLLPSPDPLXLAWLLAKSWVRNSDFQLHEIQH 360
QY 360 LLRGLHMAEVIVVATMRCLPSIHPFKLIIPHLRYTLEINVRARTGLVSDMGIFDQIMST 419
Db 361 LLNTHLVAEVIATVATMRCLPGLHPIFKELPHIHYTWEINTRARTQLISDGGIFDKAVST 420
QY 420 GGGHVQLLKQAGAFITYSSFCPPDDADRGLLGVKSSFYAQDALRLWEIYRYVEGIVS 479
Db 421 GGGHVQLLRRAAQLTVCSLCPDDDLADRGLLGLPGALYAHDALRLWEIYRYVEGIVH 480
QY 480 LHYKTDVAVKDDPELOTWCREITEIGLQAGDRGFPVSLQARDQVCHFTWCTICTGQH 539
Db 481 LFYQRDDIVKGDPELOAWCREITEVGLCQAGDRGFPVFSQSQCCHFLTWCVFCTTAQH 540
QY 540 ASVHLGOLDWYSWVPNAPCTMELPPTTK-DATLETVMATLPNFHOASIQMSITWOLGRR 598
Db 541 AAINQGQDWDYAWVPNAPCTMRMPPTTKBEDVTXATVMSLDPVQACIQMAISWHLGRR 600
QY 599 QPVMVAVGQHEEYFSGPEKAVLKKFREELAALDKIEIRNAKLDMPYELRPSWVENS 658
Db 601 QPDMVPLGHKKEKYFSGPKPAVLNQFRDLEKLEKEITARNEQLDWPYELKPSCIENS 660
QY 659 VAI 661
Db 661 VTI 663
```

```
RESULT 11
US-10-498-788-27
; Sequence 27, Application US/10498788
; Publication No. US2005011859A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: Chawla, Narinder K.
; APPLICANT: Lee, Soo Yeun
; APPLICANT: Ring, Huijun Z.
```

```

; APPLICANT: Lee, Ernestine A.
; APPLICANT: Forsythe, Ian J.
; APPLICANT: Khare, Reena
; APPLICANT: Tran, Uyen K.
; APPLICANT: Kable, Amy E.
; APPLICANT: Richardson, Thomas W.
; APPLICANT: Emerling, Brooke M.
; APPLICANT: Lindquist, Brika A.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Hafalia, April J. A.
; APPLICANT: Jin, Pei
; APPLICANT: Swarnakar, Anita
; APPLICANT: Li, Joana X.
; APPLICANT: Marquis, Joseph P.
; APPLICANT: Lee, Sally
; APPLICANT: Gorvad, Ann E.
; APPLICANT: Sprague, William W.
; APPLICANT: Becha, Shanya D.
; APPLICANT: Elliott, Vicki S.
; TITLE OF INVENTION: ENZYMES
; FILE REFERENCE: PF-1312 PCT
; CURRENT APPLICATION NUMBER: US/10/498,788
; CURRENT FILING DATE: 2004-06-14
; PRIOR APPLICATION NUMBER: US 60/340,357
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/342,962
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: US 60/343,558
; PRIOR FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: US 60/351,107
; PRIOR FILING DATE: 2002-01-22
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PERL Program
; SEQ ID NO 27
; LENGTH: 399
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7487231CD1
US-10-498-788-27

Query Match 56.0%; Score 1969; DB 17; Length 399;
Best Local Similarity 94.2%; Pred. No. 4.7e-186;
Matches 374; Conservative 2; Mismatches 7; Indels 14; Gaps 2;

QY 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHGAAALGKRLWPARG-ETELKVEVPEYLGPL 59
DB 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHGAAALGKRLWPARGKETELKVEVPEYLGPL 60
QY 60 LFVKLRKRHLKDDAWFCNWSVQGPAGDEVFPCCYRWVEGNGVLSLPEGTGRTVGEDP 119
DB 61 LFVKLRKRHLKDDAWFCNWSVQGPAGDEVFPCCYRWVEGNGVLSLPEGTGRTVGEDP 120
QY 120 QGLFQKHREELBERKLYRWGNWKDGLILNMAKLYDLPVDERFLEKRYDVFVSLAK 179
DB 121 QGLFQKHREELBERKLYRWGNWKDGLILNMAKLYDLPVDERFLEKRYDVFVSLAK 180
QY 180 GLADLAIKOSLNVLTCKWLDLDFNRIFCWGQSKLAERVDSKEDALFGVQFLNGANPVV 239
DB 181 GLADLAIKOSLNVLTCKWLDLDFNRIFCWGQSKLAERVDSKEDALFGVQFLNGANPVV 240
QY 240 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLDDGIKANVILCSQOHLAAPL 299
DB 241 LRRSAHLPARLVFPFGMEELQAQLEKEGGTLFEADFSLDDGIKANVILCSQOHLAAPL 300
QY 300 VMLKLPDQDKLLPMVTLQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDQFQHLQSH 359
DB 301 VMLKLPDQDKLLPMVTLQQLPRTGSPPPPLFLPTDPPMAWLLAKCWRSSDQFQHLQSH 360
QY 360 LLRGHLMAEVI-----VVATWRCLELSPH 383
DB 361 LLRGHLMAEVIICCGHHEVPAVDTSYLQAVNSPPAIHP 397
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```

RESULT 12
US-10-240-305-14
; Sequence 14, Application US/10240305
; Publication No. US20030162193A1
; GENERAL INFORMATION:
; APPLICANT: GLAXO GROUP LIMITED
; APPLICANT: ANDERSON, WAYNE H.
; APPLICANT: EDWARDS, Lisa D.
; APPLICANT: EMMETT, Amanda H.
; APPLICANT: PILLAJ, Sreekumar
; APPLICANT: SPRANKEL, Catherine S.
; TITLE OF INVENTION: Medicine Response Assay in Respiratory Disease
; FILE REFERENCE: P03958 & P04254
; CURRENT APPLICATION NUMBER: US/10/240,305
; CURRENT FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 674
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-305-14
```

```

Query Match 37.0%; Score 1298.5; DB 14; Length 674;
Best Local Similarity 39.7%; Pred. No. 4e-119;
Matches 269; Conservative 140; Mismatches 248; Indels 21; Gaps 11;

QY 1 MGLYRIRVSTGASLYAGSNNOVLWVGQHG---EALGKRLWP--ARGETE-LKVEVPE 54
DB 1 MPSYIVTVATGSQWPAFTDDYIYLSVGSAGSEKHLDDKPFYNDFERGAVDSDYTVDE 60
QY 55 YLGPILLFVKLRKRHLKDDAWFCNWSVQGPAGDEVFPCCYRWVEGNGVLSLPEGTGRT 114
DB 61 ELGEIQLVRIEKKRYWLNDDWLVKYLTKTP-HGDIIEFPCCYRWITGDVEVVLDRAKL 119
QY 115 VGEDPQGLFQKHREELBERKLYRWGNWKDGLILNMAKLYDLPVDERFLEKRYDVE 174
DB 120 ARDDQIHILKQHRKELETRQKQYRWMEWNEFPPLSIDAKCHKOLPRIDQFSEKGVDFV 179
QY 175 VSLAKGLADLAIKOSLNVLTCKWLDLDFNRIFCWGQSKLAERVDSKEDALFGVQFLN 233
DB 180 LNSYKAMENLFINRPMFMFQSSWDFADPEKIFVKISITISERVNHHQEDLMFGYQFLN 239
QY 234 GANPVLLRRSAHLPARLVFPFGMEEL----QAQLEKEGGTLFEADFSLDDGIKAN-VI 288
DB 240 GCNPVLIIRRCTELPEKLPVTTMVECSLERQLSLQEVQGNIFIVDFELLDGIDANKTD 299
QY 289 LCSQOHLAAPLVMLKLPDQDKLLPMVTLQQLPRTGSPPPPLFLPTDPPMAWLLAKCWR 347
DB 300 PCTLQFLAAPICLLYKNLANKIVPIAIQINQIP---GDENPIFLPSDAKYDWLLAKIWR 356
QY 348 SSDFOLHELQSHLHRLHMAEVIIVVATWRCLELSPHPIPKLIIPHLYRTLEINVRARTGLV 407
DB 357 SSDFHVHTIITHLRTHLVSEVFGIATYRQLPAPVPIFKLLVAHVRFITAITNKAREQIL 416
QY 408 SDMGIFDQIMTSGGGHVQLLKQAGAFITYSSFCPPDDLLADRLGLG---VKSSEFYAQDAL 464
DB 417 CEGGLFDRANATGGGGHVQVQRAMKDLTYASLCFPEAIKARGMESKEDIPIYFYRDDGL 476
QY 465 RWELIYRYVEGIVSLHYKTDVAVKDDPELQTCWREITEIGLQAGQDRGFVSLQARDQV 524
DB 477 LWWEAIRFTAENVDIYVEGDQVVEEDPELQFVNDVYVYGMGRKSGSPKSVKREOL 536
QY 525 CHFTVMCIETCTGQHASVHLGOLDWYSWVPNAPCTWRLPPPTTKD-ATLETVMATLPNFH 583
DB 537 SEYLTWVITFAQAAAVNFQGYDWCMTIPNAPPTTRAPPPTAKGVVITTEIQTIDLPDRG 596
QY 584 QASLQMSITWQGRQRQPVMAVQGHREYFSGPEPKAVLKPFREELAAALDKIEIRNAKL 643
DB 597 RSCWHLGAVWALSQFQENELFLGMYPPEHFIEKPVKEAMARFRKNLEAIVSVIAERNKKK 656
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QY 644 DMPYELRPSVVENSVAI 661  
Db 657 QLPYYLSPDRIPNSVAI 674

## RESULT 13

US-10-485-310-22  
; Sequence 22, Application US/10485310  
; Publication No. US20040234950A1  
; GENERAL INFORMATION:  
; APPLICANT: Takeda Chemical Industries, Ltd.  
; TITLE OF INVENTION: A Method For Screening A Gene Related To Alzheimer's Disease  
; FILE REFERENCE: P01-0277PCT  
; CURRENT APPLICATION NUMBER: US/10/485,310  
; CURRENT FILING DATE: 2004-01-26  
; NUMBER OF SEQ ID NOS: 26  
; SEQ ID NO 22  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Human  
US-10-485-310-22

Query Match 37.0%; Score 1298.5; DB 16; Length 674;  
Best Local Similarity 39.7%; Pred. No. 4e-119;  
Matches 269; Conservative 140; Mismatches 248; Indels 21; Gaps 11;

QY 1 MGLYRIRVSTGASLYAGSNQVQLWLVGQHG---EAALGKRLWP--ARGETE-LKVEYVE 54  
Db 1 MPSYTVVTWTSQWAGTDDDIYLSLVGSAGCSEKHLDDKPFYNDFERGAVDSYDVTVD 60  
QY 55 YLGPFLFKVLRKXHLKDDAWFCNWSVQGGAGDEVFPFCYRWVGVNGVLSLPGTGRT 114  
Db 61 ELGEIQLVRIEKRKYWLNDWYLYITLKP-HGDIIEFPFCYRWITGDVEVVLDRGAKL 119  
QY 115 VGEDPQGLFOKHREBELERKLYRWGNWKGILLINMAGAKLYDLPVDERFLEDKRVDFE 174  
Db 120 ARDDQIHLKQHRKELETRQYRWEMWNPFPFLSIDAKCHKDLPRIQDFSEKGVDFV 179  
QY 175 VSLAKGLADLAIKSLNVL-TCKDLDNFRIFWCGSKLAERVRDSWKEDALFCYQFLN 233  
Db 180 LNYSKAMENLFINRPMHMFQSSWDFADFEKIFVKISNTISERVNHNQEDLMFCYQFLN 239  
QY 234 GANPVVLSRAHLPARLVFPQMBEL-----QAQLEKELEGTLPRADFSLLDGIKAN-VI 288  
Db 240 GCNPVLIIRCTELPEKLPVTTEMVECSLERQLSLEQVQOQGNIFIVDFELLDGIDANKTD 299  
QY 289 LCSQQLAALPLVMLKLPDQKLLPMVIOL-QLPRTGSPPPPLFLPTDPPMAWLLAKCVR 347  
Db 300 PCTLQFLAAPICLLYLNANKLIVPAIQNLQIP---GDENPFLPSDAKYDWLLAKIWR 356  
QY 348 SSDFQHLQSHLLRGLHMAEIVVATWRCPLSIHPIFKLIIPHLYRTLEINVRARTGLV 407  
Db 357 SSDFHVHTIITHLRTHLVSEVFGIAMYRQLPAVHIPFKLLVAHVFTIAINTKAREQLI 416  
QY 408 SDMGIFDQIMSTGGGHVQLLKQAAGAFITYSSFCPPDLDLADRLGLG---VKSSFYAQQAL 464  
Db 417 CECGLFDKANATGGGHVQVQRAMKDLTYASLCFPEAKARGMESKEDIPIYFYRDDGL 476  
QY 465 RLWELIYRVEGIVSLHYKTVAVKDDPELQWCREITEIGLQGAQDRGFPVSLQARDQV 524  
Db 477 LWWEAIRFTAEVNDIYEGDQVVEEDPELQFVNDVYVYGMGRKSSGFPKSVKSRBQL 536  
QY 525 CHFVTCMCTCGHASVHLGQDWYSVVPNAPCTMRLPPPTTKD-ATLETWMTLPNPH 583  
Db 537 SEYLVITFTASAQAANVFGYDWCSPNAPPTMRAPPPTAKGVVITIEQIVDTLPDRG 596  
QY 584 QASLQMSITWQLGRQPVVAVQHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKL 643  
Db 597 RSCWHLGAWALSQFQENELFLGMYPEEHFIEKPVKEAMARFKNLEIVSVIAERNKK 656  
QY 644 DMPYELRPSVVENSVAI 661  
Db 657 QLPYYLSPDRIPNSVAI 674

## RESULT 14

US-10-240-305-16  
; Sequence 16, Application US/10240305  
; Publication No. US20030162193A1  
; GENERAL INFORMATION:  
; APPLICANT: GLAXO GROUP LIMITED  
; APPLICANT: ANDERSON, WAYNE H.  
; APPLICANT: EDWARDS, Lisa D.  
; APPLICANT: EMMETT, Amanda H.  
; APPLICANT: PILLAI, Sreekumar  
; APPLICANT: SPRANKEL, Catherine S.  
; TITLE OF INVENTION: Medicine Response Assay in Respiratory Disease  
; FILE REFERENCE: P03958 & P04254  
; CURRENT APPLICATION NUMBER: US/10/240,305  
; CURRENT FILING DATE: 2001-04-17  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 16  
; LENGTH: 663  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-240-305-16

Query Match 35.9%; Score 1261.5; DB 14; Length 663;  
Best Local Similarity 39.6%; Pred. No. 1.8e-115;  
Matches 262; Conservative 136; Mismatches 242; Indels 21; Gaps 11;

QY 18 SNNOQLWLVGQHG---EAALGKRLWP--ARGETE-LKVEYVEYVGLPLFKVLRKXHLK 71  
Db 7 TDDIYLSLVGSAGCSEKHLDDKPFYNDFERGAVDSYDVTVDDELGEIQLVRIEKRKYWL 66  
QY 72 DDWFCNWSVQGGAGDEVFPFCYRWVGVNGVLSLPGTGRTVGEDPQGLFOKHREBEL 131  
Db 67 NDDWYLYITLKP-HGDIIEFPFCYRWITGDVEVVLDRGAKLARDDDQIHLKQHRREL 125  
QY 132 EERKLYRWGNWKGILLINMAGAKLYDLPVDERFLEDKRVDFEVLAKGLADLAIKDSL 191  
Db 126 ETRQYRWEMWNPFPFLSIDAKCHKDLPRIQDFSEKGVDFVLYNYSKAMENLFINRPMH 185  
QY 192 VL-TCKDLDNFRIFWCGSKLAERVRDSWKEDALFCYQFLNGANPVVLSRAHLPARL 250  
Db 186 MFQSSWDFADFEKIFVKISNTISERVNHNQEDLMFCYQFLNGCNPVLIIRCTELPEKL 245  
QY 251 VFPQMBEL-----QAQLEKELEGTLFEADFSLLDGIKAN-VILCSQQLAALPLVMLKIQ 305  
Db 246 PVTTEMVECSLERQLSLEQVQOQGNIFIVDFELLDGIDANKTDPTLQFLAAPICLLYKN 305  
QY 306 PDGKLLPMVIOL-QLPRTGSPPPPLFLPTDPPMAWLLAKCVRSSDPOLHELOSHLLRGLH 364  
Db 306 LANKIVPAIQNLQIP---GDENPFLPSDAKYDWLLAKIWRSSDPFHVHTIITHLRTH 362  
QY 365 LMAEIVVATWRCPLSIHPIFKLIIPHLYRTLEINVRARTGLVSDMGIFDQIMSTGGGH 424  
Db 363 LVSEVFGIAMYRQLPAVHIPFKLLVAHVFTIAINTKAREQLICECGLFDKANATGGGH 422  
QY 425 VOLKQAGAFITYSSFCPPDLDLADRLGLG---VKSSFYAQQALRLWEIYRYVEGIVSLH 481  
Db 423 VQVQRAMKDLTYASLCFPEAKARGMESKEDIPIYFYRDDGLLWWEAIRFTAEVNDIY 482  
QY 482 YKTDVAVKDDPELQWCREITEIGLQGAQDRGFPVSLQARDQVCHVFTWMTCTTCTGQHAS 541  
Db 483 YEGQVVEEDPELQFVNDVYVYGMGRKSSGFPKSVKSRBQLSEYLTWVITFTASAQA 542  
QY 542 VHLQGLDWSVVPNAPCTMRLPPPTTKD-ATLETWMTLPNPHQASLQMSITWQLGRQPV 600  
Db 543 VNFQYDWCSPNAPPTMRAPPPTAKGVVITIEQIVDTLPDRGSCWHLGAWALSQFQE 602  
QY 601 VMVAVQHEEYFSGPEPKAVLKKFRELAALDKIEIRNAKLDMPEYELRPSVVENSVA 660  
Db 603 NELFLGMYPEEHFIEKPVKEAMARFKNLEIVSVIAERNKKQLPYIYLSLSPDRIPNSVA 662





GenCore version 5.1.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 11:52:27 ; Search time 6694.65 Seconds

(without alignment)  
18330.926 Million cell updates/sec

Title: US-10-688-676A-3

Perfect score: 3224

Sequence: 1 cagcttcagtagagagcta.....gtcataaatgattcattcc 3224

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_hic:\*

4: gb\_est3:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_gsei:\*

9: gb\_gsei2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3218.4	99.8	3269	3 AK028724	AK028724 Mus muscu
2	1101	34.2	2965	3 BC033294	BC033294 Homo sapi
3	1041.2	32.3	2612	3 AK076343	AK076343 Mus muscu
4	704.4	21.8	720	9 BX972732	BX972732 Reverse s
5	641	19.9	659	5 BP766317	BP766317
6	606	18.8	655	1 AV241044	AV241044 AV241044
7	586.8	18.2	648	2 BB613007	BB613007 BB613007
8	578.4	17.9	892	4 BG743633	BG743633 602633993
9	571.8	17.7	833	4 BG675395	BG675395 602621712
10	571.6	17.7	2136	9 AY415194	AY415194 Homo sapi
11	565.2	17.6	685	2 BB612677	BB612677 BB612677
12	558.8	17.3	876	4 BG674800	BG674800 602620931
13	558.6	17.3	2136	9 AY415196	AY415196 Mus muscu
14	539	16.7	863	4 BG696031	BG696031 602658180
15	529.8	16.4	875	5 BX371550	BX371550 BX371550
16	527.8	16.4	840	4 BG740579	BG740579 602633094
17	525.6	16.3	732	6 CB518927	CB518927 UI-M-GH0-
18	525.6	16.3	832	4 BG698185	BG698185 602660087
19	524.2	16.3	916	4 BG739941	BG739941 602630892
20	520.6	16.1	865	4 BG742611	BG742611 602633205
21	520.6	16.1	881	5 BX371551	BX371551 BX371551
22	517.6	16.1	893	4 BG741964	BG741964 602633405
23	516.2	16.0	845	4 BG740763	BG740763 602632735
24	512.4	15.9	843	4 BG739709	BG739709 602630403

25	495.2	15.4	761	4 BG740246	BG740246 602630664
26	492.4	15.3	494	2 BF789593	BF789593 602103693
27	491.4	15.2	697	4 BG739860	BG739860 602630592
28	478	14.8	1057	5 BX343731	BX343731 Pan trogl
29	464.6	14.4	2125	9 AY415195	AY415195 Pan trogl
30	463.8	14.4	885	4 BG743327	BG743327 602634623
31	460.2	14.3	637	1 AV241224	AV241224 AV241224
32	453	14.1	464	1 AA117154	AA117154 mo60d12.r
33	436.6	13.5	605	4 BF489877	BF489877 603031627
34	421.2	13.1	580	5 BP326139	BP326139 BP326139
35	414.6	12.9	867	4 BG697910	BG697910 602661342
36	414	12.8	850	4 BG675344	BG675344 602621653
37	409.8	12.7	678	6 CA405703	CA405703 1001852 H
38	396.8	12.3	1826	3 BC040450	BC040450 Homo sapi
39	396.8	12.3	1844	3 BC034464	BC034464 Homo sapi
40	391.4	12.1	585	5 BP306241	BP306241 BP306241
41	366	11.4	377	1 AA117205	AA117205 mo61e01.r
42	362.2	11.2	862	4 BG740949	BG740949 602634555
43	357.2	11.1	583	6 CD610811	CD610811 56004502H
44	351	10.9	604	6 CD610812	CD610812 56004502J
45	349.4	10.8	601	7 CV029325	CV029325 8061 Full

## ALIGNMENTS

RESULT 1	AK028724	3269 bp	mRNA	linear	HTC 03-APR-2004
LOCUS	AK028724	Mus musculus	10 days neonate skin cDNA, RIKEN full-length enriched library, clone:4732445G22	product:arachidonate 15-lipoxygenase,	
DEFINITION	AK028724	second type, full insert sequence.			
ACCESSION	AK028724	1	GI:26324661		
VERSION	AK028724	1	GI:26324661		
KEYWORDS	HTC; CAP trapper.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Carninci, P. and Hayashizaki, Y.				
TITLE	High-efficiency full-length cDNA cloning				
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)				
MEDLINE	99279253				
PUBMED	10349636				
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.				
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes				
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)				
MEDLINE	20499374				
PUBMED	11042159				
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuana, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.				
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer				
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)				
MEDLINE	20530913				
PUBMED	11076861				
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.				
TITLE	Functional annotation of a full-length mouse cDNA collection				
JOURNAL	Nature 409, 685-690 (2001)				
PUBMED					
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research				

TITLE JOURNAL REFERENCE AUTHORS	Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 3269)		QY Db	65 61	GGGGAAGCCTGTGGGGCTGGCACAATGGACAAAGTGTCTGTGAGCATCTGTGGGAACCCAC 124 GGGGAAGCCTGTGGGGCTGGCACAATGGACAAAGTGTCTGTGAGCATCTGTGGGAACCCAC 120	
	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.				125 GGAGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGAGTTGAGCCCGGTCTGNA 184 121 GGAGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGAGTTGAGCCCGGTCTGNA 180 185 GAAGATTCGAGGTGACGCTTCCCAGGACGTAGGACATGTGCTGATGCTGGAGTCCAC 244 181 GAAGATTCGAGGTGACGCTTCCCAGGACGTAGGACATGTGCTGATGCTGGAGTCCAC 240 245 AAAGCACCCTGGAGGTGCTCCCTCCCGCTTATGTCTTCCGTTCTGATGCTGCTTCTGC 304 241 AAAGCACCCTGGAGGTGCTCCCTCCCGCTTATGTCTTCCGTTCTGATGCTGCTTCTGC 300 305 CGCTGTTGAGAGTGGAGTGGCTACCTGGGGCTGACATCCACTTCCCTCTGTTATCAGTGG 364 301 CGCTGTTGAGAGTGGAGTGGCTACCTGGGGCTGACATCCACTTCCCTCTGTTATCAGTGG 360 365 CTGGAAGGGGGGGGAGCTGTGTCTGAGAGGGGAGCAGCAAGGTGTCTTGGCAAGAC 424 361 CTGGAAGGGGGGGGAGCTGTGTCTGAGAGGGGAGCAGCAAGGTGTCTTGGCAAGAC 420 425 CATCACTTACATCTGAGGATCAGCCAGAGGAGTGTGATCCAGGACAGAGTGTGATC 484 421 CATCACTTACATCTGAGGATCAGCCAGAGGAGTGTGATCCAGGACAGAGTGTGATC 480 485 AGCTGGAAGATTCATTTGAAGTGGCTGCTGCTGCTGACCAAGAGTGTGAAAGAC 544 481 AGCTGGAAGATTCATTTGAAGTGGCTGCTGCTGCTGACCAAGAGTGTGAAAGAC 540 545 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTTTAAAGCCAC 604 541 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTTTAAAGCCAC 600 605 TCCCGGTATAGCGAGCTGAAAGTCAAAGGGCTCTTGGACCGCAGCAGGACTCTGGAAGG 664 601 TCCCGGTATAGCGAGCTGAAAGTCAAAGGGCTCTTGGACCGCAGCAGGACTCTGGAAGG 660 665 CTGAGGAGATGAGAGGCTGTTAACTTCGCAAGACTCCAGGACGAGAGTATGTGTT 724 661 CTGAGGAGATGAGAGGCTGTTAACTTCGCAAGACTCCAGGACGAGAGTATGTGTT 720 725 GCACATCGCAGGAAGATGCTTCTTCCCTCCAGTTCCTAAATGGCATCAACCCGGTC 784 721 GCACATCGCAGGAAGATGCTTCTTCCCTCCAGTTCCTAAATGGCATCAACCCGGTC 780 785 CTGATTCGCGCTGTCAAGTCTCCCAAAACAATTTCCCGGTCACTGATGAATGGTGCC 844 781 CTGATTCGCGCTGTCAAGTCTCCCAAAACAATTTCCCGGTCACTGATGAATGGTGCC 840 845 CGAGTGTGGGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904 841 CGAGTGTGGGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 900 905 GTGATCATGCGATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCTCAGTTC 964 901 GTGATCATGCGATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCTCAGTTC 960 965 TCTGAGGCGCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAT 1024 961 TCTGAGGCGCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAT 1020 1025 GCCATCCAGCTCAACAGACTCCCGGGCCAGAACCCCATCTTCTGCGCCAGCATGAC 1084 1021 GCCATCCAGCTCAACAGACTCCCGGGCCAGAACCCCATCTTCTGCGCCAGCATGAC 1080 1085 ACGTGGGAGTGTCTGCGCAAGACCTGGGTTCCCAATCTCTGAGTCTTACATCATGAG 1144 1081 ACGTGGGAGTGTCTGCGCAAGACCTGGGTTCCCAATCTCTGAGTCTTACATCATGAG 1140	
TITLE JOURNAL	Direct Submission Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)		QY	305	CGCTGTTGAGAGTGGAGTGGCTACCTGGGGCTGACATCCACTTCCCTCTGTTATCAGTGG 364 301 CGCTGTTGAGAGTGGAGTGGCTACCTGGGGCTGACATCCACTTCCCTCTGTTATCAGTGG 360 365 CTGGAAGGGGGGGGAGCTGTGTCTGAGAGGGGAGCAGCAAGGTGTCTTGGCAAGAC 424 361 CTGGAAGGGGGGGGAGCTGTGTCTGAGAGGGGAGCAGCAAGGTGTCTTGGCAAGAC 420 425 CATCACTTACATCTGAGGATCAGCCAGAGGAGTGTGATCCAGGACAGAGTGTGATC 484 421 CATCACTTACATCTGAGGATCAGCCAGAGGAGTGTGATCCAGGACAGAGTGTGATC 480 485 AGCTGGAAGATTCATTTGAAGTGGCTGCTGCTGCTGACCAAGAGTGTGAAAGAC 544 481 AGCTGGAAGATTCATTTGAAGTGGCTGCTGCTGCTGACCAAGAGTGTGAAAGAC 540 545 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTTTAAAGCCAC 604 541 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTTTAAAGCCAC 600 605 TCCCGGTATAGCGAGCTGAAAGTCAAAGGGCTCTTGGACCGCAGCAGGACTCTGGAAGG 664 601 TCCCGGTATAGCGAGCTGAAAGTCAAAGGGCTCTTGGACCGCAGCAGGACTCTGGAAGG 660 665 CTGAGGAGATGAGAGGCTGTTAACTTCGCAAGACTCCAGGACGAGAGTATGTGTT 724 661 CTGAGGAGATGAGAGGCTGTTAACTTCGCAAGACTCCAGGACGAGAGTATGTGTT 720 725 GCACATCGCAGGAAGATGCTTCTTCCCTCCAGTTCCTAAATGGCATCAACCCGGTC 784 721 GCACATCGCAGGAAGATGCTTCTTCCCTCCAGTTCCTAAATGGCATCAACCCGGTC 780 785 CTGATTCGCGCTGTCAAGTCTCCCAAAACAATTTCCCGGTCACTGATGAATGGTGCC 844 781 CTGATTCGCGCTGTCAAGTCTCCCAAAACAATTTCCCGGTCACTGATGAATGGTGCC 840 845 CGAGTGTGGGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904 841 CGAGTGTGGGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 900 905 GTGATCATGCGATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCTCAGTTC 964 901 GTGATCATGCGATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCTCAGTTC 960 965 TCTGAGGCGCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAT 1024 961 TCTGAGGCGCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAT 1020 1025 GCCATCCAGCTCAACAGACTCCCGGGCCAGAACCCCATCTTCTTCTGCGCCAGCATGAC 1084 1021 GCCATCCAGCTCAACAGACTCCCGGGCCAGAACCCCATCTTCTTCTGCGCCAGCATGAC 1080 1085 ACGTGGGAGTGTCTGCGCAAGACCTGGGTTCCCAATCTCTGAGTCTTACATCATGAG 1144 1081 ACGTGGGAGTGTCTGCGCAAGACCTGGGTTCCCAATCTCTGAGTCTTACATCATGAG 1140	
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers 1. 3269 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="PANTOM DB:4732445G22" /db_xref="taxon:10090" /clone="4732445G22" /tissue_type="skin" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="10 days neonate" 31. 2064 /note="unnamed protein product; arachidonate 15-lipoxygenase, second type (MGI:1098228, GB Y14696, evidence: BLASTN, 100%, match=3203) putative" /codon_start=1 /protein_id="BAC26085.1" /db_xref="GI:26324662" /translation="MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHGKE FSAGAEDEFVLPQDVGLVLMRVHKAPPEVSLPMFRSDAWFCRWFELWLPAA LHPCYQWLEAGELVREGAAKVSQDHPHTLPQORKELESQKRWKTYTGWP RCLDHETVKDLNLTYSAMKNAKLFKHAHSYTELKGLDLRGLMSRLREMLRF NFKTPAAEYVFAHQEDAPFASQFLNGINPVLIRCHSLPNFVPTBWMVAPLVGP TSLOALEKSLPLVDHGLTSGVHTNLLNGKQFSAAPMTLLHQSNGSGLLPIALQ KQTPGDPNIFLPSDDTWLLAKTWNRNSEYIIEAHTLLHHLHLEVEFALATLRQ LPRCHPLFKLLIRYTHINTLARELVAPGLIDKSTGLGTGGSFSLIKRNMELQ NSVLCLPEDIPIARGVEDIPGYVITDDGQIMGAIKSFVSEIVSYIYPSDTSVQDDQE LQAWREIFSEGLFGSMPSLLDTRALVQYITWVFTCSAKHAAVSSQFDSQV WPNLPPTMQLPPTPSKQARPEFIATLPAVNSSYHILALMLLSAPGQORPLGHY PDEHTEDAPRSVAAFQRLQISKIRERNRGLALPYTLLDPLLIENSVI"		QY	305	CGCTGTTGAGAGTGGAGTGGCTACCTGGGGCTGACATCCACTTCCCTCTGTTATCAGTGG 364 301 CGCTGTTGAGAGTGGAGTGGCTACCTGGGGCTGACATCCACTTCCCTCTGTTATCAGTGG 360 365 CTGGAAGGGGGGGGAGCTGTGTCTGAGAGGGGAGCAGCAAGGTGTCTTGGCAAGAC 424 361 CTGGAAGGGGGGGGAGCTGTGTCTGAGAGGGGAGCAGCAAGGTGTCTTGGCAAGAC 420 425 CATCACTTACATCTGAGGATCAGCCAGAGGAGTGTGATCCAGGACAGAGTGTGATC 484 421 CATCACTTACATCTGAGGATCAGCCAGAGGAGTGTGATCCAGGACAGAGTGTGATC 480 485 AGCTGGAAGATTCATTTGAAGTGGCTGCTGCTGCTGACCAAGAGTGTGAAAGAC 544 481 AGCTGGAAGATTCATTTGAAGTGGCTGCTGCTGCTGACCAAGAGTGTGAAAGAC 540 545 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTTTAAAGCCAC 604 541 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTTTAAAGCCAC 600 605 TCCCGGTATAGCGAGCTGAAAGTCAAAGGGCTCTTGGACCGCAGCAGGACTCTGGAAGG 664 601 TCCCGGTATAGCGAGCTGAAAGTCAAAGGGCTCTTGGACCGCAGCAGGACTCTGGAAGG 660 665 CTGAGGAGATGAGAGGCTGTTAACTTCGCAAGACTCCAGGACGAGAGTATGTGTT 724 661 CTGAGGAGATGAGAGGCTGTTAACTTCGCAAGACTCCAGGACGAGAGTATGTGTT 720 725 GCACATCGCAGGAAGATGCTTCTTCCCTCCAGTTCCTAAATGGCATCAACCCGGTC 784 721 GCACATCGCAGGAAGATGCTTCTTCCCTCCAGTTCCTAAATGGCATCAACCCGGTC 780 785 CTGATTCGCGCTGTCAAGTCTCCCAAAACAATTTCCCGGTCACTGATGAATGGTGCC 844 781 CTGATTCGCGCTGTCAAGTCTCCCAAAACAATTTCCCGGTCACTGATGAATGGTGCC 840 845 CGAGTGTGGGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904 841 CGAGTGTGGGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 900 905 GTGATCATGCGATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCTCAGTTC 964 901 GTGATCATGCGATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCTCAGTTC 960 965 TCTGAGGCGCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAT 1024 961 TCTGAGGCGCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAT 1020 1025 GCCATCCAGCTCAACAGACTCCCGGGCCAGAACCCCATCTTCTTCTGCGCCAGCATGAC 1084 1021 GCCATCCAGCTCAACAGACTCCCGGGCCAGAACCCCATCTTCTTCTGCGCCAGCATGAC 1080 1085 ACGTGGGAGTGTCTGCGCAAGACCTGGGTTCCCAATCTCTGAGTCTTACATCATGAG 1144 1081 ACGTGGGAGTGTCTGCGCAAGACCTGGGTTCCCAATCTCTGAGTCTTACATCATGAG 1140	
FEATURES source	Query Match 99.8%; Score 3218.4; DB 3; Length 3269; Best Local Similarity 100.0%; Pred. No. 0; Matches 3219; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 5 TTGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 64 1 TGGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 60		QY	5	TTGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 64 TGGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 60	
CDS			QY	5	TTGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 64 TGGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 60	
ORIGIN	Query Match 99.8%; Score 3218.4; DB 3; Length 3269; Best Local Similarity 100.0%; Pred. No. 0; Matches 3219; Conservative 0; Mismatches 1; Indels 0; Gaps 0; 5 TTGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 64 1 TGGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 60		QY	5	TTGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 64 TGGCAGTAGAGCTAACTGTCAGGAGGATGGCGAATGCGAGGTGAGAGTATCCACG 60	

QY 1145 GCTGTACACATCTCTGTCATGCCCATCTGATTCCAGAAAGTCTTTGCTTGGCCACATTA 1204  
DB 1141 GCTGTACACATCTCTGTCATGCCCATCTGATTCCAGAAAGTCTTTGCTTGGCCACATTA 1200  
QY 1205 CGTCAGCTCCCTAGGTGTCAACCTCTCTTCAAGCTATTGATTCTCTCAATTCGGTACACA 1264  
DB 1201 CGTCAGCTCCCTAGGTGTCAACCTCTCTTCAAGCTATTGATTCTCTCAATTCGGTACACA 1260  
QY 1265 CTGCACATCAACACGCTTGGCCGGAGCTGCTGCTGGCCCTGGGAAGTGTGATAGACAAG 1324  
DB 1261 CTGCACATCAACACGCTTGGCCGGAGCTGCTGCTGGCCCTGGGAAGTGTGATAGACAAG 1320  
QY 1325 TCCACAGGCTTGGCACTGGGGGATTTCTGACCTGATAAAGAGAAAATGAGAGCAGCTG 1384  
DB 1321 TCCACAGGCTTGGCACTGGGGGATTTCTGACCTGATAAAGAGAAAATGAGAGCAGCTG 1380  
QY 1385 AACTACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCCA 1444  
DB 1381 AACTACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCCA 1440  
QY 1445 GGCTACTATTACCGAGATGATGGGATGAGATCTGGGGGGCAATAAAGAGCTTTGTCTCT 1504  
DB 1441 GGCTACTATTACCGAGATGATGGGATGAGATCTGGGGGGCAATAAAGAGCTTTGTCTCT 1500  
QY 1505 GAAATAGTCAGCATCTATCTCAAGTGACATCCGTCGAAGATGACCAAGAGCTCCAG 1564  
DB 1501 GAAATAGTCAGCATCTATCTCAAGTGACATCCGTCGAAGATGACCAAGAGCTCCAG 1560  
QY 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCCGAGAAAGCTCAAGGTATGCC 1624  
DB 1561 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCCGAGAAAGCTCAAGGTATGCC 1620  
QY 1625 TCCTTTGTTGGATAACCCGGGAAGCCCTGTCAGTATATCAACATGGTGATATCACTTCG 1684  
DB 1621 TCCTTTGTTGGATAACCCGGGAAGCCCTGTCAGTATATCAACATGGTGATATCACTTCG 1680  
QY 1685 TCAGCAGCATGACGTCTCAGTTCAGGCGAGTTCGACTCTTGTGTTGGATGCCAAT 1744  
DB 1681 TCAGCAGCATGACGTCTCAGTTCAGGCGAGTTCGACTCTTGTGTTGGATGCCAAT 1740  
QY 1745 CTGCCACCTACATGACGTACCAACCACTTCTTCCAAAGCGCAGGCCCGGCTGAGAGT 1804  
DB 1741 CTGCCACCTACATGACGTACCAACCACTTCTTCCAAAGCGCAGGCCCGGCTGAGAGT 1800  
QY 1805 TTCTATAGCCAAGCTCCAGAGTTAATTCGTAAGTTATCATCATATGCTCTCTGGCTG 1864  
DB 1801 TTCTATAGCCAAGCTCCAGAGTTAATTCGTAAGTTATCATCATATGCTCTCTGGCTG 1860  
QY 1865 CTAAGCGCAGAACCTGGGGACCAAGGCCCTGGGCCACTATCCAGATGAACACTTCACA 1924  
DB 1861 CTAAGCGCAGAACCTGGGGACCAAGGCCCTGGGCCACTATCCAGATGAACACTTCACA 1920  
QY 1925 GAGGATGCCCCCGGCGAAGCGTGGCTCTCCAGAGAAAGCTGATCCAGATCTCCAAG 1984  
DB 1921 GAGGATGCCCCCGGCGAAGCGTGGCTCTCCAGAGAAAGCTGATCCAGATCTCCAAG 1980  
QY 1985 GGCAATCAGGGAGAGAAACCGAGGCTTGSCACTGCCCCTACACTTGGATCCTCCCTC 2044  
DB 1981 GGCAATCAGGGAGAGAAACCGAGGCTTGSCACTGCCCCTACACTTGGATCCTCCCTC 2040  
QY 2045 ATTGAGAACAGTGTCTCATCTTAACATCTTGGAGAGACAGTCTGTGTGACATATAGAA 2104  
DB 2041 ATTGAGAACAGTGTCTCATCTTAACATCTTGGAGAGACAGTCTGTGTGACATATAGAA 2100  
QY 2105 CTCCTTGACCAAGCTCTCCAGGCTAAGTCCCGGTATGCTTCTCTGGACACCAAGCCCC 2164  
DB 2101 CTCCTTGACCAAGCTCTCCAGGCTAAGTCCCGGTATGCTTCTCTGGACACCAAGCCCC 2160  
QY 2165 ATCTTTACACACACACACACACACACCTTAATAAATAAGAAACAGAAAAACCTAAACT 2224  
DB 2161 ATCTTTACACACACACACACACACACCTTAATAAATAAGAAACAGAAAAACCTAAACT 2220  
QY 2225 CCCACAGAAAGGCAAGATCTCTACACAGCAGAGAGGCCAATCCAAATGTTTGGAGACCCCTGAGC 2284

## RESULT 2

BC033294 2965 bp mRNA linear HTC 19-NOV-2003  
LOCUS Homo sapiens arachidonate 15-lipoxygenase, second type, mRNA (cdna  
DEFINITION clone IMAGE:4780620), with apparent retained intron.

DB 2221 CCCACAGAAAGCAAGATCTACACAGCAGAGAGCCATCCAAATGTTTGGAGACCCCTGAGC 2280  
QY 2285 TTCAGCTCTGATTAAACGGCTTTGCTGGTTTGTCTTCTATTCCATTAAACCAATGAC 2344  
DB 2281 TTCAGCTCTGATTAAACGGCTTTGCTGGTTTGTCTTCTATTCCATTAAACCAATGAC 2340  
QY 2345 GGTAAACAGAAAGCAACAGACCCCTGGTTCACTGCAAAAGCCACTGAGATCTCACCCCTCAC 2404  
DB 2341 GGTAAACAGAAAGCAACAGACCCCTGGTTCACTGCAAAAGCCACTGAGATCTCACCCCTCAC 2400  
QY 2405 CTGACACAAAGGCGAGCTATCATACAGGCTTATCAGGAAACACAGAAATTTGTCCAAATCAA 2464  
DB 2401 CTGACACAAAGGCGAGCTATCATACAGGCTTATCAGGAAACACAGAAATTTGTCCAAATCAA 2460  
QY 2465 GCCTACCCACTAGTTCATCGTACCTACAGACCTCACTGGCATGCTTTAGCTTTGAGA 2524  
DB 2461 GCCTACCCACTAGTTCATCGTACCTACAGACCTCACTGGCATGCTTTAGCTTTGAGA 2520  
QY 2525 AGGGATTACTGGAGTCAGGTACGAAAGAGGACAGGACGAGGATGGCTCCATGTGGA 2584  
DB 2521 AGGGATTACTGGAGTCAGGTACGAAAGAGGACAGGACGAGGATGGCTCCATGTGGA 2580  
QY 2585 AGAACATATCTGCTTTCCAGATGACCCAGGCTAGCTCACAGCCATGTCTCAATCTCTAACTC 2644  
DB 2581 AGAACATATCTGCTTTCCAGATGACCCAGGCTAGCTCACAGCCATGTCTCAATCTCTAACTC 2640  
QY 2645 CAGAGGCTCTTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACCACTAGACACCA 2704  
DB 2641 CAGAGGCTCTTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACCACTAGACACCA 2700  
QY 2705 AAATTAATCTTTTAAAGAGAGGAATGGGCTGAGAGATGGCTCAGCGGTAAAGAGCAC 2764  
DB 2701 AAATTAATCTTTTAAAGAGAGGAATGGGCTGAGAGATGGCTCAGCGGTAAAGAGCAC 2760  
QY 2765 TGACGTCTCTTCCAGAGATCTGAGTTCAATTCACAGCAACCACTGCTGCTCACACACC 2824  
DB 2761 TGACGTCTCTTCCAGAGATCTGAGTTCAATTCACAGCAACCACTGCTGCTCACACACC 2820  
QY 2825 ATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGCGACAGTGTATGCA 2884  
DB 2821 ATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGCGACAGTGTATGCA 2880  
QY 2885 CATATATAAATAAATAAATCTTTAAATAAACAAGAGAGAGGAGCATGTACCAATT 2944  
DB 2881 CATATATAAATAAATAAATCTTTAAATAAACAAGAGAGAGGAGCATGTACCAATT 2940  
QY 2945 TCTACCTCACTTCTTCAAGCCACCCCTTAAAGTGAATTCGTAACCCAGGTCCTCTTGC 3004  
DB 2941 TCTACCTCACTTCTTCAAGCCACCCCTTAAAGTGAATTCGTAACCCAGGTCCTCTTGC 3000  
QY 3005 AGAGAGTTAGAAGATATTCTCAAACCTCTAATACCTTCACTCTAAATCCATCTTCATT 3064  
DB 3001 AGAGAGTTAGAAGATATTCTCAAACCTCTAATACCTTCACTCTAATCCATCTTCATT 3060  
QY 3065 CCAAAATTCAAATATTTATATACATCTCCAGTTTGGTGGTGGGGTGTGTTTTGT 3124  
DB 3061 CCAAAATTCAAATATTTATATACATCTCCAGTTTGGTGGTGGGGTGTGTTTTGT 3120  
QY 3125 TTGGTTTGGTTTGGTGGGGTGTGTTTTGTGTTTTGTTTTGTTTTCTCTGCTTCAGA 3184  
DB 3121 TTGGTTTGGTTTGGTGGGGTGTGTTTTGTGTTTTGTTTTGTTTTCTCTGCTTCAGA 3180  
QY 3185 CTCCTAGGACGTTCAATTAATGTATAAATGAGTTCAATTC 3224  
DB 3181 CTCCTAGGACGTTCAATTAATGTATAAATGAGTTCAATTC 3220

ACCESSION	BC033294	Matches 1674;	Conservative 0;	Mismatches 415;	Indels 294;	Gaps 3;
VERSION	BC033294.1	GI:23959040				
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
AUTHORS	1 (bases 1 to 2965) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.					
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences					
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)					
MEDLINE	22388257					
PUBMED	12477932					
REFERENCE	2 (bases 1 to 2965)					
AUTHORS	Strausberg, R.					
TITLE	Direct Submission					
JOURNAL	Submitted (26-JUN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA					
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>					
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgabs-r@mail.nih.gov">cgabs-r@mail.nih.gov</a> Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a> Contact: <a href="mailto:amg@bcm.tmc.edu">amg@bcm.tmc.edu</a> Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.					
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAK Plate: 29 Row: m Column: 14 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557308 This clone has the following problem: retained intron. Location/Qualifiers 1. .2965 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:4780620" /tissue_type="Skin, normal" /clone_lib="NCI CGAP_Skn3" /lab_host="DH10B" /note="Vector: pCMV-SPORT6.1"					
source						
ORIGIN	Query Match 34.2%; Score 1101; DB 3; Length 2965; Best Local Similarity 70.2%; Pred. No. 6.8e-279;					







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Query Match      21.8%; Score 704.4; DB 9; Length 720;
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Matches 708; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2391 GATCTCAGCCTCAGCTGACACAAAGGAGCTATCATACAGGCTTATCAGGAAACAGAGAA 2450
Dbb|||||
7 GATCTCAGCCTCAGCTGACACAAAGGAGCTATCATACAGGCTTATCAGGAAACAGAGAA 66

2451 TTGTGCCAATCAAGCTTACCCACTAGTGTCCATCTGACCTAGCAGCTCAGACTGGCATG 2510
Dbb|||||
67 TTGTGCCAATCAAGCTTACCCACTAGTGTCCATCTGACCTAGCAGCTCAGACTGGCATG 126
Dbb|||||

2511 CTTTGTAGCTTTGAGAGGGATTACTGAGTCAAGTACAGTACAGAGAGAGAGAGAGGCA 2570
Dbb|||||
127 CTTTGTAGCTTTGAGAGGGATTACTGAGTCAAGTACAGTACAGAGAGAGAGAGAGGCA 186
Dbb|||||

2571 TGGCTCCATGTGGAAAGAACATATCTGCTCTTCCAGATGACAGGGTAGCTCAGGCCATG 2630
Dbb|||||
187 TGGCTCCATGTGGAAAGAACATATCTGCTCTTCCAGATGACAGGGTAGCTCAGGCCATG 246
Dbb|||||

2631 TGTCAATTTCACTCAGAGGCTCTAGTGGCCATGAAGACTCCAGGATTCAGGGGATAT 2690
Dbb|||||
247 TGTCAATTTCACTCAGAGGCTCTAGTGGCCATGAAGACTCCAGGATTCAGGGGATAT 306
Dbb|||||

2691 ACCAGTACACCAAAATATATCTTTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2750
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Dbb|||||

2751 GCGGTAAAGAGACACTGACTGCTCTTCCAGAGATCTGAGTTCAAATCCAGCAACACAT 2810
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2931 GACATGCTACCAATTTCTACCTCAGTCTTCTCAAGCCACCCCTAAAGTGAATTTGTAAC 2990
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547 GACATGCTACCAATTTCTACCTCAGTCTTCTCAAGCCACCCCTAAAGTGAATTTGTAAC 606
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2991 CAGGTCCCTTTGACAGAGATTGAGATATTTCTCAAACTCTAATACCTTCAATCTAA 3050
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Dbb|||||

3051 AATCATCTTCAATCCAAATTCGAATTTTATATACATCTCCAGTTGGTG 3104
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LOCUS BP766317 mouse (C57BL/6) pancreatic islet library with
DEFINITION recombination-based method Mus musculus cDNA clone mid10051 3',
mRNA sequence.
ACCESSION BP766317
VERSION BP766317.1 GI:50225015
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 659)
AUTHORS Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioka,H.,
Takeda,J., Ohara,O. and Seino,S.
```

TITLE Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray

JOURNAL Unpublished (2004)

COMMENT Contact: Susumu Seino  
Division of Cellular and Molecular Medicine  
Kobe University Graduate School of Medicine  
7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan  
Tel: 81-78-382-5360  
Fax: 81-78-382-5370  
Email: seino@med.kobe-u.ac.jp.

FEATURES  
Location/Qualifiers  
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Matches 641; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 2584 AAGACATATCTGCTTCCAGATGACCCAGGAGTGTCTCAGCCATGTCTATTCTAACT 2643  
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659 AAGACATATCTGCTTCCAGATGACCCAGGAGTGTCTCAGCCATGTCTATTCTAACT 600  
Dbb|||||  
2644 CCAGAGGTCTCTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACCAGTAGACACC 2703  
Dbb|||||  
599 CCAGAGGTCTCTAGTGGCCATGAAGACTCCAGGCAATTCAGGGGATATACCAGTAGACACC 540  
QY 2704 AAAATATATCTTTTAAAGAGAGAGAGATGGGCTGGAGAGATGGCTCAGCGGTTAAGAGCA 2763  
Dbb|||||  
539 AAAATATATCTTTTAAAGAGAGAGAGATGGGCTGGAGAGATGGCTCAGCGGTTAAGAGCA 480  
QY 2764 CTGACTGCTCTTCCAGAGATCTGAGTTCATTCGCCCAACCATGCTGGCTCAGACAC 2823  
Dbb|||||  
479 CTGACTGCTCTTCCAGAGATCTGAGTTCATTCGCCCAACCATGCTGGCTCAGACAC 420  
QY 2824 CATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGGAGAGAGTGTATGC 2883  
Dbb|||||  
419 CATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGGAGAGTGTATGC 360  
QY 2884 ACATATATAAATAAATAAATCTTTTAAATAAACAAGAGAGAGAGAGAGAGTGTATGCAT 2943  
Dbb|||||  
359 ACATATATAAATAAATAAATCTTTTAAATAAACAAGAGAGAGAGAGAGAGTGTATGCAT 300  
QY 2944 TTCTACCTCAGTCTTCTCAAGCCACCCCTAAAGTGAATTTGTGAACAGGTCCTCCCTTTG 3003  
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299 TTCTACCTCAGTCTTCTCAAGCCACCCCTAAAGTGAATTTGTGAACAGGTCCTCCCTTTG 240  
QY 3004 CAGAGAGTTAGAAGATATTTCTCAAACTCTAATACCTTCAATCTTCAATCTTCAATCTTCAAT 3063  
Dbb|||||  
239 CAGAGAGTTAGAAGATATTTCTCAAACTCTAATACCTTCAATCTTCAATCTTCAATCTTCAAT 180  
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Dbb|||||  
179 TCCAAATTTCAATATTTTATATACACTCTCCAGTTTGGTGGGTGAGGGTGTGTTTTTGG 120  
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119 TTGCTTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGG 60  
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TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nhl.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA library Preparation: Life Technologies, Inc.  
cDNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10635 row: j column: 23  
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/note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN  
Query Match 17.9%; Score 578.4; DB 4; Length 892;  
Best Local Similarity 79.3%; Pred. No. 5.6e-141;  
Matches 698; Conservative 0; Mismatches 181; Indels 1; Gaps 1;

QY 1099 GCTGGCCAGACCTGGGTTTCGCAATCTCAGATTTTACATPCCATGAGGCTGCACACATCT 1158  
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QY 1159 GCTGCATGCCATCTGATTCAGAGAGTCTTTGCCCTTGGCCACATTCAGTCACTGCTAG 1218  
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QY 1219 GTGTACCCCTCTTCACGCTATTGATTCCTCACATTTGGTACACAGTGCACATCAACAC 1278  
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QY 1279 GCTTGCCCGGAGCTGCTCGTTGCCCTCGGAGTTGATAGACAAATGCACAGGCTTGG 1338  
DB 181 ACTGCGCCGGAGCTGCTTATCGTCGACGGCAGGTGGTGGACAGTCCACAGGCATCGG 240

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QY 1459 AGATGATGGATGTCAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAATAGTCAGCAT 1518  
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QY 1519 CTACTATCCAGTGACACATCCGTCCAGATGACCAAGAGTCCAGGCTGGGTGAGGA 1578  
DB 421 CTACTACCCAAAGTATGATGCTGTCTCAAGATGACAGAGAGCTCCAGGCTGGGTGAGGA 480

QY 1579 GATCTTCTCTGAGGCTTCTCGGCGGAGAAAGCTCAGTATGCCCTCTCTTCTTGATAC 1638  
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QY 1639 CCGGGAAGCCCTGGTCCAGTATATCACCATGCTGATTAATTCAGTGTCCCAAGCATGC 1698  
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QY 1699 AGCTGTCACTCAGGCCAGTTCGACTTTGTGTGTGTGGATGCCCAATCTGCCACCTACCAT 1758  
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Db 601 GGCTGTCACTGAGGCGAGTTTGACTCTCTGTGTTGGATGCCCAACCTGCCACCCAGCAT 660

QY 1759 GCAGCTACCAACACACTACTTCCAAAGGCCAG-GCCCGGCCTGAGAGTTTTCATAGCCAGC 1817

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QY 1818 TCCACAGAGTTAAATTCGTCAAGTTATCAATCATCTCTCTGGTCTGTAAAGCGGAGAAC 1877

Db 721 TCCCACTCTGTCAGTGCCACATGTATGTATCTCTCTCTCTGTGTGTGACGAAGGAGC 780

QY 1878 CTGGGACCAAGGCCCTGGCCACTATCCAGATGAACACTTTCACAGAGGATGCCCCC 1937

Db 781 CTGGAGACCAAGGCCCTGGCCACTATCCAGATGAACACTTTCACAGAGGAGGCCCTCG 840

QY 1938 GCGAAGGCTGGCTGCCCTTCCAGAGAAAGCTCATCCAGAT 1977

Db 841 GCGAAGCATCGGCCACTTCCAGAGCGCTGACCAGAT 880

RESULT 9  
BG675395 833 bp mRNA linear EST 01-MAY-2001  
LOCUS 602621712F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4755122 5',  
DEFINITION mRNA sequence.  
ACCESSION BG675395  
VERSION BG675395.1 GI:13906791  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 833)  
NIH-MGC http://mgc.ncl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nhl.gov  
Tissue Procurement: James Cleaver, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA  
Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM10617 row: h column: 03  
High quality sequence stop: 828.

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Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.5kb. Library constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN  
Query Match 17.7%; Score 571.8; DB 4; Length 833;  
Best Local Similarity 82.1%; Pred. No. 3e-139;  
Matches 682; Conservative 0; Mismatches 147; Indels 2; Gaps 2;

QY 914 GGCATTTCTTGGAGTCCACACCAACATCTCATGGAAGAGCCCTCAGTTCTTCAGCC 973

Db 1 GGCATTTCTTGGAGTCCACACCAACATGTCTAATGGAAGAGCCCTCAGTTCTTCAGCC 60

QY 974 CGATGACCTCTGTATACACAGAGCTCAGGTCGCGACCCCTCTTCCCATTCGCCATCCAG 1033

Db 61 CCATGACCTCTGTATACACAGAGCCAGGCTCGGGCGCTCTGCTCTCGCCATCCAG 120

QY 1034 CTCAAACAGACTCCGGGCGCAGAACCCCATCTTCTTCCGCCAGCATGACACGTGGGAC 1093



1464	Db	TTTCTGCTTCCGGACAGCCCTGCGGCGCGCGCTCTGGCTATCCCCAATACACCTA	1523
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1516	Qy	CATCTATATCCAAAGTGACACATCCGCTCCAAGATGACCAAGAGCTCCAGGCTGGGTGAG	1575
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1576	Qy	GGAGATCTTCTTGAGGGCTTCTCGGCCAGAAAGCTCAGGTATGCGCTCTCTGTGTGA	1635
1644	Db	CGAGATTTTGTCTCAGCGCTTCTGGGCGCGGAAAGCTCAGGTTTCCAAAGCCGGCTGTG	1703
1636	Qy	TACCCGGGAAGCCCTGGTCCAGTATATCACATGGTGATATTCACCTGTCTCAGCCAAGCA	1695
1704	Db	CACCCAGGAGAGATGGTGAAGTTCTCACTGCAATCATCTTCAATTGCTCTGCCACGA	1763
1696	Qy	TGCAGCTGTCTCAGTTTCAGGCCAGTCGACTCTTGTGTTGGATGCCCAATCTGCCACTAC	1755
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1944	Db	NNNNNNNNNNNAGGCCCTTGGGCACCTACCCAGATGAGCACTTCACAGAGAGGCCCC	2003
1936	Qy	CCGGCAAGCGTGGCTGCTTCCAGAAAGCTGATCCAGATCTCCAAGGGCATCAGGGA	1995
2004	Db	GAGCGGAGCATCGCCGCTTCCAGAGCGCGCTGGCCCACTTCAGAGGACATCCAGGA	2063
1996	Qy	GAGGAACCGAGGCTTGSCATGCGCCTACACTCTGGATCTCTCCCTCATTTGAGAACAG	2055
2064	Db	GCGGAACAGGGTCTGSCATGCGCCTACACTCTGGA CCGTCCCTCATTTGGAACAG	2123
2056	Qy	TGTCTCCATCTAA	2068
2124	Db	CGTCTCCATCTAA	2136

RESULT	11
BB612677	
LOCUS	BB612677 RIKEN full-length enriched, 10 day neonate skin Mus linear EST 26-OCT-2001
DEFINITION	musculus cDNA clone 4732402E02 5', mRNA sequence.
ACCESSION	BB612677
VERSION	BB612677.1 GI:16453584
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 685)
AUTHORS	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama.T., Miyazaki A., Nomura,K., Ono,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa.A., Shiraki,T., Sugabe,Y., Suzuki.H., Tagami.M., Tagawa,A., Takahashi.F., Takeda.Y., Tanaka.T., Toyota.T., Muramatsu.M. and Hayashizaki,Y.
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)
COMMENT	Unpublished (2001) Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suenhiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9216  
 Email: genome-res@genome.gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.  
 Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo, S., Shingawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa, K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and Hayashizaki, Y.  
 Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (<http://genome.gsc.riken.go.jp/>) for further details.  
 e mouse tissues.  
 Location/Qualifiers  
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 /notes="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGGAGAGAGGATCCAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGGAGAGAGTCTCGAGTTAATTAATTCCTCCCTCC sequence [3', cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"]  
 Query Match 17.6%; Score 566.2; DB 2; Length 685;  
 Best Local Similarity 97.7%; Pred. No. 8.6e-138;  
 Matches 585; Conservative 0; Mismatches 13; Indels 1; Gaps 1;  
 Qy 5 TTGCAGGTAGAGAGCTAAACTGGTCAGAGAGATGGCGAAATTCAGGGTGCAGATATCCACG 64  
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 Qy 65 GGGGAAGCCCTGTGGGGTGGGCACATGGGACAAAGTGTCTGTACAGATCGTGGGAACCCAC 124  
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VERSION	AY415196.1	GI:39771155	
KEYWORDS	GSS.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 (bases 1 to 2136) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
COMMENT	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
FEATURES	Location/Qualifiers		
source	1..2136 /organism="Mus musculus" /mol_type="genomic DNA" /db_xref="taxon:10090" <1..>2136 /gene="ALOXE3" /locus_tag="HCM5476"		
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ORIGIN			
Query Match	17.3%;	Score 558.6;	DB 9; Length 2136;
Best Local Similarity	57.7%;	Pred. No. 1.3e-135;	
Matches	835;	Conservative 0;	Mismatches 610; Indels 3; Gaps 1;
QY	621	TCAAAGTCAAGGGCTCTGGACCCACAGGACTCTGGAGGAGTCTGAGGAGATGAGAA	680
DB	692	TGAAGATTCGAGTCTCTGGACCGCAGGGCTCTCGAAGAGGGCTGGACGACATCCCGA	751
QY	681	GGCTGTTTAACTTCGCGAAGATCCAGACAGAGATGATGTTTGACACTGCGCAGGAAG	740
DB	752	ACATCTTCGTGGTGCATAGACTTCACTTCAGAGTACGTCACCGAGCATTCGTGAGG	811
QY	741	ATGCTCTTCGCTCCAGATTCCTAAATGGGCATCAACCCGGTCTCTGATTCGCCGCTGTC	800
DB	812	ACAGCTTCTTTGGTACCAGTACCTGAATGGTGTCAACCCCTGTCATGCTTCATTGCTCT	871
QY	801	ACAGTCTCCCAACAACTTCCGGTCACTGATGAATGGTGGCCCGCAGTGGGCCCTG	860
DB	872	CCAGCTTGCCCAAGAGCTGCTGTGACCAATGACATGGTGGCACCTTTGCTGGGACCA	931
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DB	932	GCACTGCTCAAAACAGAGCTAGAGAGGGGCAACATCTTCTGGCGGACTACTGATCC	991
QY	921	TTTCTGGAGTCCACACCAATCTTCAATGGAAAGCCTCAGTTCTCTCGAGCCCCGATGA	980
DB	992	TGGCGGAGGCCCCAGTCCATTGCATAAAGGGTCTCCAAACAGTACGTAAACAGGCCCTCT	1051
QY	981	CCCTGTTACACAGAGCTCAGGTCGGGACCCCTGCTTCCCATTCGCATCCAGCTCAAC	1040
DB	1052	GCTGTGTGGTCTCAACCCACAG---GGGGTGTCTGCTGCATTTGGCAATCCAGCTCAGCC	1108
QY	1041	AGACTCCCGGGCAGACAAACCCCATCTTCTGCCAGCGCATGACAGCTGGGACTGGTGC	1100
DB	1109	AGACACGAGGCCGAGAGGCCCACTTTCTGCCCACTGATTCGCGAGTTGGACTGGCTGC	1168
QY	1101	TGGCCAAAGACCTGGGGTTCGCAATTCAGTTTATCATTCATCATGAGGCTGTCAACATCTGC	1160
DB			

Db	1169	TGGCCAAAGACGTGGGTGCGCAACTCTGTAGTTTGGTGCACGAGAAACACGCAATTTTC	1228
QY	1161	TGCATGCCCATCTGATTCAGAAAGTCTTTGCTTGGCCACATTTAGCTCAGCTGCCTAGGT	1220
DB	1229	TGTGCACGCATTTGCTATGCGAGGCTTCTCCATGGCTACACTGCTGCTCAGCTGCCGCTCT	1288
QY	1221	GTCACCTCTCTTCAAGCTATTGATTTCTCATATTTCGCTACACACTGACATCAACAGGC	1280
DB	1289	GTCATCCAGTCTACAAGCTCTGCTTCTCTCATCTACACGCTGCAAGTGAACACCA	1348
QY	1281	TTGCCCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1340
DB	1349	TGCAGAGCCACGCTGCTCAACCCAGAGGCTCTGTCGAGAGGTCACGTCATCGGTA	1408
QY	1341	CTGGGGGATTTCTGACCTGATTAAGAGAAACATGGAGCAGCTGAATCTACTCTGCTCT	1400
DB	1409	GGCAGGGCTCATCTACCTCATGAGCACGGGCTGGCCCATCTTACCTTACAGGATTTCT	1468
QY	1401	GTCCTCTGAAGATATCCGAGCCGAGGTGTGGAAGACATCCAGGCTACTATTACCGAG	1460
DB	1469	GCCTACCGGATAGCATACGGGCTCGTGGCTCTGACCAITCCCAACTACCACTACCGAG	1528
QY	1461	ATGATGGAGTGCAGATCTGGGGGGCAATAAAGAGCTTTGTCTCTGAAATAGTCAGATCT	1520
DB	1529	ACGACGGCTGAAGATCTGGGGGGCTATTGAGAGGTTTGTCTCAGAGATTGTGATTTACT	1588
QY	1521	ACTATCCAAAGTGACACATCCGTCCAAGATGACCAAGAGCTCCAGGCTGGGTGAGGAGA	1580
DB	1589	ATTATCCAGCGATCGCTCTGTGACGAGGACTGTGAATCGAGGCTTGGTGGGTGAGA	1648
QY	1581	TCTTCTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGGTATGCCCTCTTGTGTTGGATACC	1640
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QY	1701	CTGTCAGTTCAGGCCAGTTCGACTCTTGTGTTGGATGCCAAATCTGCGCACCTACCATGC	1760
DB	1769	CGTCAATAGTGGGCGAGNN	1828
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QY	1821	CAGCAGTTAATCGTCAAGTTATCACATCATTTGCTCTCTGGCTGTGAAGCCAGAACCTG	1880
DB	1889	NN	1948
QY	1881	GGGACCAAGGCCCTGGGCCACTATCCAGATGAACACTTCCAGAGGATGCCGCCCGCCG	1940
DB	1949	NNNNNNNAGACTCTGGGCACTTACCAGATGAACATTTCAAGAGGAGGCCCCACCGC	2008
QY	1941	GAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAGGCAATCAGGGAGAGA	2000
DB	2009	AGAGCATCGACGCTTCCAGAACTGCTGGGCCAGATCTCAAAGGACATCAGGAGCGCA	2068
QY	2001	ACCGAGGCTGGCCTGCTTACACCTACCTGATCTCCCTCATTTGAGACAGCTGTCT	2060
DB	2069	ACCGAGGCTGGCCTGCTTACCTTGGATCTTGGATCTTCCACTTCAATTGAGAACAGTGT	2128
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RESULT 14

BG696031

LOCUS 602658180F1 NCI\_CGAP\_Skn3 Homo sapiens cDNA clone IMAGE:4801026 5', mRNA sequence.

ACCESSION BG696031

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VERSION      BG696031.1  GI:13960753
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SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE        1 (bases 1 to 863)
JOURNAL      NIH-MGC http://mgi.nci.nih.gov/
COMMENT      National Institutes of Health, Mammalian Gene Collection (MGC)
              Unpublished (1999)
              Contact: Robert Strausberg, Ph.D.
              Email: cgabbs-remail.nih.gov
              Tissue Procurement: James Cleaver, M.D.
              cDNA Library Preparation: Life Technologies, Inc.
              cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA
              Sequencing by: Incyte Genomics, Inc.
              Clone distribution: MGC clone distribution information can be
              found through the I.M.A.G.E. Consortium/LLNL at:
              http://image.llnl.gov
              Plate: LLAM10692 row: p column: 19
              High quality sequence stop: 842.
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                  /clone="IMAGE:4801026"
                  /lab_host="DH10B (T1 phage-resistant)"
                  /clone_lib="NCI CGAP Skn3"
                  /note="Organ: skin; Vector: pCMV-SPORT6; Site 1: NotI;
                  Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.5kb. Library constructed by Life
                  Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
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  Best Local Similarity 81.4%; Pred. No. 1.4e-130;
  Matches 673; Conservative 0; Mismatches 150; Indels 4; Gaps 4;

QY 1274 AACACGCTGCGCGGAGCTGCTGCTGCCCCGCGGAGTTGTATAGACAAGTCCACAGGC 1333
DB 1 AACACACTCGCGCGGAGCTGCTTATCGTGCC-AGGCAGGTGTGACAGGTCACAGGC 59

QY 1334 CTGGCACTGGGGGATTTCTGACCTGATTAAGAGAAATGAGACAGTGAATCTCT 1393
DB 60 ATCGCATTTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGTGAATTTCT 119

QY 1394 GTCCTGTCTCTCCGAGATATCCGAGCCGAGGTGTGGAAGACATCCAGGCTACTAT 1453
DB 120 CTCCTGTCTGCTGTGAGATATCCGAGCCGAGGAGTTGAAGACATCCAGGCTACTAC 179

QY 1454 TACCCAGATGATGGATGCAGATCTGGGGGGCAATAAAGAGCTTTGTCTCTGAATAGTC 1513
DB 180 TACCGTGATGATGGATGCAGATCTGGGGTGAGTGGAGAGCTTTGTCTCTGAATCATC 239

QY 1514 AGCATCTACTA-TCCAAGTGAACATTCGCTCAAGATGACCAAGAGCTCCAGGCTGGGT 1572
DB 240 GGTATCTACTACCCCAAGTGTGAGTCTGTCTCAAGATGACAGAGAGCTCCAGGCTGGGT 299

QY 1573 GAGGAGATCTCTCTGAGGCTTCTCGGCCGAGAAAGCTCAGTATGCCCTCTTGT 1632
DB 300 CAGAGAGATCTTCTCAAGGGGCTTCTTAACAGAGAGAGCTCAGGTATACCTCTCACT 359

QY 1633 GGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACTGTCTCAGCCAA 1692
DB 360 GGAGACCCGGGAGAGCCCTGGTCCAGTATGTACCATGTGTGATATTCACTGTCTCGCCAA 419

QY 1693 GCATCAGCTGTCACTCAGGCCAGTTCAGTCTTTGTGTGGATGCCCAATCTGCCACC 1752
DB 420 GCATCGGCTGTCACTCAGGCCAGTTCAGTCTTTGTGTGGATGCCCAATCTGCCACC 479

QY 1753 TACCATGAGCTTACACCACTTCTTCCAAAGGCCAGGCCGCGCTGAGAGTTTCATAGC 1812
DB 1753 TACCATGAGCTTACACCACTTCTTCCAAAGGCCAGGCCGCGCTGAGAGTTTCATAGC 1812

Db 480 CAGCATGCGCTGCCACCACCCACCTCCAAAGGCTGTGGCAACATGCGAGGGCTTCATAGC 539
QY 1813 CACGCTCCACAGCTTAATTCGTCAAGTTATCACATCATTCCTCTCTGCTGCTAAGGC 1872
DB 540 CACCTCCACCTGTCAATGCCACATGTGATGTCATCTCTGCTGCTGCTGAGCAA 599
QY 1873 AGAACCTGGGACCAAAAGGCCCTGGGCCACTATCCAGATGAACACTTCCACAGAGGATGC 1932
DB 600 GGAGCTGGAGACCAAAAGGCCCTGGGCCACTATCCAGATGAGCACTTCCACAGAGGAGGC 659
QY 1933 CCCCGCGGAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCAAGGGGAT-CA 1991
DB 660 CCTCTGGCGAGCATGCGCACCTTCCAGAGCGCGCTGGCCAGATCTCGAGGGGATCCA 719
QY 1992 GGGAGAGAAACGAGGCGCTGGCACTGCGCTACCTACCTACCTGATCCTCCCTCATTTGGA 2051
DB 720 GGAAGCGAAACGCGGCGCTGGTGTGCGCTACCTACCTACCTAGACCTACCTCATCGAGA 779
QY 2052 ACAGTGTCTCCATCAACATCTTGGAGAAAGACAGTCTCTGTGTGACAT 2098
DB 780 ACAGGTCTCCATCTAA-ATCCAGGGAACAGGCCCATGACAT 825

RESULT 15
LOCUS      BX371550 875 bp mRNA linear EST 23-APR-2004
DEFINITION BX371550 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
              clone CSODI016YB10 3-PRIME, mRNA sequence.
ACCESSION  BX371550
VERSION    BX371550.2 GI:46556307
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
REFERENCE   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS     Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE       1 (bases 1 to 875)
JOURNAL     Li W.B., Gruber C., Jessee, J. and Polayes, D.
COMMENT     Full-length cDNA libraries and normalization
              Unpublished (2001)
              On May 8, 2003 this sequence version replaced gi:30433898.
              Contact: Genoscope
              Genoscope - Centre National de Sequencage
              2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
              Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
              1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
              end enriched, double-strand cDNA was digested with Not I and cloned
              into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
              was normalized. Library was constructed by Life Technologies, a
              division of Invitrogen. This sequence belongs to sequence cluster
              8973.f
              For more information about this cluster, see
              http://www.genoscope.cns.fr/cdna?s=CSOBA1018ZA06_CS01673_1&c=8973.f

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                       /note="1st strand cDNA was primed with a NotI-oligo (dT)
                       primer. Five prime end enriched, double-strand cDNA was
                       digested with Not I and EcoR V sites of the Not I and EcoR V
                       sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN
  Query Match      16.4%; Score 529.8; DB 5; Length 875;
  Best Local Similarity 78.4%; Pred. No. 3.9e-128;
  Matches 686; Conservative 0; Mismatches 182; Indels 7; Gaps 4;

QY 956 CCTCAGTTCTTCGAGCCCCGATGACCTGTGTACACAGAGCTCAGGGTCCGAGCCCTG 1015
DB 956 CCTCAGTTCTTCGAGCCCCGATGACCTGTGTGTACACAGAGCTCAGGGTCCGAGCCCTG 1015
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Db 875 CCTCAGTTTTTTGGCGGCCCCAATGCCCCCTCTTAAACCAAGCCCCAGGCTGGGGCCCTT 816  
QY 1016 CTTCCCATG---CCATCCAGCTCAAAAGAGACTCCCGGGCCAGACAAOCCCATC--TTCC 1070  
Db 815 TTTTGTTTTTTGGCTTATCAAGTCAGCCAAGACCCCGGGCCAAATCAGCCCTATCTTCT 756  
QY 1071 TGCCAGGAGATGACACGTGGGACTGGTTGCTGGCCAAAGACCTGGGTTGCAATTCAGT 1130  
Db 755 TGCCCACTGATAACACAGTGGGACTGGTGC-GGCCAAAGGCTGGGTGGCAATGCCAGT 697  
QY 1131 TTATCATCATGAGCTGTCAACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTG 1190  
Db 696 TCTCCTTCATAAGGCCCTTACGGCACTTGTGCACTCAATCTGCTGCTGAGGTTCTCA 637  
QY 1191 CCTTGGCCACATTTAGTTCAGCTGCTAGGTGTCAOCTCTTTCAAGCTATTGATTCTC 1250  
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QY 1251 ACATTCGGTACACTGTCAATCAACACGCTTTCGCCGGAGCTGTCTGTTGCCCTGGGA 1310  
Db 576 ACACCGGATACACCTGTGCACATCAACACACTCGCCCGGGAGCTGTATCGTGCAGGGC 517  
QY 1311 AGTTGATAGACAGTCCACAGGCTTGGCACTGGGGGATTTCTGACCTGATAAAGAGAA 1370  
Db 516 AGTGGTGGACAGGTCCACAGGCTCGGCANTTGAAGGCTTCTCGAGTTGATACAGAGGA 457  
QY 1371 ACATGGAGCAGCTGAACCTACTCTGTCTGTGTCTCCTGGAAGATATCCGAGCCGAGGTG 1430  
Db 456 ACATGAGCAGCTGAACCTATTTCTCTGTGTGTCTGCTGAGGATATCCGGACCCGAGGAG 397  
QY 1431 TGGAAAGACATCCAGGCTACTATTACCGAGATGATGGGATGAGATCTGGGGGGCAATAA 1490  
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QY 1671 TGATATTCACTGTCTCAGCCAAAGCATGACGTGTCAAGTTTCAGGCCAGTTTCGACTCTTGTG 1730  
Db 156 TGATATTCACTGTCTCGGCAAGCATGCGGCTGTCAAGTGCAGGGCAGTTTGACTCCTGTG 97  
QY 1731 TTTGGATGCCCAATCTGCCACCTACCATGCAGTACCACCTACTTCCAAAGGCCAGG 1790  
Db 96 CTTGGATGCCCAACCTGGCCACCAGATGAGCTGCCACCCACCTCCAAAGGCCCTGG 37  
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Db 36 CAACATGGAGGGCTTCAAGAGCCACCTCCACCC 2

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Job time : 6704.65 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 08:58:53 ; Search time 9122.36 Seconds  
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Perfect score: 3224

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Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hg.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_ats.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3203	99.3	3203	10	MMALOX8S	Y14696 Mus musculus
2	3178	98.6	3205	6	AR142986	AR142986 Sequence
3	3178	98.6	3205	6	AR430491	AR430491 Sequence
4	3178	98.6	3205	10	MMU93277	U93277 Mus musculus
5	2921.6	90.6	2942	10	BC015253	BC015253 Mus muscu
6	1792.8	55.6	2244	10	AP415240	AP415240 Rattus no
7	1398.4	43.4	2673	9	BC035217	BC035217 Homo sapi
8	1398.4	43.4	2686	9	BC063647	BC063647 Homo sapi
9	1395.2	43.3	2685	6	AR142985	AR142985 Sequence
10	1395.2	43.3	2685	6	AR430490	AR430490 Sequence
11	1395.2	43.3	2685	6	AX770522	AX770522 Sequence
12	1395.2	43.3	2685	9	HSU78294	U78294 Homo sapien
13	1382.8	42.9	2031	9	AF468051	AF468051 Homo sapi
14	1381.6	42.9	2527	11	BV174905	BV174905 sqm75173
15	1340	41.6	261224	10	AL645527	AL645527 Mouse DNA
16	1292.8	40.1	2111	9	AF468054	AF468054 Homo sapi
17	1291.8	40.1	2101	4	AF107263	AF107263 Bos tauru
18	1232.4	38.2	1944	9	AF468052	AF468052 Homo sapi
19	998.8	31.0	1809	9	AF468053	AF468053 Homo sapi

20	659.6	20.5	3320	6	AX358607	AX358607 Sequence
21	659.6	20.5	3384	6	BD262777	BD262777 Novel lip
22	659.6	20.5	3384	6	AR345064	AR345064 Sequence
23	658.6	20.4	2136	6	AX358609	AX358609 Sequence
24	658	20.4	2236	6	BD262765	BD262765 Novel lip
25	658	20.4	2236	6	AR345052	AR345052 Sequence
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27	658	20.4	2701	6	AR345050	AR345050 Sequence
28	658	20.4	3082	9	AF182218	AF182218 Homo sapi
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30	657	20.4	2189	6	CQ724666	CQ724666 Sequence
31	657	20.4	2604	6	BD262774	BD262774 Novel lip
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33	656.4	20.4	3674	9	AK122822	AK122822 Homo sapi
34	652.2	20.2	2136	6	AX304470	AX304470 Sequence
35	648.8	20.1	2536	10	MMALOXE3	Y14695 Mus musculu
36	565.8	17.5	2278	9	AF059250	AF059250 Homo sapi
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42	537.4	16.7	2182	5	BC081087	BC081087 Xenopus 1
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45	466.2	14.5	1383	6	AR345055	AR345055 Sequence

## ALIGNMENTS

RESULT 1  
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DEFINITION. Mus musculus mRNA for arachidonate 8(S)-lipoxxygenase.  
ACCESSION. Y14696  
VERSION. Y14696.1 GI:3036863  
KEYWORDS. alox8 gene; arachidonate 8(S)-lipoxxygenase.  
SOURCE. Mus musculus  
ORGANISM. Mus musculus  
REFERENCE. 1. Krieg, P., Kinzig, A., Heidt, M., Marks, F. and Furstenberger, G. cDNA cloning of a 8-lipoxxygenase and a novel epidermis-type lipoxxygenase from phorbol ester-treated mouse skin Biochim. Biophys. Acta 1391 (1), 7-12 (1998)  
AUTHORS. Krieg, P.  
TITLE. Direct Submission  
JOURNAL. Submitted (26-AUG-1997) P. Krieg, German Cancer Research Center, Research Program 2, Im Neuenheimer Feld 280, D-69120 Heidelberg, FRG  
REMARK. Revised by [3]  
REFERENCE. 3 (bases 1 to 3203)  
AUTHORS. Krieg, P.  
TITLE. Direct Submission  
JOURNAL. Submitted (29-OCT-1997) P. Krieg, German Cancer Research Center, Research Program 2, Im Neuenheimer Feld 280, D-69120 Heidelberg, FRG  
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ORGANISM Unclassified.  
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AUTHORS Brash,A.R., Boeglin,W.E. and Jisaka,M.  
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AUTHORS Brash,A.R., Boeglin,W.E. and Jisaka,M.
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RESULT 4
LOCUS      MMU93277
DEFINITION Mus musculus 8S-lipoxygenase mRNA, complete cds.
ACCESSION U93277
VERSION    U93277.1
KEYWORDS   GI:2439986
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE  1 (bases 1 to 3205)
AUTHORS   Jisaka,M., Kim,R.B., Boeglin,W.E., Nanney,L.B. and Brash,A.R.
TITLE     Molecular cloning and functional expression of a phorbol
          ester-inducible 8S-lipoxygenase from mouse skin
JOURNAL   J. Biol. Chem. 272 (39), 24410-24416 (1997)
MEDLINE   97450967
PUBMED    9305900
REFERENCE  2 (bases 1 to 3205)
AUTHORS   Jisaka,M. and Brash,A.R.
TITLE     Direct Submission
JOURNAL   Submitted (12-MAR-1997) Clinical Pharmacology, Vanderbilt
          University, 23rd Ave. at Pierce, Nashville, TN 37232-6602, USA
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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DB      61  AAAGTGTCTGTGAGCATCGTGGGAACCCACGAGAGAGCCCTTAGTACCTCTGGACCAT 120
QY      155 CTGGGCAAGGAGTTCAGCGCGGTGCTGAAGAAGACTTCGAGGTGACGCTTCCCGCAGGAC 214
DB      121 CTGGGCAAGGAGTTCAGCGCGGTGCTGAAGAAGACTTCGAGGTGACGCTTCCCGCAGGAC 180
QY      215 GTAGGCACTGTCTGATGCTGAGATCCACAAAGCAACCCCGGAAGTGTCCCTCCCGCTT 274
DB      181 GTAGGCACTGTCTGATGCTGAGATCCACAAAGCAACCCCGGAAGTGTCCCTCCCGCTT 240
QY      275 ATGTCTTTCCGTTCTGATGCTGAGTCTTTCGCGCTGGTTCGAGCTGGAGTGGCTACCTGG 334
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901  ACCACATCTCAATGGAAAGCCCTCAGTCTCTCGAGCCCGGATGACCTGTTTACACCAAG 960
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1175  ATTCAGAAAGTCTTGTGCTTGGCCACATTCAGTCAAGTGCCTTAGGTGTCAACCTCTCTTC 1234
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1235  AAGCTATTGATTCTTCATTCATTCGGGTACACTGACATCAACAGCTTCCCGGAGCTG 1294
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1295  CTGTTGGCCCTTGGGAAGTTGATAGCAAGTTCACAGCCCTTGGCACTGGGGGATCTCT 1354
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ABRAMSON, R. D., MULLAHY, S. J., BOEAK, S. A., MCEWAN, P. J., MCKERNAN, K. J., MALEK, J. A., GUNARATNE, P. H., RICHARDS, S., WOLEY, K. C., HALE, S., GARCIA, A. M., GAY, L. J., HULYK, S. W., VILLALON, D. K., MUZNY, D. M., SODERGREN, E. J., LU, X., GIBBS, R. A., FAHEY, J., HELTON, E., KETTEMAN, M., MADAN, A., RODRIGUES, S., SANCHEZ, A., WHITING, M., MADAN, A., YOUNG, A. C., SHEVCHENKO, Y., BOUFFARD, G. G., BLAKESLEY, R. W., TOUCHMAN, J. W., GREEN, E. D., DICKSON, M. C., RODRIGUEZ, A. C., GRIMWOOD, J., SCHMUTZ, J., MYERS, R. M., BUTTERFIELD, Y. S., KRZYWINSKI, M. I., SKALSKA, U., SMAIUS, D. E., SCHNERCH, A., SCHEIN, J. E., JONES, S. J., SKALSKA, U., MARRA, M. A.	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgapbs-remail.nih.gov">cgapbs-remail.nih.gov</a> Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: <a href="http://www.shgc.stanford.edu">http://www.shgc.stanford.edu</a> Contact: (Dickson, Mark) <a href="mailto:mcd@paxil.stanford.edu">mcd@paxil.stanford.edu</a> Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.	Query Match Best Local Similarity 90.6%; Score 2921.6; DB 10; Length 2942; Matches 2924; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
TITLE	human and mouse cDNA sequences	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)	
PUBMED	12477932	
REFERENCE	2 (bases 1 to 2942)	
AUTHORS	Strausberg, R.	
TITLE	Direct Submission	
JOURNAL	Submitted (01-OCT-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	
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COMMENT		
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QY	2821	AACCATCTGTAATGGGATTCGATGCCCTCTTCTGGCGTGTCTGAAGACAGCGACAGTGTA	2880
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QY	2881	TGCACATATATAAATAAATAAATCTTTAAAAAACAACAAAGAGAGA	2928
Db	2881	TGCACATATATAAATAAATAAATCTTTAAAAAACAACAAACAAAAA	2928
RESULT 6			
AF415240			
LOCUS			
DEFINITION			
Rattus norvegicus 15-lipoxygenase-2 (Alox15b) mRNA, complete cds.			
ACCESSION			
AF415240			
VERSION			
AF415240.1 GI:22652396			
KEYWORDS			
Rattus norvegicus (Norway rat)			
SOURCE			
ORGANISM			
Rattus norvegicus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
1 (bases 1 to 2244)			
Boeglin,W.E., Schneider,C. and Brash,A.R.			
A 15-lipoxygenase in the rat, homolog of human 15-lipoxygenase-2			
and mouse 8-lipoxygenase			

JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 2244)
AUTHORS	Boggin, W.E., Schneider, C. and Brash, A.R.
TITLE	Direct Submission
JOURNAL	Submitted (31-AUG-2001) Clinical Pharmacology, Vanderbilt University, 23rd Avenue South at Pierce, Nashville, TN 37232, USA
FEATURES	Location/Qualifiers
source	1..2244
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gene	/db_xref="taxon:10116"
	1..2244
	/gene="Alox15b"
CDS	37..2070
	/gene="Alox15b"
	/note="similar to Homo sapiens ALOX15b"
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	/product="15-lipoxygenase-2"
	/protein_id="AA03708.1"
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	/translation="MAKFRVRLVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHGKE FSAGAEDEFVTLQDVTLMLRIHKAPPEAPLPLSPDPDAWYCRWFLEWLPFGAA LRFPCYQWLEGAGELVLRGAAKVSQWDRHTLQDQKELSKDMYSWKTYIEGW HCLDHETVKDLNLIKYSAMNAKFFPKAQSATFELFKGLLDRGLWRSIREKRMF NFHTPAEYVPAHQEDAPFASQFLNGLNPLVIRRCRLPENPVTDEMVAIVLPG TSLQAELEKSLFVLDHGLISGVQTNVINGKPFQSAAPMTILLYOSPGGPLPILAIQL KOTQEPDNPILFSDDKWDLAKTNVNAEFSIHEALTHLHAHLIPEVFALATLRQ LPHCHPLPKGLIPHTRYTLHINTLARELLIAPGVKVDKSLGLIGFSDLIKRMEQL SVYLCLPDLFRADVGLPGVYRDGMQIWSAIRSVSBIVDIYPSDASVRDQOE LOAMVGETFSFGLSIOSSGMPSSLDTQELVQVYVMVIFTCSAKHAASVASQFSDCV WPNLIPSMQRLPPTSKQASPEGFATLPVAVNATCDVILIALWLLSKPGRRLGHY PDEHFTBEVPRISAAPFORKUIQISSGIRKRNQSLAUPYTYLDPLIENSVSI"
ORIGIN	
Query Match	55.6%; Score 1792.8; DB 10; Length 2244;
Best Local Similarity	91.1%; Pred. No. 0;
Matches 1905; Conservative	0; Mismatches 187; Indels 0; Gaps 0;
Qy	7 GCAGTAGAGAGCTAACTGGTCAGGAGGATGGCAAAATGCAGGGTGAGAGTATCCACGGG 66
Db	9 GCAGTAGAGAGCCAGCTGGTCAGGAGGATGGCTAAATTCAGGGTGAGAGTATCCACGGG 68
Qy	67 GGAAGCCTGTGGGCTGCACATGGGACAAAGTGTCTGTACGATCGTGGGAACCCACGG 126
Db	69 GGAAGCCTGTGGGCTGCACATGGGACAAAGTGTCTGTACGATCGTGGGAACCCATGG 128
Qy	127 AGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGAGTTTCAGCGCGGTGTGGAAGA 186
Db	129 AGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGAGTTTCAGCGCTGGAGCTGAAGA 188
Qy	187 AGACTTCGAGGTGACGCTTCCCGAGAGCTAGGCACTGTGTGATGTGTGCGAGTCCACAA 246
Db	189 AGACTTCGAGGTGACGCTTCCCGAGAGCTTGGCACTGTGTGATGTGTGCGAATACAA 248
Qy	247 AGCACCCTGGAGTGTCTCCCGCTTATGTCTTTTCGGTCTGTGATGCTGGTTCGCG 306
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Qy	307 CTGTTTCGAGCTGGAGTGTGCTTACCTGGGCTGCATCCACTTCCCTCTGTATCAGTGGCT 366
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Qy	367 GGAAGGGCTGGGAGCTGTGCTGAGAGAGGAGCAGCAAGGTGTCTCTGGCAAGACCA 426
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Db	429 CCACCGTACGCTGCAAGATACAGCGCCAGAGAGCTTGAAGTTCAGGCGAGAGATGAAG 488
Qy	487 CTGGAGAGCTTACATGAAGTGTGCTTCCCTCGCTTCCCTGACACGAGACTGTGAAGACTT 546
Db	489 CTGGAGAGCTTACATGAAGTGTGCTTCCCTCGCTTCCCTGACACGAGACTGTGAAGACTT 548

Qy	547 GGACCTCAACATCAAGTACTCTCGATGAGAAATGCCAACTCTTCTTTAAAGCCCACTC 606
Db	549 GGACCTCAACATCAAGTACTCTCGATGAGAAATGCCAACTCTTCTTTAAAGCCCACTC 608
Qy	607 GCGCTATACGAGCTGAAAGTCAAGGGCTCTCGACCGCACAGACTCTCGAGGAGTCT 666
Db	609 TGCCTTTACAGAGCTGAATTCAGAGGGCTCTCGACCGCACAGACTCTCGAGGAGTCT 668
Qy	667 GAGGAGATGAGAAAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTAGTGTGTTGC 726
Db	669 GAGGAGATGAGAAAGGATGTTTAACTTCCCAACACTCCAGCAGCAGAGTAGTGTGTTGC 728
Qy	727 AACTGCGAGAGATGCTTCTTGGCTCCAGTCTCTAAATGGCATCAACCCGGTCTCT 786
Db	729 AACTGCGAGAGATGCTTCTTGGCTCCAGTCTCTAAATGGCTCAACCCAGTCTCT 788
Qy	787 GATTTCGCGCTGTCAACAGTCTCCCAAACTCCCGGTCACTGATGAAATGGTGGCCCC 846
Db	789 GATTTCGCGCTGTCCAGACTCCAGAGAACTTCCAGTCACTGATGAAATGGTGGCTCC 848
Qy	847 AGTCTGGGCGCTGGAAACCACTCTGCAAGCTGAGTTGGAGAAGGCTCCCTGTTCTGGT 906
Db	849 AGTCTGGGCGCTGGGACCACTCTGCAAGCTGAGTTAGAGAAGGCTCCCTGTTCTGGT 908
Qy	907 GGATCATGGCATTTCTTCTGGAGTCCACCAACATCTCAATGGAAGACCTCAGTTCTC 966
Db	909 GGACCATGGAATTTCTTCTGGAGTCCAAACCAATGTATCAATGGAAGACCTCAGTTCTC 968
Qy	967 TGCAGCCCCGATGACCTGTGTACACAGAGCTCAGGCTCCGAGCCCTGCTTCCCATTCG 1026
Db	969 AGCAGCCCCGATGACCTGTATATACAGAGTCCAGGGTCCGAGCCCTGCTTCCCATCGC 1028
Qy	1027 CATCAGCTCAACACAGACTCCCGGGCCAGACAAACCCATCTTCTGCGCAGGATGACAC 1086
Db	1029 CATCAGCTCAACACAGACTCCCGGGCCAGACAAACCCATCTTCTGCGCAGGATGACAA 1088
Qy	1087 GTGGGACTGTGTGTGCGCAAGACTCGGTTTCGCAATCTCTGAGTTTTCATCCATGAGGC 1146
Db	1089 GTGGGACTGTGTGTGCGCAAGACTCGGTTTCGCAAGCTGAGTTTTCATCCATGAGGC 1148
Qy	1147 TGTACACATCTGTGTGATGCCATCTGATTCAGAGAGTCTTTCGCTTGGCCACATTCAG 1206
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Qy	1207 TCAGTCTGCTAGTGTCACTCTCTTCAAGCTATTCATTCCTCACATTCGCTACACACT 1266
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Qy	1267 GCACATCAACACACGCTTCCCGGGAGCTGCTGTTGCTGGGAAGTTGATAGACAAGTC 1326
Db	1269 GCACATCAACACACGCTTCCCGGGAGCTGCTGTTGCTGGGAAGTTGATAGACAAGTC 1328
Qy	1327 CAGAGGCTTGGCACTGGGGATTTCTGACCTGATTAAGAGAAACATGGAGAGCTGAA 1386
Db	1329 CAGAGGCTTGGCACTGGGGATTTCTGACCTGATTAAGAGAAACATGGAGAGCTGAG 1388
Qy	1387 CTACTCTGCTGTGTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACATCCCAAG 1446
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Qy	1447 CTACTATTAACGAGATGATGGATGCGAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGA 1506
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Qy	1507 AATAGTCAGCATCTACTATCCAGTGACATCCGTCCNAGATGACCAAGAGCTCCAGGC 1566
Db	1509 GATAGTTGACATCTATTAACCAAGTGCATCTGTCCGAGATGACCAAGAGCTCCAGGC 1568
Qy	1567 CTGGGTGAGGAGACTTCTCTCTGAGGCTTCTCCGCGCGAGAAAGCTCAGGTATGCTCTC 1626
Db	1569 CTGGGTGAGGAGACTTCTCTCTGAGGCTTCTCCGCGCGAGAAAGCTCAGGTATGCTCTC 1628

QY	1627	CTTTGGTATACCCGGGAAGCCCTGTGTCAGTATATACCATGTTGATATTCACCTGCTC	1686
Db	1629	CTTTGGTATACCCGGGAAGCCCTGTGTCAGTATATTCACCTGCTC	1688
QY	1687	AGCCAGCATGAGCTGTGAGTTCAGGTCAGTTCGACTCTTGTGTTGATGCCCAATCT	1746
Db	1689	AGCCAGCATGAGCTGTGAGTTCAGGTCAGTTCGACTCTTGTGTTGATGCCCAATCT	1748
QY	1747	GCCACCTACCATGACGCTACCAACCACTACTTCCAAAGGCCAGGCCGCCCTGAGAGTTT	1806
Db	1749	GCCACCTTCATGACGCTACCAACCACTACTTCCAAAGGCCAGGCCGCCCTGAGAGTTT	1808
QY	1807	CATAGCCAGCTCCAGCAGTTAATTCGTAAGTTATCATCATTCATGCTCTCTGCTGCT	1866
Db	1809	CATAGCCAGCTCCAGCAGTTAATTCGTAAGTTATCATCATTCATGCTCTCTGCTGCT	1868
QY	1867	NAGCGCAGAACCTGGGAGCAAGGCGCCCTGGGCCACTATCCAGATGAACACTTCACAGA	1926
Db	1869	AAGCAAGSAGCCAGGGGACCGTAGGCGCCCTGGGCCACTATCCAGATGAACACTTCACAGA	1928
QY	1927	GGATGCCCCCGCGGAAGCGTGGCTCCCTTCAGAGAAAGCTGATCCAGATCTCCAAGGG	1986
Db	1929	GGAGTCCCGCGGAGCATGCGGCCCTTCAGAGAAAGCTGATCCAGATTCAGTGG	1988
QY	1987	CATCAGGAGAGAACCGGAGCGTGGCACTGCCCTACACCTACCTGATCCCTCCAT	2046
Db	1989	CATCAGGAGAGAACCGGAGCGTGGCACTGCCCTACACCTACCTGATCCCTCCAT	2048
QY	2047	TGAGAACAGTGTCTCATCTAATCTTTCGAGAGACAGTCTCTGTGTGAT	2098
Db	2049	CGAGAACAGTGTCTCATCTAATCTTTCGAGAGACAGTCTCTGTGTGAT	2100

RESULT 7	BC035217	2673 bp	mRNA	linear	PRI 29-JUN-2004
LOCUS	Homo sapiens arachidonate 15-lipoxygenase, second type, mRNA (CDNA clone MGC:24958 IMAGE:4778890), complete cds.				
DEFINITION	BC035217.1 GI:23270880				
ACCESSION	BC035217				
VERSION	MGC.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 2673)				
AUTHORS	Strausberg,R.L., Feigold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Schetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raja,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullaly,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakeley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalhus,D.S., Scherch,A., Schein,J.E., Jones,S.J. and Marra,M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 2673)				
AUTHORS	Strausberg,R.				
TITLE	Direct Submission				
JOURNAL	Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer				

REMARK COMMENT	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgapbs@mail.nih.gov">cgapbs@mail.nih.gov</a> Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center Center code: BCM-HGSC Web site: <a href="http://www.hgsc.bcm.tmc.edu/cdna/">http://www.hgsc.bcm.tmc.edu/cdna/</a> Contact: <a href="mailto:amg@bcm.tmc.edu">amg@bcm.tmc.edu</a> Gunnarane, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Loulseged, H., Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati, A.N., Gibbs, R.A.				
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAK Plate: 29 Row: 1 Column: 2 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein. Location/Qualifiers 1..2673 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:24958 IMAGE:4778890" /tissue_type="Skin, normal" /clone_lib="NCI CGAP_Skn3" /lab_host="DH10B" /note="Vector: pCMV-SPORT6.1" 1..2673 /gene="ALOX15B" /db_xref="LocusID:247" /db_xref="MIM:603697" 59..2089 /gene="ALOX15B" /codon_start=1 /product="arachidonate 15-lipoxygenase, second type" /protein_id="AAH35217.1" /db_xref="GI:23270881" /db_xref="LocusID:247" /db_xref="MIM:603697" /translation="MASERVSVTEAGFAGTWDKVSIVTGRESPLPLDNLGKE FTAGABDFQVLTEDVGRVLLLRVHKAPVPLPLGLAPADAFWCRWQLPFRGGHL LFPCYQMLEGAGTIVLQEGTAKVSWADHPVLQQOQEEQARQEMQWKAYNPGWPH CLDEKTVDELNTKYSTAKNANFYLQAGSAFAEMKIKGLDLKGLWRSINEMKRFN FRPTAAEHAFAHEWQEDAFASQFLNGINPVLIRRHCHLVNPFVTDAMVASVLGPGT SLOAELEKGSFLVDHGLSGITQTNVINGKQFSAAPMTLLYQSPGCPPLPLATOLS QTGPNSPIFLPTDDKMDLLAKTVRNAEFSFEALTHLLHSHLLPEVFTLATLROL PHCLPFKLLIPHTYTHLINTLARELLIVPGQVDRSTGIGEGFSLIQNMKQLN YSLCLPEDIIRTRGVEDIPGYIYRDGQIMGAVRFVSEIIGIYPSDESVDQDREL QAWNREIFSKGLNBSGIPSSLETRALVQYVTWVITCSAKHAAVSAQOFDSCAW MPNLPPSNQLPPTTSKGLATCEGTIATLPVNTATCDVILALWLLSKEPDORPLGTPY DEHTEEAPRESIATFQSRLAQISRGIQERNRGLVLPYTYLDPPLIENSVS1"				
gene					
CDS					
ORIGIN	Query Match 43.4%; Score 1398.4; DB 9; Length 2673; Best Local Similarity 79.9%; Pred. No. 0; Matches 1673; Conservative 0; Mismatches 416; Indels 5; Gaps 2;				
QY	7	GCACCTAGACCTAACT--GGTCAGGAGGATGGCGAATGCAGGTCAGAGTATCCACG	64		
Db	29	GCCCTAGAGAGCTGAGCTTAGCTGGCAGATGGCCGAGTTCAGGGTCAGGTCACCC	88		
QY	65	GCGGAAGCCTGTGGGCTGGCACATGGGACAAAGTGTCTGTACAGATCGTGGGAACCCAC	124		
Db	89	GGAGAGCCTTCGGGCTGGCACATGGGACAAAGTGTCTGTACAGATCGTGGGACCCGG	148		
QY	125	GGAGAGCCTTCCTTAGTACCTCTGACCATCTGGGCAAGGAGTTCAGGCCCGCTCTGAA	184		

Db 149 GGAGAGAGCCCCACTGCCCCCTGGACAATCTCGGCAAGAGTTCACTGCGGGCGCTGAG 208  
Qy 185 GAAGACTTCGAGGTGACGTTTCCCCAGGACGTAGGACACTGTGCTGATGCTGCGAGTCCAC 244  
Db 209 GAGGATTTCCAGTTCAGCTCCCGGAGGACGTAGGCGAGTCTGCTGTCGCGCTGCAC 268  
Qy 245 AAAGCACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGTGATGCTGTTCTGC 304  
Db 269 AAGGGCCCCC---AGTGTGCCCCCTGCTGGGGCCCCCTGGCCCCCGATGCTGTCTGTCG 325  
Qy 305 CCCTGTTTCGAGCTGGAGTGGCTACTCTGGGGCTGCACCTCCACTTCCCTCTGTTTATCAGTGG 364  
Db 326 CCGTGGTTCACGCTGCACCGCGCGGGGGCGCCACCTCTCTTCCCTGCTACAGTGG 385  
Qy 365 CTGGAAGGGGGCGGGGAGCTGTGTCTGAGAGAGGAGAGCAAGGTGTCTGGCAAGAC 424  
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Qy 425 CATCACTACACTGCAGGATCAGCGCCAGAGGAGCTTGAGTCCAGGCAGAGATGTAC 484  
Db 446 CACCACTCTGTCTCCAGCAAGCGCCAGGAGGAGCTTCAGGCCCGGAGGAGATGTAC 505  
Qy 485 AGCTGGAAGACTTACATTTGAAGTTGGCTCGCTGCTTGACACGAGACTGTGAAAGAC 544  
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Qy 605 TCCGGTATACGGAGCTGAAGTCAAGGGCTCTGGACCGCACAGGACTCTGGAGGAGT 664  
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Qy 665 CTGAGGGAGATGAGAGGCTGTGTTAACTTCGCAAGACTCCAGCAGCAGAGTATGTGTTT 724  
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Db 806 CTGATTCGCGCTGTCACTACCTCCCAAGAACTTCCCGCTCACTGATGCCATGTGGCC 865  
Qy 845 CCAGTGTGGGCCCTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904  
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Qy 905 GTGGATCATGGCATTTCTTTCTGGAGTCCACACCAACATCTCTCAATGGAAAGCCTCAGTTT 964  
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Qy 1025 GCATCCAGCTCAACAGACTCCGGGCGCAGACAACCCATCTCTCTGCCAGCGATGAC 1084  
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Qy 1085 ACGTGGGACTGTTGCTGGCCAAAGACCTGGGTTCCGAATTTCTGAGTTTTTACATCATCAG 1144  
Db 1106 AAGTGGGACTGTTGCTGGCCAGACCTGGGTGGCNAATGCCAGTTCTCTCTTCCATGAG 1165  
Qy 1145 GCTGTACACATCTCTGCTGATGCCCATCTGATTCAGAAAGTCTTTGCTTGGCCACATTA 1204  
Db 1166 GCGCTCAGGCACCTGCTGCACTACATCTGCTGCTGAGGCTTTCACCCCTGGCTACCCCTG 1225  
Qy 1205 GGTGAGCTGCTAGTGTGACCCCTCTCTCAAGCTATTGATTCCTACATTCGGTACACA 1264  
Db 1226 GGTGAGCTGCCCCACTGGCAACCTCTCTTCAAGCTGTGATCCCGCACACCCGATACACC 1285

Qy 1265 CTGCACATCAACACGCTTGGCCGGGAGCTGCTGTTGGCCCTGGGAAGTTGATAGACAG 1324  
Db 1286 CTGCACATCAACACACTCGCCCGGGAGCTGTTATTCGTGCGCAGGSCAGGTGGTGACAGG 1345  
Qy 1325 TCCACAGCCCTTGGCACCTGGGGGATTTCTGCACTGATAAAGAGAAACATGAGGACAGCTG 1384  
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Qy 1745 CTGCCACCTACCATGCACTACCACTACCTATCTTCCAAAGGCCAGGCCCGCTCAGAGT 1804  
Db 1766 CTGCCACCTACCATGCACTGCGCACCCACCTCCAAAGGCCCTGGCAACATGCGAGGSC 1825  
Qy 1805 TTCAATAGCCAGCTCCAGCAGGTTAAATTCGTCAAGTTATACATCATTCCTCTCTGGCTG 1864  
Db 1826 TTCAATAGCCACCTCCACCTGTCAATGCCACATGTGATGTCACTCTCTCTCTGGTTG 1885  
Qy 1865 CTAAGCCAGAACCTGGGGACCAAGGCCCTTGGSCCACTATCCAGATGAACACTTCCACA 1924  
Db 1886 CTGAGCAAGGAGCTTGGAGACCAAGGCCCTTGGSCACCTATCCGGATGAGCACTTCCACA 1945  
Qy 1925 GAGGATGCCCCCGCGAAGCTGTGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAG 1984  
Db 1946 GAGGAGGCCCTCGGGGAGCATCGCCACCTTCCAGAGCCGCTGGCCCGCAGATCTCGAGG 2005  
Qy 1985 GGCAATCAGGAGAGAAACCGAGGCTTGCACTGCCCCATACACTTACCTGATCTCCCTC 2044  
Db 2006 GGCAATCAGGAGCGAAACCGGGGCTGTGTGCTGCTGCTACACTTACAGACCTCCCTC 2065  
Qy 2045 ATTGAGACAGTGTCTCATCTTAACATCTTGGAGAGACAGTCCCTGTGTGACAT 2098  
Db 2066 ATCAGAAACAGCTCTCATCTTAATCCAGGGGAACACAGGCCCGCAGATGACAT 2119

RESULT 8  
BC063647

LOCUS BC063647 2686 bp mRNA linear PRI 30-JUN-2004  
DEFINITION Homo sapiens arachidonate 15-lipoxygenase, second type, mRNA (cdna clone MGC:75485 IMAGE:4804186), complete cds.

ACCESSION BC063647

VERSION BC063647.1 GI:39645887

KEYWORDS MGC.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2686)

AUTHORS Strausberg,R.L., Feingold,B.A., Grouse,L.H., Derge,J.G.,  
Klausner,R.D., Collins,F.S., Wagner,J., Shenmen,C.M., Schuler,G.D.,



Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Heieh, F., Diatchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Schaeetz, T. E., Brownstein, M. J., Uedlin, T. B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S. S., Iaquellano, N. A., Peters, G. J., Abramson, R. D., Mulhany, S. J., Bossak, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., Wille, K. C., Rodriguez, A. C., Grimwood, J., Schmutz, J., Myers, R. M., Butlerfield, Y. S., Krzyzanski, M. I., Skalska, U., Smalilus, D. E., Schnerch, A., Schein, J. E., Jones, S. J. and Marra, M. A.	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a> Contact: MGC help desk Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: James Cleaver, M.D. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: <a href="http://www.nisc.nih.gov/">http://www.nisc.nih.gov/</a> Contact: <a href="mailto:nisc_mgc@hgrl.nih.gov">nisc_mgc@hgrl.nih.gov</a> Akter, N., Ayle, K., Beckstrom-Sternberg, S. M., Benjamin, B., Blakesley, R. W., Bouffard, G. G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N. L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Maduro, Q. L., Masiello, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C., McDowell, J., Pearson, R., Stantrop, S., Thomas, P. J., Touchman, J. W., Tsugeon, C., Vogt, J. L., Walker, M. A., Wetherby, K. D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E. D.	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Series: IRAK plate: 134 Row: n Column: 5 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557308.
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ORGANISM Unknown.  
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AUTHORS Brash,A.R., Boeglin,W.E. and Jisaka,M.  
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Genes and proteins for prevention, prediction, prognosis and
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QY	1805 TTCAATAGCCACGCTCCAGCAGTTAATTGTCGAAGTATFACATCATTTGCTCTCTGGGTG 1864	
Db	1839 TTCAATAGCCACCTCCACCTGTCAATGCAATGTGATGTCTCTCTGCTCTCTGGTGTG 1898	
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QY	1925 GAGGATGCCCCCGCGAAGCGTGGCTTCTCCAGAGAAAGCTGATCCAGATCTCCAAG 1984	
Db	1959 GAGGAGGCCCTTCGGGGAGCATTCGCCACTTCCAGAGCCGCTGGCCACAGATCTCGAGG 2018	
QY	1985 GGCATCAGGGAGAGAACCGAGGCTTGCACTGCCCTTACACCTA CTTGATCTCTCCCTTC 2044	
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RESULT 12
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LOCUS
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ACCESSION   U78294
VERSION     U78294.1 GI:2224906
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2685)
AUTHORS     Brash,A.R., Boeglin,W.E. and Chang,M.S.
TITLE       Discovery of a second 15S-lipoxigenase in humans
JOURNAL     Proc. Natl. Acad. Sci. U.S.A. 94 (12), 6148-6152 (1997)
MEDLINE     97322340
PUBMED      9177185
REFERENCE   2 (bases 1 to 2685)
AUTHORS     Brash,A.R., Boeglin,W.E. and Chang,M.S.
TITLE       Direct Submission
JOURNAL     Submitted (14-NOV-1996) Clinical Pharmacology, Vanderbilt
University, MRB1 510 23rd Ave S. at Pierce, Nashville, TN
37232-6602, USA
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                   /db_xref="GI:2224907"
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Query Match      43.3%; Score 1395.2; DB 9; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

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QY      65 GGGGAAGCCTGTGGGGCTGGGCATGGGACAAAGTCTGTGTCAGCATGTGGGAACCCAC 124
Db      102 GGAGAAGCCTTCGGGGCTGGGCATGGGACAAAGTCTGTGTCAGCATGTGGGGACCCGG 161
QY      125 GGAGAGAGCCCTTAGTACTCTCGACCATCTGGGCAAGGAGTTCAGCGCCGGTCTGAA 184
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QY      185 GAAGACTTCGAGGTGACCGTCTCCCGAGGACGTAGGCATGTGTCGATGTCGAGTCCAC 244
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QY      245 AAGACACCCCGGAGTGTCCCTCCCGCTTATGTCTTCCGTTCTGATGCCCTGTCTGC 304
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QY      605 TCCCGGTATACGAGCTGAAGTCAAAAGGGCTCCCTGGACCGCAGCAGGACTCTGGAGGAGT 664
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QY      665 CTGAGGAGAGTAGAAGGCTGTTTAACTTCCGCAAGACTCCAGCAGCAGAGTATGTGTTT 724
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QY      725 GCACACTGGCAGGAAGATGCTTCTTCCGCTCCAGGTTCTTAAATGGCATCAACCCGCTC 784
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QY      785 CTGATTCCGCGCTGTCAAGTCTCCCAAAACAATCTCCCGGTCACTGATGAATGGTGGCC 844
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Db      1059 GCCATCCAGCTCAGCCAGACAGCCCGGCCCAACAGCCCACTCTTCTGCCCCATGATGAC 1118
QY      1085 ACGTGGGACTGCTGTGGCCAAAGACCTGGGTTCGCAATTCAGATTTTATCATCCATGAG 1144
Db      1119 AAGTGGGACTGCTGTGGCCAAAGACCTGGGTTCGCAATTCAGATTTTATCATCCATGAG 1178
QY      1145 GCTGTACACATCTGTGTCATGCCCCTCTGATTCAGAAAGTCTTGGCTTGGCCACATTA 1204
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Qy	755	TCCAGATTCTTAATGGGATCAACCCGGTCTCTGATTTGCGCGCTGTACAGTCTCCCAAC	814	
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RESULT 14

BVL 74905  
LOCTIS

### DEFINITION

1  
2  
3  
4  
5  
6  
7  
8  
9  
10

ACCESSION  
VEDSTON

## KEYWORDS

**SOURCE**

## ORGANISMI

## REFERENCE

## AUTHORS

**TITLE**

...

**JOURNAL**

COMMENT:

## FEATURES

**Sources**

41

OPTCTN  
STS

NOTES

Query M:

Best Local Similarity 79.7%; Pred. No. 0; Matches 1669; Conservative 0; Mismatches 419; Indels 6; Gaps 3;									
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QY	485	AGCTGAAGACTTACATTTGAAGGTGGCCCTCGCTGCTTGGACCAAGACTGTGAAAGAC	544						
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QY	725	GCACACTGGCAGGAGATGCTTCTTCGCTCCCACTTCCAGTTCCTAAATGGCATCAACCGGTC	784						
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QY	785	CTGATTTCGCGCTGTCACTAGTCTCCCAAAACAACTTCCCGGTCACTGATGAATGTTGGCC	844						
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QY	965	TTCTGAGCCCGCATGATCCCTGTGTACACAGAGCTCAGGGTCCGGACCCCTGTCTCCATT	1024						
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Job time : 9131.36 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 05:18:47 ; Search time 1096 Seconds  
(without alignments)  
17413.610 Million cell updates/sec

Title: US-10-688-676A-3

Perfect score: 3224

Sequence: 1 cagcttgagtagagagcta.....gtcataaagagttcattccc 3224

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N\_Geneseq\_16Dec04.\*

- 1: Geneseq1980a.\*
- 2: Geneseq1990a.\*
- 3: Geneseq2000a.\*
- 4: Geneseq2001a.\*
- 5: Geneseq2001bs.\*
- 6: Geneseq2002a.\*
- 7: Geneseq2002bs.\*
- 8: Geneseq2003a.\*
- 9: Geneseq2003bs.\*
- 10: Geneseq2003cs.\*
- 11: Geneseq2003ds.\*
- 12: Geneseq2004a.\*
- 13: Geneseq2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	3205	99.4	3232	12 ADQ91764	Adq91764 Mouse 8S-
3	1395.2	43.3	2647	2 AAX23827	Aax23827 Human 15S
4	1395.2	43.3	2685	5 AAD04501	Aad04501 Human 15S
5	1395.2	43.3	2685	6 ABK92181	Abk92181 Prostate
6	1395.2	43.3	2685	6 ABK64747	Abk64747 Human ben
7	1395.2	43.3	2685	8 ACA89907	ACA89907 Gene diff
8	1395.2	43.3	2685	12 ADQ91798	Adq91798 Human lip
9	1395.2	43.3	2685	12 ADQ37895	Adq37895 DNA encod
10	734.4	22.8	3127	13 ACN42888	ACN42888 Human dia
11	659.6	20.5	3320	6 ABA05968	ABA05968 Human lip
12	659.6	20.5	3320	10 RAD60556	Rad60556 Human lip
13	659.6	20.5	3384	3 AAC61761	Aac61761 cDNA enco
14	659.6	20.4	2136	12 ADQ48420	Adq48420 Human lip
15	658	20.4	2236	3 AAC61749	Aac61749 cDNA enco
16	658	20.4	2701	3 AAC61747	Aac61747 cDNA enco
17	658	20.4	2307	6 ABZ11921	Abz11921 Human pol
18	657	20.4	2307	12 ADM44439	Adm44439 Novel hum
19	657	20.4	2307	12 AAC61758	Aac61758 cDNA enco
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21	652.2	20.2	2136	6 ABA96003	Ab96003 Human lip
22	565.8	17.5	2469	3 AAS59659	Aas59659 DNA encod
23	565.8	17.5	2469	6 AAD34466	Aad34466 Human 12R
24	565.8	17.5	2469	12 ADG46601	Adg46601 Human 12R
25	565.8	17.5	2469	12 ADN04290	Adn04290 Antipsoi
26	466.2	14.5	1383	3 AAC61752	Aac61752 cDNA enco
27	466.2	14.5	1848	3 AAC61751	Aac61751 cDNA enco
28	466.2	14.5	2316	3 AAC61760	Aac61760 cDNA enco
29	442.6	13.7	2499	1 AAN90366	Aan90366 Synthetic
30	441.8	13.7	2500	3 AAA35130	Aaa35130 Human ade
31	441.8	13.7	2500	3 AAF21252	Aaf21252 Human low
32	441.8	13.7	2500	10 ABZ96946	Abz96946 Human nuc
33	441.8	13.7	2500	11 ABD20795	Abd20795 Human pul
34	441.8	13.7	11151	3 AAA35133	Aaa35133 Human ade
35	441.8	13.7	11181	3 AAF21255	Aaf21255 Human low
36	441.8	13.7	11181	10 ABZ96949	Abz96949 Human nuc
37	441.8	13.7	11181	11 ABD20798	Abd20798 Human pul
38	440.6	13.7	2497	3 AAA35132	Aaa35132 Human ade
39	440.6	13.7	2497	3 AAF21254	Aaf21254 Human low
40	440.6	13.7	2497	6 ABL65632	Ab165632 Lung canc
41	440.6	13.7	2497	6 ABL67646	Ab167646 Oesophagu
42	440.6	13.7	2497	6 ABL67509	Ab167509 Thyroid c
43	440.6	13.7	2497	6 ABT11115	Abt11115 Human 5-1
44	440.6	13.7	2497	6 ABK83762	Abk83762 Human cDN
45	440.6	13.7	2497	6 AAD24664	Aad24664 Human 5-1

#### ALIGNMENTS

RESULT 1  
AAD04502  
ID AAD04502 standard; cDNA; 3232 BP.  
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AC AAD04502;  
XX  
DT 04-JUL-2001 (first entry)  
XX  
DE Mouse 8S-lipoxygenase (8-Lox) cDNA.  
XX  
KW Mouse; 8S-lipoxygenase; 8-Lox; non-haeme iron dioxygenase;  
KW arachidonic acid; feed additive; livestock; antigen; ss.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT 5'UTR 1..27  
FT CDS /tag= a  
FT CDS 28..2061  
FT CDS /tag= b  
FT CDS /product= "Mouse 8S-lipoxygenase (8-Lox) protein"  
XX  
PN US6204037-B1.  
XX  
PD 20-MAR-2001.  
XX  
PF 16-APR-1998; 98US-00061768.  
XX  
PR 16-APR-1998; 98US-00061768.  
XX  
PA (UVA-) UNIV VANDERBILT.  
XX  
PI Brash AR, Boeglin WE, Jisaka M;  
XX  
DR WPI; 2001-289517/30.  
DR P-FSDB; AAE00936.  
XX  
PT New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed  
PT additives for livestock, or as antigens for producing antibodies.  
XX  
PS Example 2; Fig 5A-5C; 5lpp; English.  
XX  
CC The present sequence is mouse 8S-lipoxygenase (8-Lox) cDNA. Lipoxygenases

CC are a structurally related family of non-haeme iron dioxygenases that  
CC function in the production of fatty acid hydroperoxides. 8-Lox acts in  
CC the metabolism of arachidonic acid to 8S-hydro(pero)xyeicosatetraenoic  
CC acid. Lipoxigenase DNA can be used as diagnostic tools to detect normal  
CC and abnormal DNA sequences derived from patient cells, for detecting and  
CC isolating other members of the polypeptide family and related  
CC polypeptides from a DNA library potentially containing the sequences, as  
CC primers for hybridising to related sequences for amplifying those  
CC sequences or for altering native lipoxigenase DNA sequences. The  
CC lipoxigenase is useful as feed additives for livestock and as antigens  
CC for producing antibodies. Note: The present sequence is also shown in  
CC column 51-58 of the specification, but lacks 27 nucleotides at its 5' end  
XX  
SQ Sequence 3232 BP; 823 A; 872 C; 782 G; 755 T; 0 U; 0 Other;

Query Match 99.4%; Score 3205; DB 5; Length 3232;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3216; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 8 CAGTAGAGAGCTAAACTGGTTCAGGAGGATGGCGAAATGCAGGGTGAGAGTATCCACGGGG 67  
DB 1 CAGTAGAGAGCTAAACTGGTTCAGGAGGATGGCGAAATGCAGGGTGAGAGTATCCACGGGG 60  
QY 68 GAAGCCTGTGGGGCTGGCAGATGGGACAAAGTGTCTGTCAAGCATCTGTGGGAACCCACGGA 127  
DB 61 GAAGCCTGTGGGGCTGGCAGATGGGACAAAGTGTCTGTCAAGCATCTGTGGGAACCCACGGA 120  
QY 128 GAGAGCCCTTAGTACTCTCGACCATCTGGGCAAGAGTTTCAGGCCCGGTCTGAAGAA 187  
DB 121 GAGAGCCCTTAGTACTCTCGACCATCTGGGCAAGAGTTTCAGGCCCGGTCTGAAGAA 180  
QY 188 GACTTCGAGGTGACCGCTTCCCAGGACGTAGGCACCTGTGATGCTGGAGTCCACAAA 247  
DB 181 GACTTCGAGGTGACCGCTTCCCAGGACGTAGGCACCTGTGATGCTGGAGTCCACAAA 240  
QY 248 GCACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCCCTGGTTCTGCCGC 307  
DB 241 GCACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCCCTGGTTCTGCCGC 300  
QY 308 TGGTTCCAGCTGGAGTGGCTACTCTGGGGCTGCATCCACTTCCCTGTTTACGTGGGCTG 367  
DB 301 TGGTTCCAGCTGGAGTGGCTACTCTGGGGCTGCATCCACTTCCCTGTTTACGTGGGCTG 360  
QY 368 GAAGGGCGGGGAGCTGTGTGTGAGAGGGAGCAGCAAGGTGTCTTGGCAAGACCAT 427  
DB 361 GAAGGGCGGGGAGCTGTGTGTGAGAGGGAGCAGCAAGGTGTCTTGGCAAGACCAT 420  
QY 428 CACCTTACATCTGAGGATCAGGCCAGAGAGGAGCTTGTAGTCCAGGAGAAAGATGTACAGC 487  
DB 421 CACCTTACATCTGAGGATCAGGCCAGAGAGGAGCTTGTAGTCCAGGAGAAAGATGTACAGC 480  
QY 488 TGGAGACTTACATTGAAGTTGGCTCGCTGCTTGACACGAGACTGTGAAGACTTG 547  
DB 481 TGGAGACTTACATTGAAGTTGGCTCGCTGCTTGACACGAGACTGTGAAGACTTG 540  
QY 548 GACCTCAACATCAAGTACTCTGGATGAAGATGCAAACTCTTCTTTAAAGCCCACTCC 607  
DB 541 GACCTCAACATCAAGTACTCTGGATGAAGATGCAAACTCTTCTTTAAAGCCCACTCC 600  
QY 608 GCGTATACGAGGTGAAAGTCAAAAGGGCTCTGGACCGCAGCAAGGACTCTTGGAGGAGTCTG 667  
DB 601 GCGTATACGAGGTGAAAGTCAAAAGGGCTCTGGACCGCAGCAAGGACTCTTGGAGGAGTCTG 660  
QY 668 AGGGAGATGAGAGGCTGTGTTAACTTCGCAAGACTCCAGCAGCAGAGATGTGTTTGA 727  
DB 661 AGGGAGATGAGAGGCTGTGTTAACTTCGCAAGACTCCAGCAGCAGAGATGTGTTTGA 720  
QY 728 CACTGCGAGAGATGCCCTTCTTCGCTCCCACTTCTTAAATGGCATCAACCGGTCTTG 787  
DB 721 CACTGCGAGAGATGCCCTTCTTCGCTCCCACTTCTTAAATGGCATCAACCGGTCTTG 780  
QY 788 ATTTCGGCTGTACAGTCTCCAAACAACTTCCGGTCACTGATGAATGGTGGCCCA 847

DB 781 ATTCCCGCGCTGTGCACAGTCTCCAAAACAACTTCCCGGTCACTGATGAATAATGTGGCCCCA 940  
QY 848 GTGCTGGGCGCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAAAGGCTCCCTGTTCTTGGTG 907  
DB 841 GTGCTGGGCGCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAAAGGCTCCCTGTTCTTGGTG 900  
QY 908 GATCATGGCATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCCTCAGTTCTCT 967  
DB 901 GATCATGGCATTTCTTTCTGGAGTCCACCAACATCTCTCAATGGAAAGCCTCAGTTCTCT 960  
QY 968 GCAGCCCCGATGACCCCTGTTCACAGAGCTCAGGGTCCGAGCCCTGCTGCCCATGCC 1027  
DB 961 GCAGCCCCGATGACCCCTGTTCACAGAGCTCAGGGTCCGAGCCCTGCTGCCCATGCC 1020  
QY 1028 ATCCAGCTCAAAACAGACTCCCGGGCGAGAACACCCCATCTTCTCCGCCAGCGATGACAG 1087  
DB 1021 ATCCAGCTCAAAACAGACTCCCGGGCGAGAACACCCCATCTTCTCCGCCAGCGATGACAG 1080  
QY 1088 TGGGACTGGTTGCTGGCCAAAGACTCTGGGTTCGCAATCTGAGTTTATCATCATGAGGCT 1147  
DB 1081 TGGGACTGGTTGCTGGCCAAAGACTCTGGGTTCGCAATCTGAGTTTATCATCATGAGGCT 1140  
QY 1148 GTCAACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTGCCCTTGGCCACATTAAGT 1207  
DB 1141 GTCAACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTGCCCTTGGCCACATTAAGT 1200  
QY 1208 CAGCTGCCCTAGGTGTCAACCTCTTCTCAAGCTATTGATTCTCTCAATTCGGGTACACACTG 1267  
DB 1201 CAGCTGCCCTAGGTGTCAACCTCTTCTCAAGCTATTGATTCTCTCAATTCGGGTACACACTG 1260  
QY 1268 CACATCAACACGCTTGGCCGGAGCTGCTCGTTGCCCTTGGAAAGTTGATAGCAAGTCC 1327  
DB 1261 CACATCAACACGCTTGGCCGGAGCTGCTCGTTGCCCTTGGAAAGTTGATAGCAAGTCC 1320  
QY 1328 ACAGGCTTGGCACTGGGGGATCTCTGACCTGTATAAGAGAAACATGAGCAGCTGAAC 1387  
DB 1321 ACAGGCTTGGCACTGGGGGATCTCTGACCTGTATAAGAGAAACATGAGCAGCTGAAC 1380  
QY 1388 TACTCTGCTGTGCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCAGGC 1447  
DB 1381 TACTCTGCTGTGCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCAGGC 1440  
QY 1448 TACTATTACCGAGATGATGGGATGAGATCTGGGGGCAATAAAGAGCTTTGCTCTGAA 1507  
DB 1441 TACTATTACCGAGATGATGGGATGAGATCTGGGGGCAATAAAGAGCTTTGCTCTGAA 1500  
QY 1508 ATAGTCAGCATCTACTATCCAAAGTGCACATCCGTCGAAGATGACCAAGAGCTCCAGGC 1567  
DB 1501 ATAGTCAGCATCTACTATCCAAAGTGCACATCCGTCGAAGATGACCAAGAGCTCCAGGC 1560  
QY 1568 TGGGTGAGGAGATCTTCTTGAGGGCTTCTCCGCGCGAGAAAGCTCAGGTATGCCCTCC 1627  
DB 1561 TGGGTGAGGAGATCTTCTTGAGGGCTTCTCCGCGCGAGAAAGCTCAGGTATGCCCTCC 1620  
QY 1628 TTGTTGGATACCCCGGAAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACCTGCTCA 1687  
DB 1621 TTGTTGGATACCCCGGAAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACCTGCTCA 1680  
QY 1688 GCCAAGATGACGTGTGTCAGTTCAGGCCAGTTCGATCTTGTGTTTGGATGCCAATCTG 1747  
DB 1681 GCCAAGATGACGTGTGTCAGTTCAGGCCAGTTCGATCTTGTGTTTGGATGCCAATCTG 1740  
QY 1748 CCACCTTACATGACGTATCCACCTACTTCCAAAGGCCAGGCCCGGCTCAGAGTTTC 1807  
DB 1741 CCACCTTACATGACGTATCCACCTACTTCCAAAGGCCAGGCCCGGCTCAGAGTTTC 1800  
QY 1808 ATAGCCAGCTCCCAAGCAGTTAAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTGCTA 1867  
DB 1801 ATAGCCAGCTCCCAAGCAGTTAAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCTGCTA 1860  
QY 1868 AGCGAGAACTGTGGGACCAAGAGCCCTCGGCCATATCCAGATGAACACTTTCACAGAG 1927  
DB 1861 AGCGAGAACTGTGGGACCAAGAGCCCTCGGCCATATCCAGATGAACACTTTCACAGAG 1920





XX	Sequence	3232 BP; 823 A; 872 C; 782 G; 755 T; 0 U; 0 Other;	
SQ	Query Match	99.4%; Score 3205; DB 12; Length 3232;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 3216; Conservative	0; Mismatches 0; Indels 1; Gaps 1;	
QY	8	CAGTAGAGAGCTAAACTGTGTCAAGAGGATGGCGAAATGCAGGGTGAGAGTATCCACGGGG	67
DB	1	CAGTAGAGAGCTAAACTGTGTCAAGAGGATGGCGAAATGCAGGGTGAGAGTATCCACGGGG	60
QY	68	GAAGCTGTGGGGCTGGGCATGGGCAAAAGTGTCTGTTCAGCATCGTGGGAACCCACCGGA	127
DB	61	GAAGCTGTGGGGCTGGGCATGGGCAAAAGTGTCTGTTCAGCATCGTGGGAACCCACCGGA	120
QY	128	GAGAGCCCTTAGTACTCTCTGACCATCTGGGCAAGGAGTTCCAGGCCCGGTCTGAAGAA	187
DB	121	GAGAGCCCTTAGTACTCTCTGACCATCTGGGCAAGGAGTTCCAGGCCCGGTCTGAAGAA	180
QY	188	GACTTCGAGGTGACGCTTCCCGAGGACGTPAGGCACTGTGCTGATGTCGAGTCACACAA	247
DB	181	GACTTCGAGGTGACGCTTCCCGAGGACGTPAGGCACTGTGCTGATGTCGAGTCACACAA	240
QY	248	GCACCCCGGGAAGTGTCCCTCCGCTTAGTCTTTCCTGCTGATGCCTGTGTTCTGCCGC	307
DB	241	GCACCCCGGGAAGTGTCCCTCCGCTTAGTCTTTCCTGCTGATGCCTGTGTTCTGCCGC	300
QY	308	TGGTTTCGAGCTGGAGTGGCTACTCTGGGCTGCACTCCCACTTCCCTCTGTTATCAGTGGGTG	367
DB	301	TGGTTTCGAGCTGGAGTGGCTACTCTGGGCTGCACTCCCACTTCCCTCTGTTATCAGTGGGTG	360
QY	368	GAAGGGCGGGGAGCTGTGTCTGAGAGAGGAGCAGCAAAAGTGTCTGGCAAGACCAT	427
DB	361	GAAGGGCGGGGAGCTGTGTCTGAGAGAGGAGCAGCAAAAGTGTCTGGCAAGACCAT	420
QY	428	CACCTTACACTCCAGGATCAGCCGCAAGAGAGCTTGAGTCCAGGCAAGAGTGTACAGC	487
DB	421	CACCTTACACTCCAGGATCAGCCGCAAGAGAGCTTGAGTCCAGGCAAGAGTGTACAGC	480
QY	488	TGGAGACTTACATTGAAGGTTGGCTCGCTGCTTGACACGAGACTGTGAAGACTTG	547
DB	481	TGGAGACTTACATTGAAGGTTGGCTCGCTGCTTGACACGAGACTGTGAAGACTTG	540
QY	548	GACCTCAACATCAAGTACTCTCGATGAAGAATGCCAACTCTTCTTTAAAGCCCACTCC	607
DB	541	GACCTCAACATCAAGTACTCTCGATGAAGAATGCCAACTCTTCTTTAAAGCCCACTCC	600
QY	608	GGGTATACGGAGCTGAAGTCAAGGGCTCTGGACCGCACAGGACTCTGGAGGAGTCTG	667
DB	601	GGGTATACGGAGCTGAAGTCAAGGGCTCTGGACCGCACAGGACTCTGGAGGAGTCTG	660
QY	668	AGGGAGATCAGAAGGCTGTTTAACCTTCGCAAGACTCCAGCAGCAGAGTATGTGTTGCA	727
DB	661	AGGGAGATCAGAAGGCTGTTTAACCTTCGCAAGACTCCAGCAGCAGAGTATGTGTTGCA	720
QY	728	CACCTGCAGGAAGATGCTTCTTGGCTCCCGATTCCTAAATGGCATCAACCGGTCCTG	787
DB	721	CACCTGCAGGAAGATGCTTCTTGGCTCCCGATTCCTAAATGGCATCAACCGGTCCTG	780
QY	788	ATTGCGCGCTGTACAGTCTCCCAACCACTTCCCGGTCACTGATGAATGTTGGCCCCA	847
DB	781	ATTGCGCGCTGTACAGTCTCCCAACCACTTCCCGGTCACTGATGAATGTTGGCCCCA	840
QY	848	GTGCTGGGCGCTGGAAACAGTCTGCAAGGCTGAGTTGGAGAGGGCTCCCTGTTCTGGTG	907
DB	841	GTGCTGGGCGCTGGAAACAGTCTGCAAGGCTGAGTTGGAGAGGGCTCCCTGTTCTGGTG	900
QY	908	GATCATGGCATTTCTTTCTGAGTTCACACCAACATCTCAATGGAAAGCCTCAGTTCTCT	967
DB	901	GATCATGGCATTTCTTTCTGAGTTCACACCAACATCTCAATGGAAAGCCTCAGTTCTCT	960
QY	968	GCAGCCCGATGACCCCTGTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCATGGCC	1027

DB	961	GCAGCCCGATGACCCCTGTTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCATTGCC	1020
QY	1028	ATCCAGCTCAAAACAGACTCCCGGGGCAGACAAACCCCATCTTCTCCGCCAGCGATACACG	1087
DB	1021	ATCCAGCTCAAAACAGACTCCCGGGGCAGACAAACCCCATCTTCTCCGCCAGCGATACACG	1080
QY	1088	TGGGACTGTTGCTGGCCCAAGACCTGGGTTCGCAATTCGTAGTTTTTACATCATGAGGCT	1147
DB	1081	TGGGACTGTTGCTGGCCCAAGACCTGGGTTCGCAATTCGTAGTTTTTACATCATGAGGCT	1140
QY	1148	GTACACATCTGCTGTCATGCCCATCTGATTCAGAAAGTCTTTGGCTTGGCCACATTAAGT	1207
DB	1141	GTACACATCTGCTGTCATGCCCATCTGATTCAGAAAGTCTTTGGCTTGGCCACATTAAGT	1200
QY	1208	CAGTGCCTAGGTGTCACCTCTCTTCAAGCTATTGATTCCTCACTTCGGGTACACATG	1267
DB	1201	CAGTGCCTAGGTGTCACCTCTCTTCAAGCTATTGATTCCTCACTTCGGGTACACATG	1260
QY	1268	CACATCAACACGCTTGGCCGGAGCTGCTCGTGGCCCTGGGAAGTGTGATACAAAGTCC	1327
DB	1261	CACATCAACACGCTTGGCCGGAGCTGCTCGTGGCCCTGGGAAGTGTGATACAAAGTCC	1320
QY	1328	ACAGGCTTGGCACTGGGGGATTTCTCTGACCTGTATAAAGAGAAACATGAGCAGCTGAAC	1387
DB	1321	ACAGGCTTGGCACTGGGGGATTTCTCTGACCTGTATAAAGAGAAACATGAGCAGCTGAAC	1380
QY	1388	TACTCTGCTGTGTCTCTCGAAGATTCGAGGCCCGAGGGTGTGGAAGACATCCAGGC	1447
DB	1381	TACTCTGCTGTGTCTCTCGAAGATTCGAGGCCCGAGGGTGTGGAAGACATCCAGGC	1440
QY	1448	TACTATTACCGAGATGATGGGATGCAGATCTGGGGGGCAATAAAGAGCTTCTCTCTGAA	1507
DB	1441	TACTATTACCGAGATGATGGGATGCAGATCTGGGGGGCAATAAAGAGCTTCTCTCTGAA	1500
QY	1508	ATAGTCAGCATCTACTATCCAAAGTCACACATCCGTCCTCAAGATGACCAAGAGCTCCAGGC	1567
DB	1501	ATAGTCAGCATCTACTATCCAAAGTCACACATCCGTCCTCAAGATGACCAAGAGCTCCAGGC	1560
QY	1568	TGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCTCGCGCGAGAAAGCTCAGGTATGCCCTCC	1627
DB	1561	TGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCTCGCGCGAGAAAGCTCAGGTATGCCCTCC	1620
QY	1628	TGTTTGGATACCCGGGAAGCCCTGTCAGATATATACCATGGTATATACCTGCTCA	1687
DB	1621	TGTTTGGATACCCGGGAAGCCCTGTCAGATATATACCATGGTATATACCTGCTCA	1680
QY	1698	GCCAAAGCATGCACTGTCTGAGTTCAGGCCAGTTCGACTCTTGTGTTTGGATGCCAATCTG	1747
DB	1681	GCCAAAGCATGCACTGTCTGAGTTCAGGCCAGTTCGACTCTTGTGTTTGGATGCCAATCTG	1740
QY	1748	CCACCTACATGCACTACCCACCTACTTCCAAAGGCCAGGCCCGGCTCAGAGTTTC	1807
DB	1741	CCACCTACATGCACTACCCACCTACTTCCAAAGGCCAGGCCCGGCTCAGAGTTTC	1800
QY	1808	ATAGCCAGCTCCAGCAGTAAATTCGTCAGTATATCATCATCTCTCTGGCTGCTA	1867
DB	1801	ATAGCCAGCTCCAGCAGTAAATTCGTCAGTATATCATCATCTCTCTGGCTGCTA	1860
QY	1868	AGCGCAGAACCTGGGGACCAAGGGCCCTGGGCCACTATCCAGATGAAACACTTTCACAGAG	1927
DB	1861	AGCGCAGAACCTGGGGACCAAGGGCCCTGGGCCACTATCCAGATGAAACACTTTCACAGAG	1920
QY	1928	GATGCCCCCGCGAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAGGC	1987
DB	1921	GATGCCCCCGCGAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAGGC	1980
QY	1988	ATCAGGGAGAGAAACGAGGCTTGGCACTGCCCTACACCTACTGATCCTCCCTCAAT	2047
DB	1981	ATCAGGGAGAGAAACGAGGCTTGGCACTGCCCTACACCTACTGATCCTCCCTCAAT	2040
QY	2048	GAGAAACAGTGTCTCTCAATCTTAAACATCTTGGAGAAAGCAGTCTCTGTGTGACATATAGAATC	2107
DB	2041	GAGAAACAGTGTCTCTCAATCTTAAACATCTTGGAGAAAGCAGTCTCTGTGTGACATATAGAATC	2100



QY 125 GGAGAGAGCCCTTGTGTA CTTCTGGACCAATCTGGGCAAGAGTTTCAAGCCCGGTGCTGAA 184  
DB 162 GGAGAGAGCCCTTGTGTA CTTCTGGACCAATCTGGGCAAGAGTTTCAAGCCCGGTGCTGAA 221  
QY 185 GAAGACTTCGAGGTGAGCTTCCCAAGGAGTAGGCACTGTGCTGATGCTGGAGTCCAC 244  
DB 222 GAGGACTTCAGGTGAGCTTCCCGAGGAGCTAGGCGGAGTGTGCTGTGCTGCGCTGAC 281  
QY 245 AAAGCAACCCCGGAAGTGTCTCCCGCTTATATGTCCTTCGTTCTGATGCTGCTGCTG 304  
DB 282 AAGCGCCCCC --- AGTGTGCTCCCTGCTGGGGCCCTGCGCCCGATGCTGCTGCTG 338  
QY 305 CGCTGTTTCGAGTGGAGTGTCTGCTGGGCTGCACTCCATCTCCCTGTTATCAGTGG 364  
DB 339 CGCTGTTTCAGCTGACACCGCGCGGGCGGCACTCTCTTCCCTGCTACCAAGTGG 398  
QY 365 CTGGAGGGCGGGGAGTGTGCTGAGAGGAGGAGCAAGGTGCTTGGGCAAGAC 424  
DB 399 CTGGAGGGCGGGGAGCCCTGCTGCTGAGAGGGGTACAGCCAAAGGTGCTTGGGCAAG 458  
QY 425 CATCACTTACCTGAGGATCAGCCCAAGAGGAGCTTGAAGTCCAGGCGAGAGATGTAT 484  
DB 459 CACCACTTGTCTCAGCAACAGCGCAGGAGGAGCTTCAAGCCCGGCGAGGATGTAT 518  
QY 485 AGCTGAAAGACTTACATTTGAAGTTGGCTGCTGCTTGAACAAGAGACTGTGAAAGAC 544  
DB 519 CAGTGGAAAGGCTTACAAACAGGTTGGCTCTCACTGCTGCTGATGAAAGACAGTGGAAAG 578  
QY 545 TTGGACTCAACATCAAGTACTCTGCGATGAGAGTGCAGAACTCTTCTTAAAGCCAC 604  
DB 579 TTGGAGCTCAATATCAAAATCTCCAAGCAAGAAATGCCAACTTTTATCTAAGCTGGC 638  
QY 605 TCCGCGTATACGAGCTGAAAGTCAAAGGCTCTCTGGAACGACAGCACTCTGGAGGAGT 664  
DB 639 TCTGCTTTTCAGAGATGAATAATCAAGGGTGTCTGGAACGAGGGCTCTGGAGGAGT 698  
QY 665 CTGAGGAGATGAGAGGCTGTTTAACTTCGCAAGACTCCAGAGCAAGATGTTT 724  
DB 699 CTGAATGAGATGAAAGGATCTTCACTTCGAGGAGACCCAGAGCTGAGCAAGCATTT 758  
QY 725 GCACACTGGCAGAGATGCTTCTTGGCTCCAGTCTCTAAATGGCATCAACCCGCTC 784  
DB 759 GAGCATGGCAGAGATGCTTCTTGGCTCCAGTCTCTGAATGGTCTCAACCCCTGTC 818  
QY 785 CTGATTTGCGCGCTGTCACTGCTTCCCAACAACTTCCCGTCACTCATGAATGGTGGCC 844  
DB 819 CTGATTCGCGCGCTGTCACTACCTCCCAAGAACTTCCCGTCACTGATGCCATGGTGGCC 878  
QY 845 CCAAGTCTGGGCGCTGGAACCAAGTCTGCAAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904  
DB 879 TCAATTTGGGTCTTGGGACCAAGCTTGCAGGCTGAGCTAGAGAGGGCTCCCTGTTCTTG 938  
QY 905 GTGGATCATGGCAATCTTCTGAGTTCACACCAACATCTCTAATGGAAAGCTCAGTTC 964  
DB 939 GTGGATCATGGCAATCTCTCTGGCATCCAGCAACATGTCTAATGGGAAGCGCAGTTC 998  
QY 965 TCTGCAAGCCCGATGACCTGTTTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAT 1024  
DB 999 TCTGCGGCCCCAATGACCTGTCTATACAGAGCCAGGCTGCGGGCGCTGTGCTCTCTC 1058  
QY 1025 GCATCCAGCTCAACAGACTCCCGGGCCAGAACCCCACTCTTCTGCTCCCAAGCATGAC 1084  
DB 1059 GCCATCCAGCTCAGCCAGACCCCGGGCCCAACAGCCCCATCTTCTGCGCCACTGATGAC 1118  
QY 1085 ACGTGGAGCTGGTGTGCGCAAGACCTGGGTTCGCAATCTGAGTTTACATCCATGAG 1144  
DB 1119 AAGTGGAGCTGGTGTGCGCAAGACCTGGGTTCGCAATCTGAGTTTCTCTTCCATGAG 1178  
QY 1145 GCTGTCAACATCTGCTGATGCCATCTGATTTCCAGAAAGTCTTTCCTTTGGCCACATTA 1204  
DB 1179 GCCTCAGGACCTGCTGCACTCAATCTGCTGCTGAGGTCTTCACTTGGTACCTGCT 1238  
QY 1205 CGTCACTGCTAGGTGTCAACCTCTCTTCAAGCTATTGATTCTCTCAATTCGGTACACA 1264

## RESULT 4

AAD04501

ID AAD04501 standard; cdNA; 2685 BP.

XX AAD04501;

XX 04-JUL-2001 (first entry)

XX Human 15S-lipoxigenase (15-Lox-2) cdNA.

DE Human; 15S-lipoxigenase; 15-Lox-2; non-haeme iron dioxxygenase;

KW arachidonic acid; feed additive; livestock; antigen; ss.

XX

DB 1239 CGTCAAGCTGCCCACTGCCACCCCTCTCTCAAGCTGCTGATCCCGCACACCCGATACACC 1298  
QY 1265 CTGCACATCAACACACCTTTGCCGGAGTGTCTGTTGCCCTTGGGAAGTTGATAGCAAG 1324  
DB 1299 CTGCACATCAACACACTGCCCGGAGTGTCTTATCTGTCGCCAGGCGAGGTGGTGGACAG 1358  
QY 1325 TCACAGAGCCCTTGGCACTGGGGGATTTCTCTGACCTGATAAAGAGAAACATGAGAGAGCTG 1384  
DB 1359 TCACAGGCACTCGGCATTTGAAGGCTCTCTGAGTTGATACAGAGGAACATGAAGAGCTG 1418  
QY 1385 AACTACTCTGCTCTGCTGCTCCCTGAAAGATATCCGAGCCCGAGGTGTGGAGACATCCCA 1444  
DB 1419 AACTATTCTCTCTGCTGCTCCCTGAGGATATCCCGAGCCCGAGGAGTTGAAGACATCCCA 1478  
QY 1445 GGCTACTATTACCGAGATGATGGGATGAGATCTCGGGGGCAATAAAGAGCTTTGTCTCT 1504  
DB 1479 GGCTACTACTACCGTATGATGGGATGAGATTTGGGGTGCAGTGGAAAGCTTTGTCTCT 1538  
QY 1505 GAAATAGTCAGCATCTACTATCCAAAGTACACATCCGTCCTCAAGATGAACAAGAGCTCCAG 1564  
DB 1539 GAAATCATCGGTATCTACTA CCAAGTGA TGAAGTCTGTCCAAGATGA CAGAGAGCTCCAG 1598  
QY 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCTCGGCGGCAAGAGCTCAGGATGCCC 1624  
DB 1599 GCCTGGGTGAGGAGATCTTCTCAAGGGCTTCTTAAACCAAGGAGAGCTCAGGATCCCT 1658  
QY 1625 TCCTTGTGTTGGATACCCCGGAAGCCCTGCTCAGATATATACCATGTGTGATATTCACCTGC 1684  
DB 1659 TCCTCACTGGAGACCCCGGAAGCCCTGCTGAGTATGTCACATGTTGATATTCACCTGC 1718  
QY 1685 TCAGCAAGCATGCAAGCTGTCTAGTTTCAGGCCCAAGTTGCACTCTTGTGTTGGATGCCAAT 1744  
DB 1719 TCAGCAAGCATGCGGCTGTCTGTCAGGGCAGTTTGAAGTCTGCTGCTGGATGCCAAC 1778  
QY 1745 CTGCACACCTACATGCACTACCACTACTTCTTCAAAGGCCAGGCCGCGCTCAGAGT 1804  
DB 1779 CTGCCACCCAGCATGCACTGCTGCCACCCACCTCCAAGGGCTTGGCAACATGCGAGGCG 1838  
QY 1805 TTCTATAGCCAGCTCCCAAGCAGTTAAATTTGTCAGTGTATCATCATTTGCTCTCTGGCTG 1864  
DB 1839 TTCTATAGCAACCTCCCACTGTCTAATGGCATGTGTGATCTCTTGTCTCTGTTG 1898  
QY 1865 CTAAGCGCAGAACCTGGGGACCAAGGCCCTTGGGCCACTATCCAGATGAACAATTCA 1924  
DB 1899 CTGAGCAAGGAGCTTGGAGACCAAGGGCCCTTGGGCACTATCCGATGAGCACTTCA 1958  
QY 1925 GAGGATGCCCCCGGGAGAGCGTGGCTTCCAGAGAAAGCTGATCCAGATCTCCAG 1984  
DB 1959 GAGGAGGCCCTTGGCGGAGCATCGCCACCTTCCAGAGCCCGCTGGCCCGAGATCTCGAG 2018  
QY 1985 GGCATCAGGAGAGGAACCGAGGCTTGGCACTGCGCTACACCTAGCTGATCCTCCCCCTC 2044  
DB 2019 GGCATCCAGGAGCGGAACCGGGCCCTGTTGTCCTTACCTACCTAGACCTTCCCTC 2078  
QY 2045 ATTGAGAACAGTGTCTCCATCTTAACATCTTGGAGAAAGAGTCTGTTGTGACAT 2098  
DB 2079 ATCGAGAACAGGTCTCCATCTTAATCCAGGGGAACACAGGCCCCAGATGACAT 2132

OS Homo sapiens.  
 XX Key Location/Qualifiers  
 FH FT 72..2102  
 CDS /\*tag=a  
 /product="Human 15S-lipoxygenase (15-Lox-2) protein"  
 XX US6204037-B1.  
 XX 20-MAR-2001.  
 XX 16-APR-1998; 98US-00061768.  
 XX 16-APR-1998; 98US-00061768.  
 XX (UYVA-) UNIV VANDERBILT.  
 XX Brash AR, Boeglin WE, Jiseaka M;  
 XX WPI; 2001-289517/30.  
 DR P-PSDB; AAE00935.  
 XX New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed  
 PT additives for livestock, or as antigens for producing antibodies.  
 XX Claim 3; Col 43-48; 51pp; English.  
 XX The present sequence is human 15S-lipoxygenase (15-Lox-2) cDNA.  
 CC Lipoxygenases are a structurally related family of non-haeme iron  
 CC dioxygenases that function in the production of fatty acid  
 CC hydroperoxides. 15-Lox-2 acts in the metabolism of arachidonic acid to  
 CC 15S-hydroperoxyicosatetraenoic acid. Lipoxygenase DNA can be used as  
 CC diagnostic tools to detect normal and abnormal DNA sequences derived from  
 CC patient cells, for detecting and isolating other members of the  
 CC polypeptide family and related polypeptides from a DNA library  
 CC potentially containing the sequences, as primers for hybridising to  
 CC related sequences for amplifying those sequences or for altering native  
 CC lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives  
 CC for livestock and as antigens for producing antibodies  
 XX Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;  
 SQ  
 Query Match 43.3%; Score 1395.2; DB 5; Length 2685;  
 Beat Local Similarity 79.8%; Pred. No. 0;  
 Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;  
 7 GCAGTAGAGAGCTAAACT--GGTCAGGAGGATGGCGAAATGCAGGGTCGAGAGTATCCACG 64  
 42 GCCGTAGAGAGCTGGACTTAGGCTGGCAGCATGGCCGAGTTCAGGGTCAGGGTGTCCACC 101  
 65 GGGGAAGCCTGTGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATGTGGGAACCCAC 124  
 102 GGAGAAGCCTTCGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATGTGGGGACCCGG 161  
 125 GGAGAGAGCCCTTAGTACCTGTGACCATCTGGGCAAGAGTTCAGGCGCGGTCTGAA 184  
 162 GGAGAGAGCCCCCACTGCCCTTGACATCTCGGCAAGAGTTCAGTCCGGGCGCTGAG 221  
 185 GAAGACTTCGAGGTGACCTTCCCGAGGACGTGAGGACCTGTGCTGATGCTGGAGTCCAC 244  
 222 GAGGACTTCGAGGTGACCTTCCCGAGGACGTGAGGACGTGCTGCTGCGCGTGCAC 281  
 245 AAAGCACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCTGTTCTGCG 304  
 282 AAGGCGCCCC--AGTGTGCCCTGTGGGGCCCCCTGGCCCCCGATGCTGTTCTGCG 338  
 305 CGCTGGTTCGAGCTGGAGTGGTCACTCGGGGCTGCATCCACTTCCCTCTGTTATCAGTGG 364  
 339 CGCTGGTTCGAGCTGACACCGCGGGGGCGGCCACCTCTCTTCCCTGCTTACCACTGG 398  
 365 CTGGNAGGGCGGGGAGCTGGTGTGTGAGAGGGGAGCAGCAAGGTGTCTTGGCAGAC 424  
 399 CTGGAGGGGGGGGAGCCCTGGTGTGTGAGAGGGGTACAGCCNAGGTGTCTTGGGCGAC 458

QY 425 CATCACTCACTGCAGGATCAGCGCCAGAGAGCTTGAGTCCAGGCGAGAGATGTAC 484  
 DB 459 CACCACCTGTGTCTCCAGCAACAGCGCCAGGAGAGCTTCAGGCCCGCAGAGATGTAC 518  
 QY 485 AGCTGGAGAGCTTACATTTGAAGGTTGGCTCGCTCGCTTGGACCGAGACTGTGAAAGAC 544  
 DB 519 CAGTGGAGAGGCTTACACCAGGTTGGCTCCTCCTGCTGGATGAAAGACAGTGGAGAC 578  
 QY 545 TTGACCTCAACATCAAGTACTCTGCGATGAAGATGCCAAACTCTTCTTTAAAGCCAC 604  
 DB 579 TTGAGCTCAATATCAATACTCCACAGCCAAAGATGCCAACTTTTATCTCAAGCTGCG 638  
 QY 605 TCCGCGTATACGGAGCTGAAAGTCAAAGGCTCTCTGGAACCGCAGAGACTCTGAGGAGT 664  
 DB 639 TCTGCTTTTGAGAGATGAAATCAAGGGGTGTGGACCGCAAGGGGCTCTGAGGAGT 698  
 QY 665 CTGAGGAGATGAGAAGCTGTCTTAACTTCCGCAAGACTCCAGCAGCAGAGATGTCTGTT 724  
 DB 699 CTGAATGAGATGAAGAGATCTTCACTTCCGAGGACCCAGCAGCTGAGCAGCATTT 758  
 QY 725 GCACACTGGCAGGAGATGCTTCTTCCGCTCCAGTTCCTTAAATGGCATCAACCCGCTC 784  
 DB 759 GAGCACTGGCAGGAGATGCTTCTTCCGCTCCAGTTCCTTGAATGGTCTCAACCTCTGTC 818  
 QY 785 CTGATTCCGCGCTGTCAAGTCTCCCAAACTTCCCGGTCACTGATGAATGGTGGCC 844  
 DB 819 CTGATCCGCGCTGTCACTACTCTCCCAAGAACTTCCCGTCACTGATGCCATGGTGGCC 878  
 QY 845 CCAGTGTGGGCGCTGGAAACAGTCTCCAGCTCAGTGGAGAGGGCTCCCTGTTCTTG 904  
 DB 879 TCATTGTTGGTCTCTGGACAGCTTGCAGCTGAGCTAGAGAGGGCTCCCTGTTCTTG 938  
 QY 905 GTGATCATGTGCTTCTTCTGGAGTCCACCAACATCTCTCAATGGAAGCTCAGTTC 964  
 DB 939 GTGATCAAGGATCTCTCTGGGATCCAGACCAATGTCAATATGGAAGCGCAGTTC 998  
 QY 965 TCTGAGCGCGGATGACCTGTATACACAGAGCTCAGGGTCCGAGCCCTGTTCCCAT 1024  
 DB 999 TCTGCGGCCCAATGACCTGTATACAGAGCCAGGCTCGGGCGCTGCTGCTCTC 1058  
 QY 1025 GCCATCAGCTCAACAGACTCCCGGGCCAGAACCCCACTTCTTCCCGCCAGCATGAC 1084  
 DB 1059 GCCATCAGCTCAGCCAGAGACCCCGGCCCAACAGCCCACTTCTTCCCGCCAGCATGAC 1118  
 QY 1085 ACGTGGGACTGTTGCTGGCCAGACCTGGGTTCGCAATCTGAGTTTTTACATCCATGAG 1144  
 DB 1119 AAGTGGGACTGTTGCTGGCCAGACCTGGGTGGCAATGCCGAGTCTCTCTTCCATGAG 1178  
 QY 1145 GCTGTCAACATCTGTGCTGATGCCCATCTGATTCAGAAAGTCTTTGCTTGGCCACATTA 1204  
 DB 1179 GCCCTCAGCAGCTGTGCTCACTCACTGTGCTGAGGTCTTCACTGCTGCTGCTGCTG 1238  
 QY 1205 CGTCAGCTGCTAGGTGTCACTCTTCAAGCTATTTGATTCCTCACTTCCGTTACACA 1264  
 DB 1239 CGTCAGCTGCCCCACTGCCACCTCTTCAAGCTGTGATGCCGCAACCCGATACACC 1298  
 QY 1265 CTGCACATCAACAGCTTGGCCGGAGCTGTCTGCTGCCCCCTGGGAAGTTGATAGACAAG 1324  
 DB 1299 CTGCACATCAACACTTGGCCCGGAGCTGCTTATCGTGCAGGCGGAGGTGGTGGACAG 1358  
 QY 1325 TCCAAGGCGCTTGGCACTGGGGGATCTTGAACCTGATTAAGAGAAACATGGAGAGCTG 1384  
 DB 1359 TCCACAGGCTCGGCAATGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418  
 QY 1385 AACTACTCTGTCTGTCTCTCCCTGAAGATATCCAGCCCGAGGTGTGGAGACATCCCA 1444  
 DB 1419 AACTATTCTCTCTGTCTGTCTCTGAGGATATCCGAGCCCGAGGAGTTGAAGACATCCCA 1478  
 QY 1445 GGCTACTATTACCGAGATGATGGATGAGATCTGGGGGGCAATAAGAGAGCTTTGTCTCT 1504  
 DB 1479 GGCTACTACTACCTGATGATGGATGAGATTTGGGGTGCAGTGGAAAGCTTTGTCTCT 1538





Qy	545	TTGACCTCAA	CATCAAGTACTCTGCGATGAAGTAATGCCAAACTCTCTTTTAAAGCCCAAC	604
Db	579	TTGAGCTCA	TATCAAATATCATCACAGCCAAGTAATGCCAACTTTTATCTACAAGCTGGC	638
Qy	605	TCCCGTATAC	GGAGCTGAAGTCAAAAGGGCTCTGGACCGCACAGACACTCTGAGAGGT	664
Db	639	TCTGCTTTTG	CAGAGA TGAATAATCAAGGGTTGCTGGACCCCAAGGGCTCTCGAGAGGT	698
Qy	665	CTGAGGAGAT	GAGAAGCGCTTTTAACTTCCGCAAGACTTCAGACAGCAGAGTATGTGTGT	724
Db	699	CTGAATGAG	ATGAAGAAGATCTTCAACTTCCGGAGGACCCAGCAGCTGAGCAGCATTT	758
Qy	725	GCACATGGC	GAGGAAGATGCTTCTTGCTCTCCAGTTCCTAAATGGGATCAACCCGGTC	784
Db	759	GAGCACTGG	CAGGAGATGCTTCTTGCTCTCCAGTTCTCTGAATGGTCTCAACCCGTCTC	818
Qy	785	CTGATTCCG	CGCTCTCAGCTCTCCAAAACAATCTCCGGTCACTGATGAATGGTGGCC	844
Db	819	CTGATCCG	CGCTCTGACTCTCCAAAGAACTTCCCGGTCACTGATGCCATGGTGGCC	878
Qy	845	CCAGTGTCT	GGGCCCTTGGAAACAGTCTGCAGGCTGAGTTGGAGAAGGCTCCCTGTCTTG	904
Db	879	TCAATTGT	TGGTCTCTGGGACAGCTTGACGCTGAGCTAGAGAAGGCTCCCTGTCTTG	938
Qy	905	GTGATCAT	GGCATCTTTTCTGAGTCCACACCAACATCTCAATGAAGAACTCTCAGTTC	964
Db	939	GTGATCA	CGCATCTCTCTGGCATCCAGACCAATGTCAATTAATGAAGCCGAGTTC	998
Qy	965	TCTCAGCC	CGGATGCTTTACACAGAGCTCAGGTCGGAACCCCTGCTTCCCAT	1024
Db	999	TCTGCGCC	CCCAATGACCTGCTATACAGAGCCAGGCTGCGGGCGCTGCTGCCCTCTC	1058
Qy	1025	GCCATCC	AGCTCAACAGACTCCCGGCGCAGACAAACCCATCTTCTCTGCCCAGGCGATGAC	1084
Db	1059	GCAATC	AGCTCAGCAGACAGACCCCGGCCAAAGACCCCACTCTTCTGCCCACTGATGAC	1118
Qy	1085	ACGTGGA	CTGGTTGCTGGCCAGACTGCGGTTCGCAATTTCTGAGTTTTATCATCCATGAG	1144
Db	1119	AAGTGG	AGCTGGTGGTGGCTGGCCAGACCTGGGTGGCAATGTCGAGTTCTCTCCATGAG	1178
Qy	1145	GCTGTCA	CACATCTGCTGCTATGCCCATCTGATTTCCAGAAGTCTTTGCTTGGCCACATTA	1204
Db	1179	GCCCTCA	CGCACTGTGCTCACTCATCTGCTGCTGAGGTCTTCACTCTGGCTGAGTTC	1238
Qy	1205	CGTCAG	CTGCTAGGTCACTCTTCAAGCTATTGATTCTCTCACATTCGATTCGATACCA	1264
Db	1239	CGTCAG	CTGCCCACTGCACTCTCTTCAAGTCTGATTCGCCGCAACCCGATACCC	1298
Qy	1265	CTGCAT	CAACACGCTTGCCGGAGCTGCTCGTTGCCCTGGGAAGTTGATAGACAAG	1324
Db	1299	CTGCAT	CAACACACTCGCCCGGAGCTGCTTATCGTGCAGGCGAGGTGGTGCACAG	1358
Qy	1325	TCCACAG	CGCTTGGCACTGGGGGATTTCTCTGACCTGATTAAGAGAAACATGAGAGCAG	1384
Db	1359	TCCA	CAGGCATTCGCGATTTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAG	1418
Qy	1385	AACTACT	CTGTGCTGCTCCCTGAAGATATCCGACCGCAGGTGGGAAGACATCCCA	1444
Db	1419	AACATT	TTCTCTGTGCTGCTGAGATATCCGGAACCGAGAGTTGAAGACATCCCA	1478
Qy	1445	GGCTA	CTATTACCGAGATGAGGATGCAGATCTGGGGGCAATAAAGAGCTTTGTCTCT	1504
Db	1479	GGCTACT	ACTACGCTGATGATGGGATGCAGATTTGGGGTGCAGTGGAAACGCTTTGTCTCT	1538
Qy	1505	GAATAGT	CAGCATCTACTATCCAAAGTGACACATCTCGTCCAGATGACCAAGAGCTCCAG	1564
Db	1539	GAATCAT	CGGTATCTACTACCAAGTGATGAGTCTGTCTCCAAGATGACAGAGAGCTCCAG	1598
Qy	1565	GCCTGG	GTGGAGATCTTCTCTGAGGGCTTCTCTCGCCCGAGAAAGCTCAGGTATGCC	1624
Db	1599	GCCTGG	GTGAGAGATCTTCTCTCAAGGGCTTCTCTAAACAGGAGAGCTCAGGTATCCCT	1658
Qy	1625	TCCTTGT	TGGATACCGGGAGCCCTGGTCCAGTATATCACCATGGTGAATTCACCTGC	1684

1659	Db	TCCTCACTGGAGACCGGGAAGCCCTGGTGCAATATGTCCACCATGGTGATATTCACCTGC	1718
1685	Qy	TCAGCCAAGCATCAGCTGTTCAGTTCAGGCGAGTTCGACTCTTGTTGTGTTTGGATGCCCCAAT	1744
1719	Db	TCAGCCAAGCATCGGGCTGTTCAGTGCAGGCGAGTTTGTACTTCCTGTGCTTGGATGCCCAAC	1778
1745	Qy	CTGCCACTACCATGCAGCTTACCACCACTTACTTCCAAAGGCCAGGCCCGGCCCTGAGAGT	1804
1779	Db	CTGCCACCCAGCATGCAGCTGCCACCACTCCCAAGGCCCTGCAACATCGAGGGC	1838
1805	Qy	TTCAATGACACGGTCTCCAGCAGTTAAATTCGTCAAGTTATCACAATCATTTGCTCTCTGGCTG	1864
1839	Db	TTCAATGACCACTCTCCACCTGTCAATGCCACATGTGATGTCTATCCTTGTCTCTCTGGTTG	1898
1865	Qy	CTAAGCGCAGAACCTTGGGNGCCAAAGGCCCTGGGCCACTATCCAGATGAACACTTTCACA	1924
1899	Db	CTGAGCAAGAGGCTTGAGACCAAGGCCCTGGGCACCTTATCCGGATGAGCACTTTCACA	1958
1925	Qy	GAGGATGCCCCCGCGAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCTCAAG	1984
1959	Db	GAGGAGGCCCTCTGGGGGAGCATCGCACTTTCAGAGCGCGCTGGCCCNAGATCTCGAGG	2018
1985	Qy	GGCATCAGGAGAGGAACCGAGGCCCTGGCACTGCCCTTACACTTACCTGGATCTCTCCCTC	2044
2019	Db	GGCATCCAGGAGCGGAACCGGGCCCTGGTGCTGCCCCCTACACCTTACCTAGACCCCTCCCTC	2078
2045	Qy	ATTGAGAACAGTGTCTCCCATCTTAACTTCTTGGAGAAGACAGTCTCTGTGTGACAT	2098
2079	Db	ATCGAGAACAGCGTCTCCATCTAAATCCAGGGGGAACAGAGGCCCAAGATGACAT	2132

## RESULT 6

ABK64747

ABK64747  
ID ABK64747 standard: DNA: 2685 BP.

AC ABK64747:

DT 18-JUN-2002 (first entry)

Human benign prostatic hyperplasia gene #642:

KW Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.

OS Homo sapiens.

PN WO200212440-A2.

14-FEB-2002

07-AUG-2001; 2001WO-US024708.

PR 07-AUG-2000; 2000US-0223323P.

PR 05-JUN-2001; 2001US-00873319.

PA (GENE-) GENE LOGIC INC.

PA (NISB) JAPAN TOBACCO INC.

PI Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;

DR WPI; 2002-257476/30.

Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate cells.

PS Disclosure: Page 351: 444pp: English:

CC The invention relates to a method of diagnosing (I) the onset or  
CC progression of benign prostatic hyperplasia (BPH), or screening (II) for  
CC or identifying an agent that modulates the onset or progression of BPH.  
CC The method is based on changes in gene expression in BPH tissue isolated



Db	1839	TTCAAGCACCTTCCCACTGTCAATGCACATGTGATGTCATCTTCTCTCTGTTG	1898
Qy	1865	CTAAGCGAGAACTCGGGGACCAAGAGCCCTTGGGCCACTATCCAGATGAACACTTCACA	1924
Db	1899	CTGAGCAAGGAGCCTTGAGAGCAAGAGCCCTTGGGCACCTATCCGGATGAGCACTTCACA	1958
Qy	1925	GAGGATGCCCCCGCGCAAGCGTGGCTTGTCTCCAGAGAAAGCTGATCCAGATCTCCAAG	1984
Db	1959	GAGGAGCCCTCGCGGAGCATCGCCACCTTCCAGAGCCGCTGGCCCGAGATCTCGAGG	2018
Qy	1985	GGCATCAGGAGAGAACCGAGGCTGGCACTGCGCTACACCTACCTGGATCTCCGCCCTC	2044
Db	2019	GGCATCCAGGAGCGGAACCGGGGCGCTGGTGTGCGCTTACACTACCTAGACCTCCGCCCTC	2078
Qy	2045	ATTGAGAACAGTGTCTCCATCTAAACATCTTTGGGAAGACAGTCTCTGTGACAT	2098
Db	2079	ATCGAAGAACGCGTCTCATCTAAATCCAGGGGAAACAGGGCCAGATGACAT	2132

RESULT 7  
ACA89907  
ID ACA89907 standard; cDNA; 2685 BP.

**AC ACA89907;**

DT 10-JUL-2003 (first entry)

DE Gene differentially regulated in cardiovascular disease #28.

Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;  
KW  
myocardial infarction; cardiant; antiarteriosclerotic; antianginal;  
KW  
gene therapy; differential gene expression; gene; ss.  
KW

OS Homo sapiens.

PN WO2003031650-A2.

17-APR-2003.

02-OCT-2002: 2002WO-EP011034-

08-OCT-2001: 2001GB-00024145-XX  
PRXX  
PA  
/FLAPP 1 PLAYED ACXX  
PI  
Munnes M, Gehrman M, Wick M, Schmitz G;

DR WPI: 2003-403108/38.

UR P-PSUB; ABU89/34.  
XX

PT of a polynucleotide in a biological sample comprises detecting a hybridization complex.

PS Claim 1: Page 176-178: 454pp: English.

The invention describes a method of predicting, diagnosing or prognosing a cardiovascular disease by detection of a polynucleotide in a biological sample comprises hybridising at least one of the polynucleotide to a nucleic acid material of a biological sample, thus forming a hybridisation complex, and detecting the hybridisation complex. The polynucleotides, polypeptides, antisense molecule, antibody and reagent are useful for preparing compositions for preventing, predicting or diagnosing, or a medicament for treating a cardiovascular disease, e.g. arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction. This sequence represents a gene identified in the invention, a being differentially regulated in individuals with cardiovascular disease

SQ Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;

Query Match 43.38; Score 1395.2; DB 8; Length 2685;

### Query Match

	Best Local Similarity	79.8%;	Pred No. 0;	Mismatches	418;	Indels	5;	Gaps	2;
	Matches	1671;	Conservative	0;					
Qy	7	GCAGTAGAGCTAAACT--GGTCAGGAGGATGCGGAAATCGAGGGTGAAGAGTATCCACG	64						
Db	42	GCGGTAGAGAGCTGGGACTTAGGCTGGCAGCATGGCCGAGTTCAGGGTCA GGGTGTCCACC	101						
Qy	65	GCGGGAAGCCCTGTGGGGCTGGCACATGGGACAAAGTGTCTGTCAGCATCTGTGGGAACCCAC	124						
Db	102	GGAGAAGCCTT CGGGCTGGCACATGGGACAAAGTGTCTGTCAGCATCTGTGGGACCGG	161						
Qy	125	GGAGAGGCCCTTACTCTGGACCACTCTGGCAAGAGATTCAGCGCGGTGCTGAA	184						
Db	162	GGAGAGGCCCCCACTGCCCTTGGACAACTCTCGGC AAGAGTTCATCTGGGGGCGCTGAG	221						
Qy	185	GAAGACTTCGAGTGAGCGCTTCCCCAGGACGTAGGCAC TCTGTGTATGCTGCGAGTCCAC	244						
Db	222	GAGGACTTCAGGTGACGCTCCCGGAGGAGCTAGGCGCAGTGTGCTGCTGCGCGTGAC	281						

[illegible]

Db 1059 GCCATCCAGCTCAGCAGACCCCGCGCCCAACAGCCCCCATCTTCTGCGCCCACTGATGAC 1118  
QY 1085 ACCTGGGACTGTGTCTGGCCAAAGACTGGGTTCGCAATTTCTGAGTTTACATCCATGAG 1144  
Db 1119 AAGTGGGACTGTGTCTGGCCAAAGACTGGGTTCGCAATTTCTGAGTTTACATCCATGAG 1178  
QY 1145 GCTGTACACATCTGTCTGATGCCATCTGATTTCCAGAAAGTCTTTGCTTGGCCACATTA 1204  
Db 1179 GCCTCAGCAGCCTGTCTGCACTCAGATCTGCTGCTGAGTCTTCACTCCCTGCTACCCCTG 1238  
QY 1205 CGTCACTGCTAGGTGTCACCTCTCTTCAAGCTATTGATTCCTCAGATTCGGTACACA 1264  
Db 1239 CGTCACTGCCCACTGCCACCTCTCTTCAAGCTGCTGATCCCGCACACCCGATACACC 1298  
QY 1265 CTGCACATCAACACGCTTGGCCGGGAGCTGCTGTTGCCCTGGGAAGTTGATAGACAAG 1324  
Db 1299 CTGCACATCAACACATCTGCCCGGGAGCTGCTTATCTGCTCCAGGGCAGGTGTGNCAGG 1358  
QY 1325 TCCACAGGCTTGGCACTGGGGGATTTCTGTGACCTGATTAAGAGAAACATGAGCAGCTG 1384  
Db 1359 TCCACAGGCACTGGCACTTGAAGGCTTCTGTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418  
QY 1385 AACTACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCGAGGTGTGAAGACATCCCA 1444  
Db 1419 AACTATTCTCTCTGTCTCTGCTGAGGATATCCGAGCCGAGGTGTGAAGACATCCCA 1478  
QY 1445 GGCTACTATTACCGAGATGATGGGATGTCAGATCTGGGGGCAATTAAGAGCTTTGTCTCT 1504  
Db 1479 GGCTACTACTACCGTATGATGGGATGTCAGATTTGGGGTGCAGTGAACGCTTTGTCTCT 1538  
QY 1505 GAAATAGTCAGCATCTACTATCCAAGTGACACATCCGTCCTCAAGATGACCAAGAGCTCCAG 1564  
Db 1539 GAAATCATCGGTATCTACTACCCCAAGTGATGAGTCTGTCCAAGATGACAGAGAGCTCCAG 1598  
QY 1565 GCCTGGGTAGGGAGATCTTCTCTGAGGGTTCCTCGCGCGAGAAAGCTCAGTATGCC 1624  
Db 1599 GCCTGGGTAGAGAGATCTTCTCAAGGGCTTCCTAAACAGGAGAGCTCAGGTATCCCT 1658  
QY 1625 TCCTGTGTGATACCCGGGAAGCCCTGCTCCAGTATATCACCATGTGTATATTCACCTGC 1684  
Db 1659 TCCTCACTGGAGNACCCGGGAGCCCTGCTGAGTATGTCCACATGTGTATATTCACCTGC 1718  
QY 1685 TCAGCCAAGATGACGTGCTCAGTTCAGGCCAGTTCGACTCTTGTGTTTGGATGCCAAT 1744  
Db 1719 TCAGCCAAGATGACGTGCTCAGTTCAGGCCAGTTCGACTCTTGTGTTTGGATGCCAAT 1778  
QY 1745 CTGCCACCTACCATGACGTACACACCTACTTCCAAAGGCCAGCCCGGCTGAGAT 1804  
Db 1779 CTGCCACCTACCATGACGTGACACACCTACTTCCAAAGGCCAGCCCGGCTGAGAT 1838  
QY 1805 TCCATAGCCACGCTCCCGAGCTTAATTCGTCAAGTTATCAATCATTTCTCTCTGGCTG 1864  
Db 1839 TCCATAGCCACCTCCCGAGCTTAATTCGTCAAGTTATCAATCATTTCTCTCTGGCTG 1898  
QY 1865 CTAAGCCGCAAACTCGGGGACCAAGGCCCTGGGCCACTATCCAGATGAACACTTCACA 1924  
Db 1899 CTGAGCAAGGAGCTCGAGAACCAAGGCCCTGGGCCACTATCCGATGAGCACTTCACA 1958  
QY 1925 GAGGATGCCCCCGGGGAGAGCTGGCTGCTCCAGAGAAAGCTGATCCAGATCTCCAG 1984  
Db 1959 GAGGAGGCCCTCGGGGAGCATTCGCCACCTTTCAGAGCGGCTGGCCCGAGATCTCGAG 2018  
QY 1985 GGCATCAGGGAGAGAAACAGGAGCCCTGGCACTGSCCTACACCTTACCTGATCTCCCTC 2044  
Db 2019 GGCATCAGGGAGAGAAACAGGAGCCCTGGCTGCTGCTGCTTACCTTACCTTACCTTCCCTC 2078  
QY 2045 ATTGAGAACAGTGTCTCCATCTAACTCTTTGGAGAAAGACAGTCTCTGTGTGACAT 2098  
Db 2079 ATCGAGAACAGCTCTCCATCTAACTCTTAACTCCAGGGGAAACACAGGCCCGAGATGACAT 2132

ID ADQ91798 standard; cDNA; 2685 BP.  
XX  
AC ADQ91798;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Human lipoxxygenase 15-Lox-2 cDNA.  
XX  
DE lipoxxygenase; iron ligand; arachidonic acid metabolism; human;  
KW lipoxxygenase 15-Lox-2; ss; gene.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 72..2102  
FT /tag= a  
FT /product= "Human lipoxxygenase 15-Lox-2"  
XX  
PN US2004137483-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 18-NOV-2003; 2003US-00716204.  
XX  
PR 16-APR-1998; 98US-00061768.  
PR 17-JAN-2001; 2001US-00764246.  
XX  
PA (BRAS/) BRASH A R.  
PA (BOEG/) BOEGLIN W E.  
PA (JISA/) JISAKA M.  
XX  
PI Brash AR, Boeglin WE, Jisaka M;  
XX  
DR WPI: 2004-533356/51.  
DR P-PSDB; ADQ91763.  
XX  
PT New lipoxxygenase nucleic acid segment comprises an isolated gene encoding  
PT a lipoxxygenase containing an iron ligand comprising a serine, useful for  
XX arachidonic acid metabolism.  
PS Claim 10; SEQ ID NO 1; 39pp; English.  
XX  
CC The invention describes a nucleic acid segment (I) comprising an isolated  
CC gene encoding a lipoxxygenase containing an iron ligand comprising a  
CC serine, or comprises at least a 10 nucleotides long contiguous stretch of  
CC the nucleic acid sequence not given in the specification (SEQ ID NO. 1)  
CC or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a  
CC nucleic acid segment comprising at least 10 nucleotides long contiguous  
CC stretch of the nucleic acid sequence not given in the specification (SEQ  
CC ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is  
CC a polypeptide having the amino acid sequence Trp-Leu-Ala-Lys (SEQ ID  
CC NO. 5) and Gly-Gln-Tyr-Asp-Trp (SEQ ID NO. 35). The lipoxxygenase nucleic  
CC acids and proteins are useful in arachidonic acid metabolism. This  
CC sequence encodes human lipoxxygenase 15-Lox-2.  
SQ Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;

Query Match 43.3%; Score 1395.2; DB 12; Length 2685;  
Best Local Similarity 79.8%; Pred. No. 0;  
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

QY 7 GCAGTAGAGAGCTAACT--GGTCAGGAGGATGGCGAAATGACGGGTGAGATATCCACG 64  
Db 42 GCCGTAGAGAGCTGACTTAGCTGGCAGCATGGCCGAGTTCCAGGTTCAGGTGCCACC 101  
QY 65 GGGGAAGCCTGTGGGCTGGCAGCATGGGACAAAGTGTCTGTTCAGCATGTGGGAACCCAC 124  
Db 102 GGAGAGAGCCTTCGGGGCTGGCAGCATGGGACAAAGTGTCTGTTCAGCATGTGGGGACCCG 161  
QY 125 GGAGAGAGCCTTGTAGTACCTCTGGACCATCTGGGCAAGGAGTTCCAGCGCCGCTGTGAA 184  
Db 162 GGAGAGAGCCCCCACTGCCCTCGACAATCTCGCAAGGAGTTCACTGCGGGCGCTGAG 221



```
FT /*tag= a
FT /product= "Human 15-lipoxygenase 2 protein"
PN WO2004060274-A2.
XX
XX 22-JUL-2004.
XX
XX 17-OCT-2003; 2003WO-US033139.
XX
XX 20-DEC-2002; 2002US-0435988P.
XX
XX (ALCO-) ALCON INC.
XX
XX Gianni JM, Gamache DA, Miller ST;
XX WPI: 2004-543776/52.
XX P-PSDB; ADQ37896.
XX
XX Treating dry eyes in postmenopausal women comprises administering a
XX composition comprising the 15-lipoxygenase (15-LO)-1 or 15-LO-2 gene to
XX the ocular surface cells of the post-menopausal women with dry eyes.
XX
XX Claim 1; SEQ ID NO 3; 20pp; English.
XX
XX The invention relates to a novel method for treating dry eyes. The method
XX comprises obtaining a composition containing the nucleotide sequence of
XX 15-lipoxygenase (15-LO)-1 or 15-LO-2, and administering the composition
XX to a patient suffering from dry eye under conditions such that the
XX nucleotide sequence of 15-LO-1 or 15-LO-2 is expressed. The invention
XX further comprises a composition for the treatment of dry eye, comprising
XX a vector having the above nucleotide sequence and an excipient. The 15-LO
XX compositions have ophthalmological activity and may be used in gene
XX therapy to treat disorders. The method is useful for treating dry eyes in
XX postmenopausal women. This polynucleotide sequence represents the DNA
XX encoding the 15-lipoxygenase 2 protein of the invention.
XX
XX Sequence 2685 BP; 625 A; 829 C; 721 G; 510 T; 0 U; 0 Other;
XX
XX Query Match 43.3%; Score 1395.2; DB 12; Length 2685;
XX Best Local Similarity 79.8%; Pred. No. 0;
XX Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;
XX
XX 7 GCAGTAGAGAGCTAAACT--GGTCAGGAGGATGGCGAAATGCAGGGTGAGAGTATCCACG 64
XX 42 GCCTAGAGAGCTGGACTTAGGCTGGCAGATGGCCGAGTTCAGGGTCAGGGTGTCAC 101
XX 65 GGGGAAGCCTTGGGGCTGGCAGATGGGACAAAGTGTCTGTAGCATCTGGGAACCCAC 124
XX 102 GGAGAAGCCTTCGGGGCTGGCAGATGGGACAAAGTGTCTGTAGCATCTGGGACCCGG 161
XX 125 GGAGAGAGCCCTTAGTACTCTGTGACCATCTGGGCAAGGAGTTCAGCGCCGGTGTCTGAA 184
XX 162 GGAGAGAGCCCCCACTGCCCTTGGACATCTCGGCAAGAGTTCAGTCGGGGCGCTGAG 221
XX 185 GAAGACTTCAGAGTGAACGCTTCCCAAGGACGTAGGCACCTGTGTGATGTCTGGAGTCCAC 244
XX 222 GAGGACTTCAGGTGACGCTCCCGAGGAGCTAGGCCGAGTGTCTGTCTGCGCGTGCAC 281
XX 245 AAGACACCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGGTCTGTATGCTGTCTGTCG 304
XX 282 AAGGCGCCCC---AGTGTGCCCTGTCTGGGGCCCTCGGGCCCGGATGCCTGGTTCTGC 338
XX 305 CGCTGGTTCGAGCTGAGTGGCTACCTGGGGCTGCACCTCCACTTCCCTGTGTATCAGTGG 364
XX 339 CGCTGGTTCGAGCTGACACGCGCGGGGGGGCCACCTCTCTTCCCTGTCTACAGTGG 398
XX 365 CTGGAAAGGGGCGGGGAGCTGGTGTCTGAGAGGGGACGACAAAGGTGTCTCTGGCAAGAC 424
XX 399 CTGGAGGGGGCGGGACCCCTGGTGTCTGCAGAGGGGTACAGCCAAAGGTGTCTCTGGGCAG 458
XX 425 CATCACCTTACACTGAGGATCAGGCCAGAGAGGAGCTTGTAGTCCAGGACAGAGATGTAC 484
XX 459 CACCACCCTGTGTCTCAGCAACAGCGCCAGGAGGAGCTTCAGGCCCGGCGAGAGATGTAC 518
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QY 485 AGCTGGAAAGACTTACATTGAAGGTTGGCTCGCTGCCTTGACCCAGAGACTGTGAAAGAC 544
DB |||||
DB CAGTGGAAAGGCTTACAACCCAGGTTGGCTCACTGCCTGGATGAAGACAGAGTGAAGAC 578
QY 545 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCAAACTCTTCTTTAAAGCCAC 604
DB |||||
DB TTGGAGCTCAATATCAAAATACTCCACAGCCAAAGATGCCAACTTTTATCTACAAGTGC 638
QY 605 TCCGGTATACGGAGCTGAAAGTCAAAAGGCTCCTGGACCGCAGACAGGACTCTGGAGGAGT 664
DB |||||
DB TCTGCTTTTGAGAGATGAATAATCAAGGGGTGTCTGGACCGCAGGGGCTCTGGAGGAGT 698
QY 665 CTGAGGGAGATGAGAAAGCTGTTTAACTTCCGCAAGACTCCAGCAGCAGAGTATGTGTTT 724
DB |||||
DB CTGAATGAGATGAATAAGGATCTTCAACTTCCGAGGAGCCCAAGCAGCTGAGCACGATTT 758
QY 725 GCACATCGCAGGAGATGCGCTTCTTCGCTCCAGTTCCTTAATGGGATCAACCGGTC 784
DB |||||
DB GAGCATTGCGCAGGAGATGCGCTTCTTCGCTCCCAAGTTCCTGAATGGTCTCAACCTGTC 818
QY 785 CTGATTCCGCGCTGTCACAGTCTCCCAAACTTCCCGGTCACCTGATGAATGTGGCC 844
DB |||||
DB CTGATCCCGCGCTGTCACTACTCCCAAGAACTTCCCGCTCACTGATGCCATGTGGCC 878
QY 845 CCAGTGTGGGCGCTTGGAAACAGACTCTGCAAGCTGAGTTGGAGAGGGCTCCCTGTCTTG 904
DB |||||
DB TCAATTGTTGGTCTTGGACCAAGCTTGCAGCTGAGCTAGAGAGGGCTCCCTGTCTTG 938
QY 905 GTGATCATGGATCTTCTTGGAGTCAACACCAATCTCTCAATGGAAAGCTCAGTTC 964
DB |||||
DB GTGGATCAAGGATCTCTCTGGCATCCAGACCAATGTCAATTAATGGGAAGCGCAGTTC 998
QY 965 TCTGAGCCCGCAGTACGACCTGTATACACAGAGCTCAGGCTCGGACCCCTGCTCCCAT 1024
DB |||||
DB TCTGGGGCCCAATGACCTGTATACAGAGCCAGGCTGGGGCGGCTGCTGCTCTC 1058
QY 1025 GCCATCCAGCTCAAAACAGACTCCCGGGCGCAGACCAACCCCATCTTCTGCCAGCGATGAC 1084
DB |||||
DB GCCATCCAGCTCAGCCAGACACCCCGGGCCCAACAGCCCATCTTCTGCCCATGATGAC 1118
QY 1085 AGTGGGACTGGTGTCTGGCCAGACCTGGGTTCGCAATCTGAGTTTATCATCATGAG 1144
DB |||||
DB AAGTGGGACTGGTGTCTGGCCAAAGCTGGGTGCGCAATCGGAGTTCTCTCTTCCATGAG 1178
QY 1145 GCTGTACACATCTGCTCATGCCCATCTGATTCAGAAAGTCTTTGCTTGGCCACATTA 1204
DB |||||
DB GCCCTCAGCACCTCTGCTCATCTCATCTGCTGCTGAGGTTTCACTGCTGCTACCTG 1238
QY 1205 GGTCAAGCTGCTTAGGTGTCACTCTCTTCAAGCTATTTGATTCCTCACAATTCGGTACACA 1264
DB |||||
DB GGTCAAGCTGCTTAGGTGTCACTCTCTTCAAGCTATTCCTGCTGATCCCGCACACCGATACAC 1298
QY 1265 GTGACATCAACACGCTTGGCGGAGTGTCTGTTGCCCTTGGGAGTTGATAGACAG 1324
DB |||||
DB GTGACATCAACACACTCGCGGAGTGTCTTATCGTCCAGGCGAGGTGGTGGACAG 1358
QY 1325 TCCAGAGCCTTGGCACTGGGGGATTTCTGACCTGATAAGAGAAACATGGAGGAGCTG 1384
DB |||||
DB TCCAGAGGATCGGATTTGAAGGCTTCTGTAGTTGATACAGAGAAACATGAAGAGCTG 1418
QY 1385 AACTACTGTCTGTCTCTCCCTGAAGATATCCGAGCCCGAGGTTGTGGAAGACATCCCA 1444
DB |||||
DB AACTATTCTCTCTGTCTGCTGCTGAGGATATCCCGACCCGAGGAGTTGAAGACATCCCA 1478
QY 1445 GGTACTATATCCGAGATGAGTGGAGTGCAGATCTGGGGGGCAATAAAGAGCTTTGTCTCT 1504
DB |||||
DB GGTACTACTACCGTGTGATGGAGTGCAGATTTGGGGTGCAGTGGAAAGCTTTGTCTCT 1538
QY 1505 GAATAGTGCAGATCTACTTCCAGATGCACATCCGCTCCAGATGACCAAGAGCTCCAG 1564
DB |||||
DB GAATCATCGGTATCTACTACCCAAAGTGTAGTCTGTCTCCAAAGATGACAGAGGCTCCAG 1598
```



QY 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGCGGAGAAAGCTCAGGTATGCC 1624  
Db |||||  
QY 1599 GCCTGGGTGAGAGATCTTCTTCAAGGGCTTCTTAAACAGGAGAGCTCAGGTATCCCT 1658  
Db |||||  
QY 1625 TCCTTGTGTGATACCCGGAAGCCCTGTGTCCAGTATATCACCATGGTATATTCACCTGC 1684  
Db |||||  
QY 1659 TCCTCACTGGAGACCCGGAGCCCTGTGTGAGTATGTCACCATGTGTATTCACCTGC 1718  
QY 1685 TCAGCAAGCATGACGTGTCTAGTTCAGCCAGTTCGACTCTTGTGTGGATGCCAAT 1744  
Db |||||  
QY 1719 TCAGCAAGCATGCGCTGTCTAGTGCAGGCGAGTGTGACTCTCTGTGTGGATGCCAAT 1778  
QY 1745 CTGCACTTACCATGACGTACCACTACTCTTCCAAAGCCAGCCGCGCTGAGGT 1804  
Db |||||  
QY 1779 CTGCAACCCAGCATGAGCTGCGACCCACCTTCCAAAGGCTGGCAACATGCGAGGC 1838  
QY 1805 TTCTATAGCCACCTCCAGCAGTAAATTCGTCAAGTATATCATCATATGCTCTCTGGGTG 1864  
Db |||||  
QY 1839 TTCTATAGCCACCTCCACCTGTCTAATGCCATGTGTATCTCTCTGTGTG 1898  
QY 1865 CTAAAGCGAGAACCTGGGACCAAGGCCCTTGGGCCACTATCCAGATGAACACTTCA 1924  
Db |||||  
QY 1899 CTGAGCAAGGAGCTGGAGACCAAGGCCCTTGGGCCACTATCCGATGAGCACTTCA 1958  
QY 1925 GAGGATGCCCCCGGGAAGGTGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAG 1984  
Db |||||  
QY 1959 GAGGAGGCCCTTCGCGGAGCATCGCCACTTCCAGAGCCGCTGGCCAGATCTCGAGG 2018  
QY 1985 GGCATCAGGAGAGAACCGAGGCTTGGCACTGCGCTTACACCTACTGATCTCCCTC 2044  
Db |||||  
QY 2019 GGCATCAGGAGCGGAACCGGGGCTTGGTGTGCTGCTTACCTACTAGACCTCCCTC 2078  
QY 2045 ATTGAGAACAGTGTCTTCCATCTTAACATCTTGGAGAGAGACGTCTGTGTGACAT 2098  
Db |||||  
QY 2079 ATCGAGACAGCGTCTCCATCTTAATCCAGGAGAACACAGGCCCCAGATGACAT 2132

RESULT 10  
ACN42888  
ID ACN42888 standard; cDNA; 3127 BP.  
AC ACN42888;  
XX  
DT 18-NOV-2004 (first entry)  
DE Human diagnostic and therapeutic polynucleotide SEQ ID NO:1763.  
XX  
KW ss; gene; gene therapy; human diagnostic and therapeutic polynucleotide;  
KW dithp.  
XX  
OS Homo sapiens.  
XX  
PN WO2004023973-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 12-SEP-2003; 2003WO-US028227.  
XX  
PR 12-SEP-2002; 2002US-0410259P.  
XX  
PR 12-SEP-2002; 2002US-0410260P.  
XX  
PA (INCY-) INCYTE CORP.  
XX  
PI Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen P;  
PI Harshorne TA, Suchorski MT, Altus CM, Pitts SJ, Elder LV;  
PI Mooney EM, Deleage AM, Panesar IS, Banville SC, Reddy TP;  
PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;  
PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;  
PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;  
PI Xu Y, Kwong M, Pollicky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;  
PI Patury S, Shi X, Suarez C;  
XX  
DR WPI; 2004-329368/30.

P-PSDB; ABM84236.  
New diagnostic and therapeutic polynucleotides and polypeptides, useful in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or in gene mapping.  
Claim 1; Page; 190pp; English.  
The invention relates to novel diagnostic and therapeutic polynucleotides selected from one of the 2722 sequences defined in the specification. A polynucleotide of the invention may have a use in gene therapy. The human diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be used to diagnose a particular condition, disease or disorder associated with human molecules, e.g. cell proliferative disorders, autoimmune/inflammatory disorder, developmental disorder, endocrine disorder, neurological disorders, gastrointestinal disorders, or infections caused by virus, bacteria, fungi or parasite. The dithp molecules may also be used in genetic mapping, in identifying individuals from minute biological samples, in detecting single nucleotide polymorphisms, as molecular weight markers, and for somatic or germline gene therapy. The present sequence represents a dithp polynucleotide of the invention. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO at www.wipo.int/pct/en/sequences/listing.htm  
Sequence 3127 BP; 667 A; 1014 C; 821 G; 625 T; 0 U; 0 Other;  
Query Match 22.8%; Score 734.4; DB 13; Length 3127;  
Best Local Similarity 61.2%; Pred. No. 8.9e-182;  
Matches 1248; Conservative 0; Mismatches 766; Indels 24; Gaps 3;  
QY 35 ATGCGGAAATGACGGGTGAGAGTATCCACGGGGAGAGCCCTGTGGGGCTGGCACATGGGAC 94  
Db |||||  
QY 537 ATGCGAGTGTACCGCTGTGTGTCACCACTGCTCTACTCTGAGGGCGGCACACTGGAC 596  
QY 95 AAAGTGTCTGTCAGCATCTGTGGGAACCCACGAGAGAGCCCTTAGTACTCTGACCAT 154  
Db |||||  
QY 597 AACATCTCTGTCACTGGTGGGACGCTGTGTGAAGCCCAAGCAGCGGTAGATCGA 656  
QY 155 CTGGGCAAGGAGTTCAGCGCGGTGCTGAAGAAGACTTCGAGGTGACGCTTCCCCAGGAC 214  
Db |||||  
QY 657 ATGGCAGGACTTCGCGCCCTGGATCGGTACAGAAGTACAGGTGCTGTGCACACGGAG 716  
QY 215 GTAGGCACTGTGTGATGCTCGAGTCCAAAGACACCCCGGAAGTGTCTCCCGCTT 274  
Db |||||  
QY 717 CTGGGTGAGCTTGTGCTGCTGCTGTGTACCAAGGAGCGCTACG----- 759  
QY 275 ATGTCTTTCGCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 334  
Db |||||  
QY 760 -CTTCTTTCGCAAGGACTCTTGGTACTGTAGCCGCACTCTGTGTACCGAACCGGATGGT 818  
QY 335 GCTGCACTCCACTTCCCTGTTATCAGTGGCTGGAAGGGCGGGGAGCTGTGTCTGAGA 394  
Db |||||  
QY 819 AGTGTATCCCACTTCCCTGCTATCAGTGGATGAGGCTACTGACCGTGGAGCTGAGG 878  
QY 395 GAGGAGCAGCAAAAGGTCTCTTGGCAAGACCATCACCTTACACTGCAGGATCAGCGCAG 454  
Db |||||  
QY 879 CCAGGACAGCAAGAACTATTTGTGAGGACTCTCTTCCCTCTCTCTGATCACAGGACA 938  
QY 455 AAGGAGCTTGTAGTCCAGGACAGAAATGTA----CAGCTGGAAGACTTACATTTGAAGTTGG 511  
Db |||||  
QY 939 CGGAGCTCCCGGGCCGCAAGAATGCTACGCGAGTGGGAATCGGTACTCTGCCCGCTTC 998  
QY 512 CCTCGCTGCTTGCACGAGACTGTGAAGACTTGGACCTCAACATCAAGTACTCTGCG 571  
Db |||||  
QY 999 CCCATGAAATGTACATCCCATCTGATGTATGAGGCCCAATGTTGATCTACGCC 1058  
QY 572 ATGAAGATGCAAACTCTTCTTTAAAGCCCACTCCCGGTATACGAGCTGAAGAGTCAAA 631  
Db |||||  
QY 1059 ACCAAGACGATCTCGCTGCTCTTCAATGCTCTCTGCTGCTCTTGGGAATGAAGCTTGA 1118  
QY 632 GGGCTCTCGGACCGCACAGGACTCTGAGGAGAGTCTGAGGGAGATGAGAAGGCTGTTTAC 691

Db	1119	GGGCTGTTGGATCGCAAGGGCTCTGGAAGAAGCTGGATGACATGCAGAAACATCTTCTTGG	1178
Qy	692	TTCCGCAAGACTCCAGCAGCAGAGTAGTGTGTTTGACACTGGCAGGAAGATGCTTCTTTC	751
Db	1179	TGCCATAAAGACCTTTCACGAAAGTAGTGTACAGAGCAGCTGGTGTGAAGATCACTTCTTT	1238
Qy	752	GCCTCCAGATTCTTAATGGCATCAACCCGGTCTGATTGCGCGCTGTGCACAGTCTCCCA	811
Db	1239	GGGTACCACTACCTGAATGGTGTCAATCCCGTCACTGCTCACTGCATCTCTAGCTTGCC	1298
Qy	812	AACAATTCCTCCGGTCACTGATGAATGGTGGCCCCAGTGTGGGCCCTTGAAACAAGTCTG	871
Db	1299	AGCAAGCTGCTGTCAACAAATGACATGGTGGCCCCCTTGTGTGGGACAGGACACATGCTG	1358
Qy	872	CAGCTCAGTTGGAGAGGGCTCCCTGTTCTTGGTGGATCATGGCATCTTTTCTGGAGTC	931
Db	1359	CAGACAGCTTAGAGAGGGGGAACATCTTCTAGCGGACTACTGGATCTCTGGCGAGGCC	1418
Qy	932	CACACCAACATCTCTAAATGGAAGCCTCAGTTCTCTGCAGCCCCGATGACCTGTTTACAC	991
Db	1419	CCCACCACTGCCTTAACGGCCGCCAGCAGTACGTGGCCGCCCACTGTGCTGCTGTGG	1478
Qy	992	CAGAGCTCAGGGTCCGAGCCCTGCTTCCATTTGGCATTCAGTCAAAAGACTCTCCGGG	1051
Db	1479	CTCAGCCCCAG--GGGGGGCTGGTGGCTTGGCCATCCAGTCTCAGCCAGACCCCGGG	1535
Qy	1052	CCAGACAACCCCATCTTCTGCGCCAGCGATGACAGCTGGGACCTGGTGTGCGCCAGAGCC	1111
Db	1536	CCTGACAGCCCCATCTTCTGCCCCACATGACTCCGAATGGGAGCTGGTCTGGGCCAGAGC	1595
Qy	1112	TGGGTTCCGCAATCTGAGTTTTCATCCATGAGGCTCTCACACATCTGCTGCAATGCCCAT	1171
Db	1596	TGGGTGGCAACTCTGAGTTCTCTGGTGCAAGAAAACAACGGCACTTTCTGTGCACGCAT	1655
Qy	1172	CTGATCCAGAAGTCTTTGGCTTTGGCCACAATTAGTCAAGTGGCTAGGTTCACTCTTC	1231
Db	1656	TTGCTGTGCAGGCTTTCGCCATGGCCACGCTGGCCAGCTGGCGCTCTGCCACCCCATC	1715
Qy	1232	TTCAAGCTATGATTCCTCATATTCGATGATGACACTGACACATCAACAGCTTCCCGGAG	1291
Db	1716	TACAAGCTCTTACTCTCCCCACATCGATACACGCTGCAGGTGAACCACTCGCGAGGCC	1775
Qy	1292	CTGCTCGTTCGCCCTGGGAAAGTTGATAGACAAAGTCCACAGCGCTTGGCACTGGGGATTC	1351
Db	1776	ACGCTGCTCAACCCGAGGGCCTCGTGCACAGGTCAAGTCCATCGGAGGCAAGGCCTC	1835
Qy	1352	TCTGACTCTGATAAAGAGAAACATGGAGGAGCTGAACTACTCTGTCTGTCTCTCCCTGAA	1411
Db	1836	ATCTACCTCATGACACGGGCTGGCCCACTTCACTTACCAATTTCTGCCTTCGGAC	1895
Qy	1412	GATATCCGAGCCGAGGTGTGGAAGACATCCAGGCTACTATTACCGAGATGATGGGATG	1471
Db	1896	AGCCTGGGGCCCGCGGCTCTGGCTATCCCCAACTACCACTACCGAGACGCGGCTG	1955
Qy	1472	CAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAAATAGTCAAGCATCTACTATCCAAGT	1531
Db	1956	AAGATCTGGGGGCCATTTGAGAGCTTTGTCTCAGAAATCGTGGGCTACTATTATCCAGT	2015
Qy	1532	GACACATCCGTCCAAGATGACCAAGAGCTCCAGGCTGGGTGAGGGAGATCTTCTCTGAG	1591
Db	2016	GAGCACTCTGTGCAGCAGGATTCGGAGCTGCGGCTCGGAGTGGCGGAGATTTTGTCTCAG	2075
Qy	1592	GGCTTCCTCGGCGAGAAAGCTCAGGTATGCCCTCTTGTGGTATCCCGGGAGCCCTG	1651
Db	2076	CGCTTCTGGCGGGAAAGCTCAGGTTTCCCAAGCCGGCTGTGTCAACCCAGGAGAGATG	2135
Qy	1652	GTCAGTATATCACATGGTGTATTCACCTGTCTCAGCCAGCAAGCATGCAGTGTCTGATCA	1711
Db	2136	GTGAAGTTCCTCACTGCAATCATCTTCAATTGCTCTGCCAGCAGCTGTGTCTCAACAGT	2195
Qy	1712	GGCCAGTTCGACTCTTGTGTTTGGATGCCCAATCTGCCACTTACCATGCAGCTACCAACA	1771

Db	2196	GGG	CAGCATGAC	TTTGGGG	CCTGGATGCCCAATGTCTCCATCATCATGAGCGAGCCCCCA	2255
Qy	1772	CCTACT	TCCAAAGCCAGG	CCCGGCCTTGAGAGTTT	CATAGCCACGCTCCCGAGCAGTTAAT	1831
Db	2256	CCC	GACCAAGGGG	ACCACCCCTGAAGACTT	ACTTAGACACCTCCCTGGAAGTGAAC	2315
Qy	1832	TCG	TCAAAGTTATCACATP	ATGTCTCTCTTGCTGCTTAAGCCGAGAAC	CTTGGGGACCAAGG	1891
Db	2316	ATCAGCTGT	TAAACAACCTCTCTCTTCTGCTGTGGTTAGCCAAGAACAACCAAGGACCAAGG			2375
Qy	1892	CCCTGGCGCACATATCCAGATGAACACTTCACAGAGGATGCCCCCGCGCGAAGCGTGCT				1951
Db	2376	CCCCCTGGGCACCTTACCCAGATGAGCACTTCACAGAGGAGGCCCCCGAGCGGAGCATCGCC				2435
Qy	1952	GCCTTCACAGAGAAAGCTGATCCAGATCTCCAAGGCGATCAGGGAGAGAAACCGAGGCGCTG				2011
Db	2436	GCCTTCAGAGCCGCTGGCCAGACTCAAGGGACATCCAGGAGCGGAACCAAGGCTCTG				2495
Qy	2012	GCACTGCCCTACACCTTACCTGGATGCTCTCCCTCATTTGAGAACAGTGTCTCCATCTAAC				2069
Db	2496	GCACTGCCCTACACCTTACCTGGAGCCCTCCCTCATTTGAGAACAGCGCTCTCCATCTAAC				2553
RESULT 11						
ABA05868						
XX	ID	ABA05868 standard; cDNA; 3320 BP.				
XX	AC	ABA05868;				
XX	DT	21-MAR-2002 (first entry)				
XX	DE	Human lipoxxygenase 46638 coding sequence.				
XX	KW	Human; lipoxxygenase; 46638; cytostatic; antiarrhythmic; hypotensive;				
KW		antiatherosclerotic; cardiant; vasotropic; hypertensive;				
KW		antiinflammatory; neuroprotective; nootropic; antiparkinsonian;				
KW		anticonvulsant; hepatotropic; dermatological; antipsoriatic; fungicide;				
KW		antididarrhaeic; antidiabetic; antidiabetic; antiasthmatic; antiarthritic;				
KW		antirheumatic; osteopathic; antithyroid; antiallergic; gene therapy;				
KW		ophthalmological; antianaemic; analgesic; virucide; anorectic; vulnerary;				
KW		immunomodulator; ss.				
OS		Homo sapiens.				
XX	Key	Location/Qualifiers				
FH		459..2594				
FT	CDS	/*tag= a				
FT		/product= "lipoxxygenase 46638"				
FT		/note= "this region is specifically claimed"				
XX						
XX	PN	WO200190323-A2.				
XX						
PD		29-NOV-2001.				
XX						
XX	PF	21-MAY-2001; 2001WO-US016380.				
XX						
XX	PR	19-MAY-2000; 2000US-0205675P.				
XX						
PA		(MTLL-) MILLENNIUM PHARM INC.				
XX						
FI		Meyers RA;				
XX						
DR		WPI; 2002-083104/11.				
DR		P-PSDB; ABB04578.				
XX						
PT		Novel human lipoxxygenase family member polypeptide and polynucleotide for				
PT		diagnosing, treating immune, blood vessel, cardiovascular, inflammatory,				
PT		ovarian, lung, colon, skin disorders and disorders involving placenta.				
XX						
PS		Claim 1; Page 100-102; 118pp; English.				
XX						
CC		The present invention provides the protein and coding sequences of a				
CC		human protein, which is a member of lipoxxygenase family, and is referred				





Qy	1924	AGAGGATGCCCCCGGCGGAGCGTGGCTTCCAGAGAAAAGCTGATCCAGATCTCCAA	1981
Db	2450	AGAGGAGCCCCCGGAGGCGGAGCATCGCGGCTTCCAGAGCGCGCTGGCCAGATCTCAAG	2509
Qy	1984	GGGCATCAGGAGGAGGAGAACCGAGCGCTGGCACTGCCCTACACCTACCTGGATCCTCCCT	2043
Db	2510	GGACATCCAGGAGCGGAGAACCGAGGTCCTGGCACTGCCCTACACCTACCTGGACCTCCCT	2569
Qy	2044	CATTGAGAACAGTGTCTCCATCTAAC	2069
Db	2570	CATTGAGAACAGTGTCTCCATCTAAC	2595
RESULT 13			
ADQ48418			
XX	ID	ADQ48418 standard; cDNA; 3320 BP.	
XX	AC	ADQ48418;	
XX	DT	23-SEP-2004 (first entry)	
XX	DE	Human lipoxigenase 46638, SEQ ID 22.	
XX	XX	Neuroprotective; Nootropic; Cerebroprotective; Anticonvulsant;	
XX	XX	Antiparkinsonian; Hepatotropic; Antiinflammatory; Osteopathic;	
XX	XX	Antirheumatic; Antiarthritic; Cytostatic; Antidiabetic; Antithyroid;	
XX	XX	Gastrointestinal; Antulcer; Cardiant; Immunosuppressive; Dermatological;	
XX	XX	Virucide; Haemostatic; Gene therapy; human; cytochrome P450;	
XX	XX	cytochrome P450 3312; cytochrome P450 3303; cytochrome P450 32579;	
XX	XX	dehydrogenase; reductase; dehydrogenase/ reductase 21509;	
XX	XX	dehydrogenase/ reductase 33770; lipoxigenase; lipoxigenase 46638;	
XX	XX	hydratase; hydratase 50090; gene; ss; enzyme.	
XX	OS	Homo sapiens.	
XX	XX		
XX	Key	Location/Qualifiers	
XX	FT	459..2594	
XX	FT	/*tag= a	
XX	FT	/product= "Human lipoxigenase 46638"	
XX	XX	US2004132087-A1.	
XX	XX	08-JUL-2004.	
XX	XX	11-FEB-2004; 2004US-00776871.	
XX	XX	31-MAR-2000; 2000US-0193920P.	
XX	XX	19-MAY-2000; 2000US-0205675P.	
XX	XX	15-JUN-2000; 2000US-0211727P.	
XX	XX	02-FEB-2001; 2001US-0266140P.	
XX	XX	30-MAR-2001; 2001US-00823901.	
XX	XX	02-APR-2001; 2001WO-US010720.	
XX	XX	21-MAY-2001; 2001US-0082658.	
XX	XX	21-MAY-2001; 2001WO-US016380.	
XX	XX	15-JUN-2001; 2001US-0082837.	
XX	XX	15-JUN-2001; 2001WO-US019319.	
XX	XX	04-FEB-2002; 2002US-00067668.	
XX	XX	20-JUN-2002; 2002US-00175696.	
XX	XX	(MILL-) MILLENNIUM PHARM INC.	
XX	XX	Meyers RE, Glucksmann MA, Rudolph-Owen LA;	
XX	XX	WPI; 2004-533235/51.	
XX	XX	P-PSDB; ADQ48419.	
XX	XX	New 33312, 33303, 32579, 21509, 33770, 46638, or 50090 nucleic acid	
XX	XX	molecules, useful for treating genetic disorders of the membrane	
XX	XX	transport, CNS disorders, liver disorders, skeletal muscle disorders, or	
XX	XX	cancer.	
XX	XX	Claim 1; SEQ ID NO 22; 248pp; English.	
XX	XX		

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Db 1730 GCGCCAGCTGCGGCTTCTGCGCACCCCATCTCAAGCTCTCTACTCCGCCACACTCGATACAC 1789
Qy 1264 ACTGCACATCAACAGCTTGGCCCGGAGCTGCTCGTTGGCCCTGGGAAAGTTGATAGACAA 1323
Db 1790 GTGCGAGTGAACACCATCGAGGGCCAGCTGCTCAACCCGAGGGCTCGTGGACCA 1849
Qy 1324 GTCCACAGCCCTTGGCACTGGGGGATTTCTGACCTGATGATAAAGAGAAACATGAGAGCT 1383
Db 1850 GGTCACTGCTCGGAGGCAAGGCTCATCTACCTCATGAGCAGGGCTGGCCCACTT 1909
Qy 1384 GAACACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1443
Db 1910 CACCTACACCAATTTCTGCTTCCGACAGCTGCGGGCCGCGGCTCTGCTGCTATCC 1969
Qy 1444 AGCTACTATTACCGAGATGATGGGATGAGATCTGGGGGGCAATAAAGAGCTTTGCTCTC 1503
Db 1970 CAACCTACCACTACCGAGACGAGCGCTGAAGATCTGGGGCGGCATGAGAGCTTTGCTCTC 2029
Qy 1504 TGAATAGTCAAGTCTACTATCCAGTGCACATCCGTTCAAGATGACCAAGAGCTCCA 1563
Db 2030 AGAATCGTGGGCTACTATTATCCAGTGCACATCTGTGACGAGGATTCGGAGCTGCA 2089
Qy 1564 GGCCTGGTGGAGAGATCTTCTGAGGGCTTCTCGCGGAGAAAGCTCAGGTATGCC 1623
Db 2090 GGCCTGGAGTGGGAGATTTTCTGAGGCTTCTCGCGGAGAAAGCTCAGGTATGCC 2149
Qy 1624 CTCCTGTTGGATACCGGGAAGCCCTGCTCAGATATATCACATGCTGATATTCACCTG 1683
Db 2150 AAGCCGGCTGTGCACCCGAGGAGATGCTGAGTTCCTCATGCAATCTTCAATG 2209
Qy 1684 CTCAGCCAGCATGACGTGTGCTGAGTTCAGGCGAGTTCGACTTTGTTGGATGCCAA 1743
Db 2210 CTCGCGCAGCAGCTGCTGTCAACAGTGGGAGCATGACTTTGGGGCTGGATGCCAA 2269
Qy 1744 TCTGCCACTACATCAGTACCTACCACTACTTCCAAAGCCAGGCGCGGCTGAGAG 1803
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RESULT 14  
AAC61761

ID AAC61761 standard; cDNA; 3384 BP.

XX AAC61761;

XX 06-MAR-2001 (first entry)

XX cDNA encoding a human lipoxxygenase protein.

XX Human; lipoxxygenase; leukotriene; lipid; chemotactic agent; inflammation;  
KW smooth muscle contraction; asthma; eye disease; arthritis; lung disease;  
KW cancer; acne; psoriasis; ss.

XX OS Homo sapiens.  
XX PN WO200061765-A2.  
XX PD 19-OCT-2000.  
XX PF 12-APR-2000; 2000WO-US009657.  
XX PR 12-APR-1999; 99US-0128817P.  
XX PR 24-AUG-1999; 99US-0150454P.  
XX PA (LEXI-) LEXICON GENETICS INC.  
XX PI Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;  
XX WPI; 2000-665134/64.  
XX Novel polynucleotides encoding human lipoxxygenase proteins useful for  
XX producing transgenic animals preferably mouse.  
XX Claim 1; Page 81-82; 83pp; English.  
XX The present sequence encodes a human lipoxxygenase protein. Lipoxxygenases  
XX oxidise lipids to produce leukotrienes. Leukotrienes bind cognate  
XX receptors and trigger biological effects. Leukotrienes influence a  
XX variety of biological processes, and can serve as, inter alia, potent  
XX chemotactic agents and mediators of inflammation, smooth muscle  
XX contractile agents, etc. Lipoxxygenases and leukotrienes are implicated in a  
XX variety of diseases and disorders, such as asthma, eye diseases,  
XX arthritis, lung disease, cancer, acne, psoriasis, etc

XX Sequence 3384 BP; 746 A; 1079 C; 865 G; 694 T; 0 U; 0 Other;

Query Match 20.5%; Score 659.6; DB 3; Length 3384;  
Best Local Similarity 63.9%; Pred. No. 4.2e-162;  
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;  
Qy 484 CAGCTGGAAGACTTACATTAAGAGTTGGCTGCTGCTTGTACACGAGACTGTGAAAGA 543  
Db 1053 CAGTGGGAATCGGTACCTGCCGGCTTCCCATGAAATTTGACATCCCATCCTGATGTA 1112  
Qy 544 CTTGACCTCAACATCAAGTACTCTCGATGAAGATGCCAACTTCTTTTAAAGCCCA 603  
Db 1113 CATGGAGCCCAATGTTTCGATATCTAGCCACCAAGACGATCTCGTGTCTTCAATGCCAT 1172  
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Qy 964 CTCTCAGCCCCGATGACCTCTTACACAGAGCTTCAGGGTCCGGACCCCTGCTTCCCAT 1023  
Db 1533 CGTGCGCGCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1589



QY 1024 TGCATTCAGCTCAAAAGAGATCCCGGGCCAGACAACCCCAATCTTCCTGCGCCAGCGATGA 1083  
Db 1590 GGCCATCCAGCTCAGCCAGAGACCCCGGGCCTGACAGCCCCATCTTCCTGCGCCACTGACTC 1649  
QY 1084 CACGTGGGACTGGTTGCTGGCCAGACCTGGGTTCGCAATCTGAGTTTACATCCATGA 1143  
Db 1650 CGAATGGGACTGGTCTGGCCAGACGCTGGGTGGCAACTCTGAGTTCTCTGGTGACGA 1709  
QY 1144 GGCTGTACACATCTGTGTCATGCCATCTGATTCAGAAAGTCTTTGGCTTTGGCCACAT 1203  
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Db 1950 CACCTACACCAATTTCTGCTTTCGGACAGCGCTGCGGGCCGGCGGCTCTGGGCTATCCC 2009  
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QY 1804 TTTCTAGCAGCTCCAGCAGATTAATTCGTCAAGTTATCAATCATTTGCTCTCTGCTG 1863  
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QY 1864 GCTAAGCGCAGAACTGGGGACCAAGGCCCTGGGCCACTATCCAGATGAACACTTCCAC 1923  
Db 2430 GGTTAGCCAGAACCAAGGACCGAGGCCCCCTGGGCACTTACCAGATGAGCACTTCC 2489  
QY 1924 AGAGATGCCCCCGGGGAAAGCGTGGCTGCTTCCAGAGAAAGTGATCCAGATCTCCAA 1983  
Db 2490 AGAGAGGCCCCGAGGGGAGCATCGCGCTTCCAGAGCGCGCTGGCCAGATCTCAAG 2549  
QY 1984 GGGCATCAGGAGAGAGAAACGAGGCTGGCATCTGCTTACACTTACCTGGATCTCTCCCT 2043  
Db 2550 GGACATCCAGAGGGGAAACCAAGGCTGGGCACTGGCTTACACCTTACCTTGGACCTCCCT 2609  
QY 2044 CATTGAGAACAGTGTCTCCATCTAAC 2069  
Db 2610 CATTGAGAACAGTGTCTCCATCTAAC 2635

RESULT 15  
ADQ48420  
ID ADQ48420 standard; cDNA; 2136 BP.  
XX  
AC ADQ48420;  
XX  
DT 23-SEP-2004 (first entry)  
XX  
DE Human lipoxigenase 46638, SEQ ID 24.  
XX  
KW Neuroprotective; Nootropic; Cerebroprotective; Anticonvulsant;  
KW Antiparkinsonian; Hepatotropic; Antiinflammatory; Osteopathic;  
KW Antirheumatic; Antiarthritic; Cytostatic; Antidiabetic; Antithyroid;  
KW Gastrointestinal; Antitumor; Cardiant; Immunosuppressive; Dermatological;  
KW Virucide; Haemostatic; Gene therapy; human; cytochrome P450;  
KW cytochrome P450 3312; Cytochrome P450 33303; cytochrome P450 32579;  
KW dehydrogenase; reductase; dehydrogenase/ reductase 21509;  
KW dehydrogenase/ reductase 33770; lipoxigenase; lipoxigenase 46638;  
KW hydratase; hydratase 50090; gene; ss; enzyme.  
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OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
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FT /\*tag= a  
FT /product= "Human lipoxigenase 46638"  
XX  
PN US2004132087-A1.  
XX  
PD 08-JUL-2004.  
XX  
PF 11-FEB-2004; 2004US-00776871.  
XX  
PR 31-MAR-2000; 2000US-0193920P.  
PR 19-MAY-2000; 2000US-0205675P.  
PR 15-JUN-2000; 2000US-0211727P.  
PR 02-FEB-2001; 2001US-0266140P.  
PR 30-MAR-2001; 2001US-00823901.  
PR 02-APR-2001; 2001WO-US010720.  
PR 21-MAY-2001; 2001US-00862658.  
PR 21-MAY-2001; 2001WO-US016380.  
PR 15-JUN-2001; 2001US-00882837.  
PR 15-JUN-2001; 2001WO-US019319.  
PR 04-FEB-2002; 2002US-00067668.  
PR 20-JUN-2002; 2002US-00175696.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
XX  
PI Meyers RE, Glucksmann MA, Rudolph-Owen LA;  
XX  
XX WPI: 2004-533235/51.  
XX P-PSDB; ADQ48419.  
XX  
PT New 33312, 33303, 32579, 21509, 33770, 46638, or 50090 nucleic acid  
PT molecules, useful for treating genetic disorders of the membrane  
PT transport, CNS disorders, liver disorders, skeletal muscle disorders, or  
PT cancer.  
XX  
PS Claim 1; SEQ ID NO 24; 248pp; English.  
XX  
CC The present invention relates to novel human coding sequences and  
CC proteins for cytochrome P450 proteins 33312 (ADQ48397-ADQ48399), 33303  
CC (ADQ48400-ADQ48402) and 32579 (ADQ48403-ADQ48405); dehydrogenases/  
CC reductases 21509 (ADQ48409-ADQ48411) and 33770 (ADQ48412-ADQ48414);  
CC lipoxigenase 46638 (ADQ48418-ADQ48420) and hydratase 50090 (ADQ48424-  
CC ADQ48426). The sequences are useful for diagnosing and treating  
CC disorders, such as genetic disorders of the membrane transport  
CC (aminocidurias, cystinosis), CNS disorders (Alzheimer's disease,  
CC epilepsy, Parkinson's disease), liver disorders, skeletal muscle  
CC disorders, cellular proliferative and/or differentiative disorders  
CC (cancer), hormonal disorders (diabetes, thyroid disorders), immune and  
CC inflammatory disorders (rheumatoid arthritis, osteoarthritis, ulcer),

CC	cardiovascular disorders, blood vessel disorders, neutrophil disorders
CC	(neutropenia, lupus), testicular disorder (mumps)
CC	The present sequence is a coding sequence for a lipoygenase of the
CC	invention.
XX	
SQ	Sequence 2136 BP; 459 A; 683 C; 569 G; 425 T; 0 U; 0 Other;
	Query Match 20.4%; Score 658.6; DB 12; Length 2136;
	Best Local Similarity 63.9%; Pred. No. 6e-162;
	Matches 1013; Conservative 0; Mismatches 569; Indels 3; Gaps 1;
QY	484 CAGCTGGAAGACTTACATTGAAGGTTGGCTCGCTGCTTGAACCAAGAGACTGTGAAGA 543
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	555 CAGTGGGAATCGGTACCTGCTCCGGCTTCCCATGAAAAATTGCATCCCATCCCTGATGTA 614
QY	544 CTTTGGACCTCAAATCAAGTACTCTGCGATGAAGAATGCCAAACTCTCTCTTTAAAGGCCA 603
DB	
	615 CATGGAGCCCAATGTTTCGATCTCAGCCACCAAGACGATCTCGTGTCTCTTCATGCGAT 674
QY	604 CTCGCGTATACGGAGCTGAAAGTCAAAGGCTCTCGACCGCACAGACTCTGGAGGAG 663
DB	
	675 CCCTGCGCTCTGGGAATGAAGCTTCGAGGCTGTTGGATCGCAAGGGCTCTCTGGAAGAA 734
QY	664 TCTGAGGGAGATGAGAAGGCTGTTAACTTCCGCAAGACTCCAGCAGCAGAGTATGTGTT 723
DB	
	735 GCTGGATGACATGCAGAAACTCTTCTGGTGCCATAAGACCTTCACGACAAAGTATGTGAC 794
QY	724 TGCACACTGCGCAGAGATGCTTCTTTCGCTCCCAAAACAATCCCGGTCACTGATGAAATGTGGC 783
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	795 AGAGCACTGTTGGAAGATCACTTCTTTGGGTACCACTACCTGATGTTGTCATCCCGT 854
QY	784 CTTGATTTCGCGCTGTCACTGTCTCCAAACAACATTCCTCGGTCACTGATGAAATGTGGC 843
DB	
	855 CATGCTCCACTGCATCTTAGTCTGCCCAGACAGCTGCCTGTCAACAATGACATGTGGTGC 914
QY	844 CCCAGTCTGGGCGCTGGAACCAAGTCTGZAGGCTGAGTTGGAGAGGGCTCCCTGTTCCT 903
DB	
	915 CCCCTTCTGGGACAGGACACATGCTCTGCACAGAGCTAGAGAGGGGGAAACATCTTCCT 974
QY	904 GGTGGATCATGGCAATCTTTCTGGAGTCCACCAACAATCCTCAATGGAAAGCTCAGTT 963
DB	
	975 AGCGGACTATGATCTCTGGCGAGGCCCCACCCTGCTTAACGGCGCCAGAGTA 1034
QY	964 CTCTGACGCCCCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGTCTCCAT 1023
DB	
	1035 CGTGGCGCCCCACTGTGCTGTGTGGCTCAGCCCCCAG---GGGGGGCTGGTGCCCTT 1091
QY	1024 TGCCATCCAGCTAAACAGACTCCCGGGCCAGACAAACCCCATCTTCTCTGCCACGAGTGA 1083
DB	
	1092 GGCCATCCAGCTCAGCCACAGACCCCGGGCCGTGACAGCCCCCATCTTCTCTGCCCATGACTC 1151
QY	1084 CACGTGGACTGTGTCTGCGCAAGACTGGGTTTCGCAATTTCTAGATTTTACATCCATGA 1143
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	1152 CGAATGGGAATGGTCTGTGCGCAAGAAGTGGGTGGCAACTCTGAGTTCCTGGTGCACGA 1211
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DB	
	1212 AAACACACGCACTTTCTGTGCACGCAATTTGCTGTGAGGCTTTCGCCATGGCCACGCT 1271
QY	1204 ACGTCACTGCTAGGTTGTCACCTCTCTTTCAAGCTATTGATTCCTCACATTTGGGTACAC 1263
DB	
	1272 GCGCCAGCTGCGCTGTGCCACCCCATCTACAAGCTCCTACTCCCCACACTCGATACAC 1331
QY	1264 ACTGCACATCAACACGCTTGCCGGGAGCTGCTGTTGCCCTGGGAAGTTGATAGACAA 1323
DB	
	1332 GCTGCAAGGTGAACCACTCGGAGGGGCCACGCTGCTCAACCCCGAGGGCTCTGFGACCA 1391
QY	1324 GTCCACAGGCTCTGGCACTGGGGGATTTCTCTGACTGATAAAGAGAAACATGGAGCAGCT 1383
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	1392 GGTCACTTCATCGGAGGCAAGGCCTCATCTACTCATGACACGGGCTTGCCCACTT 1451
QY	1384 GAACTACTCTGTCTGTCTCTCCTTGAGATATCCGAGCCCGAGGTGTGGAAGACATCCC 1443

Search completed: July 19, 2005, 13:18:45  
Job time : 1104 secs

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1752	Db	CTCTGCCAGCAGCGCTGCTCTCAACAGTGGGCGCATGATCTTTGGGCGCTGGATGCCCAA	1811
1744	Qy	TCGTGCCACCTTACATGCGATTAACAACAACCTTATCCAAAGGCCAGGCCCGCGCTGAGAG	1803
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1804	Qy	TTTTCATAGCACGCTCCCGACAGTTAATTCGTCAAGTTATCACATCATTTGCTCTCTGGCT	1863
1872	Db	TTTACTAGACACCTTCCCTGAAGTGAACATCAGCTGTAAACAACCTCTCTCTTCTGGTT	1931
1864	Qy	GCTAAGCGCAGAACTCTGGGACCAAAAGGCCCTTGGGCACTATCCAGATGAACACTTCAC	1923
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2052	Db	GGAATCCAGAGCGGAACCAAGGCTCTGGGCACTGCGCCCTACCTTACCTGGACCTCTCCCT	2111
2044	Qy	CATTGAAACAGTGTCTCCCATCTAA	2068
2112	Db	CATTGAAACAGTGTCTCCCATCTAA	2136

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 12:45:07 ; Search time 1284.13 Seconds  
(without alignments)  
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Title: US-10-688-676A-3

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Gapop 10.0 , Gapext 1.0

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3178	98.6	3205	9	Sequence 3, Appli
3	3178	98.6	3205	19	Sequence 3, Appli
4	1395.2	43.3	2685	9	Sequence 1, Appli
5	1395.2	43.3	2685	9	Sequence 985, App
6	1395.2	43.3	2685	10	Sequence 642, App
7	1395.2	43.3	2685	19	Sequence 1, Appli

8	659.6	20.5	3320	9	US-09-862-658-1	Sequence 1, Appli
9	659.6	20.5	3320	14	US-10-175-696-22	Sequence 22, Appli
10	659.6	20.5	3320	19	US-10-776-871-22	Sequence 22, Appli
11	659.6	20.5	3384	16	US-10-422-264-29	Sequence 29, Appli
12	658.6	20.4	2136	9	US-09-862-658-3	Sequence 3, Appli
13	658.6	20.4	2136	14	US-10-175-696-24	Sequence 24, Appli
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16	658	20.4	2301	18	US-10-422-264-1	Sequence 1, Appli
17	657	20.4	2307	16	US-10-302-172-803	Sequence 803, App
18	657	20.4	2604	16	US-10-422-264-23	Sequence 23, Appli
19	652.2	20.2	2136	17	US-10-275-998-8	Sequence 8, Appli
20	585.8	17.5	2469	9	US-09-853-053-1	Sequence 6, Appli
21	565.8	17.5	2469	17	US-10-445-484-1	Sequence 1, Appli
22	466.2	14.5	1383	16	US-10-422-264-11	Sequence 11, Appli
23	466.2	14.5	1848	16	US-10-422-264-9	Sequence 9, Appli
24	466.2	14.5	2316	16	US-10-422-264-27	Sequence 27, Appli
25	440.6	13.7	2497	9	US-09-964-824A-543	Sequence 543, App
26	440.6	13.7	2497	9	US-09-962-832-97	Sequence 97, Appli
27	440.6	13.7	2497	9	US-09-954-456-942	Sequence 942, Appli
28	440.6	13.7	2497	16	US-10-240-305-13	Sequence 13, Appli
29	440.6	13.7	2497	18	US-10-641-643-1155	Sequence 1155, Ap
30	440.6	13.7	2497	19	US-10-071-411-3	Sequence 3, Appli
31	440.6	13.7	2497	20	US-10-741-292-1	Sequence 1, Appli
32	440.6	13.7	2497	21	US-10-314-799-3	Sequence 3, Appli
33	440.6	13.7	2497	21	US-10-843-641A-3969	Sequence 3969, Ap
34	440.6	13.7	2497	21	US-10-843-641A-5846	Sequence 5846, Ap
35	440.6	13.7	2497	21	US-10-843-641A-5983	Sequence 5983, Ap
36	440.2	13.7	2484	17	US-10-191-997-91	Sequence 91, Appli
37	440.2	13.7	2484	19	US-10-283-975A-296	Sequence 296, App
38	439.8	13.6	2076	20	US-10-485-310-21	Sequence 21, Appli
39	439.6	13.6	2420	16	US-10-240-305-15	Sequence 15, Appli
40	427.8	13.3	2107	20	US-10-741-292-18	Sequence 18, Appli
41	423	13.1	2107	20	US-10-741-292-17	Sequence 17, Appli
42	407.2	12.6	1441	16	US-10-422-264-13	Sequence 13, Appli
43	336.4	10.4	2368	19	US-10-741-601-232	Sequence 232, App
44	336.4	10.4	2368	21	US-10-741-600-671	Sequence 671, App
45	336.4	10.4	2867	19	US-10-741-601-233	Sequence 233, App

ALIGNMENTS

RESULT 1

US-10-688-676A-3  
; Sequence 3, Application US/10688676A  
; Publication No. US20040248794A1  
; GENERAL INFORMATION:  
; APPLICANT: Alcon, Inc.  
; APPLICANT: Gianni, John M.  
; APPLICANT: Gamache, Daniel A.  
; APPLICANT: Miller, Steven T.  
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo-  
; TITLE OF INVENTION: Activity to Ocular Surface Cells  
; FILE REFERENCE: 2394 US  
; CURRENT APPLICATION NUMBER: US/10/688.676A  
; CURRENT FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: US 60/435,958  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 3  
; LENGTH: 3224  
; TYPE: DNA  
; ORGANISM: homo sapiens  
; ORGANISM: 676A-3

Query Match 100.0%; Score 3224; DB 20; Length 3224;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CAGTTTCGAGTAGAGCTAACTGGTCAGAGATGCCAAATGCGAGGTGAGAGTATC 60

Db 1 CAGCTTGCAGTAGAGAGCTAAACTGGTCCAGGAGGATGGCGAAATGCGAGGGTGAGAGTATC 60  
Qy 61 CACGGGGGAAGCCTGTGGGGCTGGCACATGGGACAAAGTGTCTGTCTCAGCATCGTGGGAAAC 120  
Db 61 CACGGGGGAAGCCTGTGGGGCTGGCNCATGGGACAAAGTGTCTGTCTCAGCATCGTGGGAAAC 120  
Qy 121 CCA CGGAGAGAGCCCTTTAGTACCTCTGTGACCAATCTGGGCAAGAGATTGAGCGCCGGTGC 180  
Db 121 CCA CGGAGAGAGAGCCCTTTAGTACCTCTGTGACCAATCTGGGCAAGAGATTGAGCGCCGGTGC 180  
Qy 181 TGAAGAGACTTTCGAGGTGACGCTTCCCGAGAGCTGAGCACTGTGCTGATGCTGGAGT 240  
Db 181 TGAAGAGACTTTCGAGGTGACGCTTCCCGAGAGCTGAGCACTGTGCTGATGCTGGAGT 240  
Qy 241 CCACAAGACACCCCGGAAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGTAGTGCCTGGTT 300  
Db 241 CCACAAGACACCCCGGAAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGTAGTGCCTGGTT 300  
Qy 301 CTGCCGCTGGTTTCGAGCTGGAGTGGCTACCTGGGGCTGCACCTCCACTTCCCTCTGTATCA 360  
Db 301 CTGCCGCTGGTTTCGAGCTGGAGTGGCTACCTGGGGCTGCACCTCCACTTCCCTCTGTATCA 360  
Qy 361 GTGGCTGGAAAGGGCGGGGAGCTGTGCTGAGAGAGGAGCAGCAAAAGTGTCTGGCA 420  
Db 361 GTGGCTGGAAAGGGCGGGGAGCTGTGCTGAGAGAGGAGCAGCAAAAGTGTCTGGCA 420  
Qy 421 AGACCATCACCTTACACTCAGAGTACAGCGCCAGAGGAGCTTGTAGTCCAGGACAGAGAT 480  
Db 421 AGACCATCACCTTACACTCAGAGTACAGCGCCAGAGGAGCTTGTAGTCCAGGACAGAGAT 480  
Qy 481 GTACAGCTGGAAAGACTTACATTTGAAGGTTGGCTCGCTCGCTTGACCAGAGACTGTGAA 540  
Db 481 GTACAGCTGGAAAGACTTACATTTGAAGGTTGGCTCGCTCGCTTGACCAGAGACTGTGAA 540  
Qy 541 AGACTTGGAGCTCAACATCAAGTACTCTGCGATGAAGATGCGCAACTCTTTTAAAGC 600  
Db 541 AGACTTGGAGCTCAACATCAAGTACTCTGCGATGAAGATGCGCAACTCTTTTAAAGC 600  
Qy 601 CCACTCCGCTATACCGAGCTGAAGCTCAAGGGCTCTCGGACCGCAGAGGACTCTGGAG 660  
Db 601 CCACTCCGCTATACCGAGCTGAAGCTCAAGGGCTCTCGGACCGCAGAGGACTCTGGAG 660  
Qy 661 GAGTCTGAGGAGATGAGAAGGCTGTTTAACTTCCGAAAGACTTCCAGCAGCAGAGTATGT 720  
Db 661 GAGTCTGAGGAGATGAGAAGGCTGTTTAACTTCCGAAAGACTTCCAGCAGCAGAGTATGT 720  
Qy 721 GTTTGCACACTGCGAGAGAGATGCTTCTTCCGCTCCAGTTCCTTAAATGGGCATCAACC 780  
Db 721 GTTTGCACACTGCGAGAGAGATGCTTCTTCCGCTCCAGTTCCTTAAATGGGCATCAACC 780  
Qy 781 GGTCTCTGATTCGCGCTGTACAGTCTCCAAACAACTTCCCGGTCACTGATGAATGGT 840  
Db 781 GGTCTCTGATTCGCGCTGTACAGTCTCCAAACAACTTCCCGGTCACTGATGAATGGT 840  
Qy 841 GGCCCCAGTGTGCGGCCCTGGAAACCAAGTCTGCAAGGCTGAGTTGGAAAGGGCTCCCTGTT 900  
Db 841 GGCCCCAGTGTGCGGCCCTGGAAACCAAGTCTGCAAGGCTGAGTTGGAAAGGGCTCCCTGTT 900  
Qy 901 CTTTGTGGATCATGGCAATCTTTCTGGAGTCCACCAACATCCTCAATGGAAAGCCTCA 960  
Db 901 CTTTGTGGATCATGGCAATCTTTCTGGAGTCCACCAACATCCTCAATGGAAAGCCTCA 960  
Qy 961 GTTCTCTGAGCCCGATGAGCTGTTACACAGAGCTCAGGGTCGGGACCCCTGCTCC 1020  
Db 961 GTTCTCTGAGCCCGATGAGCTGTTACACAGAGCTCAGGGTCGGGACCCCTGCTCC 1020  
Qy 1021 CATTTGCCATCCAGCTCAACAGACTCCCGGGCCAGACAAACCCCATCTTCTGCCCCAGCGA 1080  
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Qy 1081 TGA CAGTGGGACTGTTGCTGGCCAGAGCTGGGTTCCGAATCTGAGTTTATACCA 1140  
Db 1081 TGA CAGTGGGACTGTTGCTGGCCAGAGCTGGGTTCCGAATCTGAGTTTATACCA 1140

Qy 1141 TGA GCTCTCACA CATCTGCTGCA TGTGCCAT TGTCCCAT TCTGAT TCCAGAA GTCTTTTGCCTTGGCCAC 1200  
Db 1141 TGA GCTCTCACA CATCTGCTGCA TGTGCCAT TGTCCCAT TCTGAT TCCAGAA GTCTTTTGCCTTGGCCAC 1200  
Qy 1201 ATTAGCTCAGCTGCTAGGTGTCA CCGCTCTCTTCAAGCTATTGATTCCTCA CATTCGGTA 1260  
Db 1201 ATTAGCTCAGCTGCTAGGTGTCA CCGCTCTCTTCAAGCTATTGATTCCTCA CATTCGGTA 1260  
Qy 1261 CACACTGCACATCAACACGCTTGGCCCGGAGCTGCTCGTTGCCCTGGGAGTTGATAGA 1320  
Db 1261 CACACTGCACATCAACACGCTTGGCCCGGAGCTGCTCGTTGCCCTGGGAGTTGATAGA 1320  
Qy 1321 CAAGTCCA CAGGCCCTTGGCACTGGGGAT TCTGAC CTTGAT TAAAGAGAA CATCGAGCA 1380  
Db 1321 CAAGTCCA CAGGCCCTTGGCACTGGGGAT TCTGAC CTTGAT TAAAGAGAA CATCGAGCA 1380  
Qy 1381 GCTGAAC TACTCTGCTGTGTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACAT 1440  
Db 1381 GCTGAAC TACTCTGCTGTGTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACAT 1440  
Qy 1441 CCCAGGCTACTATTACCGAGATGATGGGATGCAGATCTGGGGGGCAATAAAGAGCTTTGT 1500  
Db 1441 CCCAGGCTACTATTACCGAGATGATGGGATGCAGATCTGGGGGGCAATAAAGAGCTTTGT 1500  
Qy 1501 CTCTGAAA TAGTCAGCATCTACTATCCAAGTGACACATCCGTTCCAAGATGACCAAGAGCT 1560  
Db 1501 CTCTGAAA TAGTCAGCATCTACTATCCAAGTGACACATCCGTTCCAAGATGACCAAGAGCT 1560  
Qy 1561 CGAGCCCTGGGTGAGGGAGATCTTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGGTAT 1620  
Db 1561 CGAGCCCTGGGTGAGGGAGATCTTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGGTAT 1620  
Qy 1621 GCCCTCTCTTGTGGATACCCGGGAAGCCCTGCTGCAGTATATCACCATGGTGATATTCAC 1680  
Db 1621 GCCCTCTCTTGTGGATACCCGGGAAGCCCTGCTGCAGTATATCACCATGGTGATATTCAC 1680  
Qy 1681 CTGCTCAGCCAAGCATGCAGTGTCA GGTTCAGGCCAGTTCGACTCTTGTGTTGATGCC 1740  
Db 1681 CTGCTCAGCCAAGCATGCAGTGTCA GGTTCAGGCCAGTTCGACTCTTGTGTTGATGCC 1740  
Qy 1741 CAACTGCGCA CTTACCATGCACTACCA CCACTACTTCCAAAGGCCAGGCCGCCCTGA 1800  
Db 1741 CAACTGCGCA CTTACCATGCACTACCA CCACTACTTCCAAAGGCCAGGCCGCCCTGA 1800  
Qy 1801 GAGTTTCA TAGCCAGCTCCCA CAGAGTTAA TTTGCTCAAGTTATCACATCATTTGCTCTG 1860  
Db 1801 GAGTTTCA TAGCCAGCTCCCA CAGAGTTAA TTTGCTCAAGTTATCACATCATTTGCTCTG 1860  
Qy 1861 GCTGCTAAGCGCAGAACCTTGGGAC CAAAGGCCCTGCGCCACTATCCAAGATGAACACTT 1920  
Db 1861 GCTGCTAAGCGCAGAACCTTGGGAC CAAAGGCCCTGCGCCACTATCCAAGATGAACACTT 1920  
Qy 1921 CACAGAGATGCCCCCGCGGAGAGCGTGGCTGCCCTTCCAGAGAAAGCTGATCCAGTCTC 1980  
Db 1921 CACAGAGATGCCCCCGCGGAGAGCGTGGCTGCCCTTCCAGAGAAAGCTGATCCAGTCTC 1980  
Qy 1981 CAAAGGCA TCAGGAGAGAAC CCGAGGCTGGCA CTGCCCTACCTACTCTGGATCTCC 2040  
Db 1981 CAAAGGCA TCAGGAGAGAAC CCGAGGCTGGCA CTGCCCTACCTACTCTGGATCTCC 2040  
Qy 2041 CCTCATTTGAGAA CAGTGTCTCCATCTAA CATCTTGGAGAA GACAGTCTCTGTGACATAT 2100  
Db 2041 CCTCATTTGAGAA CAGTGTCTCCATCTAA CATCTTGGAGAA GACAGTCTCTGTGACATAT 2100  
Qy 2101 AGAACTCTTGACCATGCTCTCCAGGCTAAGTCCCGGTATGCTTCTCTGGACAAACCAAG 2160  
Db 2101 AGAACTCTTGACCATGCTCTCCAGGCTAAGTCCCGGTATGCTTCTCTGGACAAACCAAG 2160  
Qy 2161 CCCCATTCTTACACACACACACACACACACACACACACCTAATAAAAAATCGAAAAACCTTA 2220  
Db 2161 CCCCATTCTTACACACACACACACACACACACACACCTAATAAAAAATCGAAAAACCTTA 2220



QY	455	AAGGAGCTTCAAGTCCAGGCAGAGATGTACAGCTGGAAGACTTACATTTGAAGGTTGGCCT	514
Db	421	AAGGAGCTTGAAGTCCAGGCAGAGATGTACAGCTGGAAGACTTACATTTGAAGGTTGGCCT	480
QY	515	CGTGCCTTGAACAAGAGACTGTGAAGAAGCTTGGACCTCAACATCAAGTACTCTGGGATG	574
Db	481	CGTGCCTTGAACAAGAGACTGTGAAGAAGCTTGGACCTCAACATCAAGTACTCTGGGATG	540
QY	575	AAGATGCCAAACTCTTTCTTAAAGCCCACTCGCGTATACGGAGCTGAAAGTCAAGGG	634
Db	541	AAGATGCCAAACTCTTTCTTAAAGCCCACTCGCGTATACGGAGCTGAAAGTCAAGGG	600
QY	635	CTCCTCGAAGCGCAGAGACTCTGGAGGAGTCTGAGGGAGATGAGAAGGCTGTTTAACTTC	694
Db	601	CTCCTCGAAGCGCAGAGACTCTGGAGGAGTCTGAGGGAGATGAGAAGGCTGTTTAACTTC	660
QY	695	CGCAAGACTCCAGCAGCAGAGTATGTGTTTGACACTGGCAGAGATGCCCTTCTTCGCC	754
Db	661	CGCAAGACTCCAGCAGCAGAGTATGTGTTTGACACTGGCAGAGATGCCCTTCTTCGCC	720
QY	755	TCCAGTTCCTTAATGGCATCAACCCGGTCTGTGATTCGCGCTGTACAGTCTCCCAAC	814
Db	721	TCCAGTTCCTTAATGGCATCAACCCGGTCTGTGATTCGCGCTGTACAGTCTCCCAAC	780
QY	815	AACCTTCCCGTCACTGATGAATGTGTGGGCCCCAGTGTGGGCCCTGGAAACCAAGTCTGCGAG	874
Db	781	AACCTTCCCGTCACTGATGAATGTGTGGGCCCCAGTGTGGGCCCTGGAAACCAAGTCTGCGAG	840
QY	875	GCTGAGTTGGAGAGGGCTCCCTGTTCTGTGTGGATCATGGCATCTTTCTGGAGTCCAC	934
Db	841	GCTGAGTTGGAGAGGGCTCCCTGTTCTGTGTGGATCATGGCATCTTTCTGGAGTCCAC	900
QY	935	ACCAACATCTCAATGGAAAGCTCAGTTCTCTGACAGCCCGATGACCTGTACACAG	994
Db	901	ACCAACATCTCAATGGAAAGCTCAGTTCTCTGACAGCCCGATGACCTGTACACAG	960
QY	995	AGCTCAGGGTCCGGACCCCTGCTTCCCATTTGCCATCCAGTCAAAACAGACTCCCGGGCCA	1054
Db	961	AGCTCAGGGTCCGGACCCCTGCTTCCCATTTGCCATCCAGTCAAAACAGACTCCCGGGCCA	1020
QY	1055	GACAAACCCATCTTCTGCGCAGCAGATGACAGTGGGAATGTTGTGTCGCCAAGACTGCG	1114
Db	1021	GACAAACCCATCTTCTGCGCAGCAGATGACAGTGGGAATGTTGTGTCGCCAAGACTGCG	1080
QY	1115	GTTTCGCAATCTGAGTTTACATCCATGAGGCTGTACACATCTGCTGCATGCCCATCTG	1174
Db	1081	GTTTCGCAATCTGAGTTTACATCCATGAGGCTGTACACATCTGCTGCATGCCCATCTG	1140
QY	1175	ATTCCAGAAAGTCTTTGCTTGGCCACATTAACGTACGTGCTGCTAGGTGTCAACCTCTCTTC	1234
Db	1141	ATTCCAGAAAGTCTTTGCTTGGCCACATTAACGTACGTGCTGCTAGGTGTCAACCTCTCTTC	1200
QY	1235	AAGCTATTGATTCCTCAATTCGGTACACATGTCACATCAACACGTTGCCCGGAGCTG	1294
Db	1201	AAGCTATTGATTCCTCAATTCGGTACACATGTCACATCAACACGTTGCCCGGAGCTG	1260
QY	1295	CTCGTTGCCCTGGGAAGTTGATAGCAAGTCCACAGGCTTGGCACTGGGGATTCCTCT	1354
Db	1261	CTCGTTGCCCTGGGAAGTTGATAGCAAGTCCACAGGCTTGGCACTGGGGATTCCTCTCT	1320
QY	1355	GACCTGATAAAGAAACATGGAGCAGCTGAATCTCTGCTGTGTCTCCCTGAAGAT	1414
Db	1321	GACCTGATAAAGAAACATGGAGCAGCTGAATCTCTGCTGTGTCTCCCTGAAGAT	1380
QY	1415	ATCCGAGCCGAGGTGTGAAGACATCCAGGCTACTATTACCGAGATGATGGGATGCGAG	1474
Db	1381	ATCCGAGCCGAGGTGTGAAGACATCCAGGCTACTATTACCGAGATGATGGGATGCGAG	1440
QY	1475	ATCTGGGGGCGCATTAAGAGCTTGTCTCTGAAATAGTCAGCATCTACTATCCAGTGCAC	1534
Db	1441	ATCTGGGGGCGCATTAAGAGCTTGTCTCTGAAATAGTCAGCATCTACTATCCAGTGCAC	1500

QY	1535	ACATCCGTTCCAGATGACCAAGAGCTCCAGGCTGGGTGAGGGAGATCTTCTCTGAGGC	1594
Db	1501	ACATCCGTTCCAGATGACCAAGAGCTCCAGGCTGGGTGAGGGAGATCTTCTCTGAGGC	1560
QY	1595	TTCCTCGGCCGAGAAAGCTCAGGTATGCCCTCTGTTGGATACCCGGGAGCCCTGGTC	1654
Db	1561	TTCCTCGGCCGAGAAAGCTCAGGTATGCCCTCTGTTGGATACCCGGGAGCCCTGGTC	1620
QY	1655	CAGTATATCACCATGGTGATATTACCTGCTCAGCAAGCATGCAGCTGTCTAGTTTCAGGC	1714
Db	1621	CAGTATATCACCATGGTGATATTACCTGCTCAGCAAGCATGCAGCTGTCTAGTTTCAGGC	1680
QY	1715	CAGTTTCGACTCTTGTGTTTGGATGCCAATCTGCCAATCTTACCATGCAGAGCTACACACCT	1774
Db	1681	CAGTTTCGACTCTTGTGTTTGGATGCCAATCTGCCAATCTTACCATGCAGCTACACACCT	1740
QY	1775	ACTTCCAAAGGCCAGGCCCGGCTGAGAGTTTCATAGCACGCTCCAGCAGTTAATTCG	1834
Db	1741	ACTTCCAAAGGCCAGGCCCGGCTGAGAGTTTCATAGCACGCTCCAGCAGTTAATTCG	1800
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Db	1801	TCAGTTATCACATCATTTGCTCTCTGGCTGTAAAGCGCAGAACTTGGGGACCAAGGCC	1860
QY	1895	CTGGGCCACTATCCAGATGAACATTTCAAGAGATGCCCCCGCGGAGCGTGCGTGCC	1954
Db	1861	CTGGGCCACTATCCAGATGAACATTTCAAGAGATGCCCCCGCGGAGCGTGCGTGCC	1920
QY	1955	TTCAGAGAAAGCTCATCCAGATCTCCAAAGGCATCAGGAGAGGAAACCGAGCCCTGGCA	2014
Db	1921	TTCAGAGAAAGCTCATCCAGATCTCCAAAGGCATCAGGAGAGGAAACCGAGCCCTGGCA	1980
QY	2015	CTGCCCTACACTACTCGATCTCCCTCTCATTTGAGAAACAGTGTCTCCATCTAAACATCTT	2074
Db	1981	CTGCCCTACACTACTCGATCTCCCTCTCATTTGAGAAACAGTGTCTCCATCTAAACATCTT	2040
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Db	2041	GGAGAAAGCAGTCTGTGTGATATAGAACTCTTTGACCATGCTCTCCAGGCTAAGTCC	2100
QY	2135	CGGTATGCTTCTCTGGGAAACCAAGCCCATCTTTACACACACACACACACACACAC	2194
Db	2101	CGGTATGCTTCTCTGGGAAACCAAGCCCATCTTTACACACACACACACACACACAC	2160
QY	2195	TAAATAAATCGAAAAACAGAAAAACCTAAATCTCCACAGAGGCAAGATCTCACACAGCAG	2254
Db	2161	TAAATAAATCGAAAAACAGAAAAACCTAAATCTCCACAGAGGCAAGATCTCACACAGCAG	2220
QY	2255	GAGCCATCCAAATGTTTGGAGACCCCTGAGCTTTCAGCTCTGATTAACGGCTTTTGTGGTTT	2314
Db	2221	GAGCCATCCAAATGTTTGGAGACCCCTGAGCTTTCAGCTCTGATTAACGGCTTTTGTGGTTT	2280
QY	2315	GCTTTGCTTCTTATTCATTAACCATGACCGTACAGAAAGCAGACAGAACCCCTGGTTAC	2374
Db	2281	GCTTTGCTTCTTATTCATTAACCATGACCGTACAGAAAGCAGACAGAACCCCTGGTTAC	2340
QY	2375	TGCACAAAGCCACTGAGATCTCACCTCACTGACACAAAGGCAGCTATCATACAGGCTT	2434
Db	2341	TGCACAAAGCCACTGAGATCTCACCTCACTGACACAAAGGCAGCTATCATACAGGCTT	2400
QY	2435	ATCAGGAAACAGAGGAATTTGTCCAAATCAAGCCTACCACTAGGTCATCTGTGACCTAG	2494
Db	2401	ATCAGGAAACAGAGGAATTTGTCCAAATCAAGCCTACCACTAGGTCATCTGTGACCTAG	2460
QY	2495	ACCTCACACTGGCATGCTTTAGCTTTGAGAGGGATTAATGGAGTCAGGTACGAGAGAA	2554
Db	2461	ACCTCACACTGGCATGCTTTAGCTTTGAGAGGGATTAATGGAGTCAGGTACGAGAGAA	2520
QY	2555	GGACAGGAGGAGGATGGCTCATGTGGAAGAAATATCTGCTCTTCCAGATGACAGG	2614
Db	2521	GGACAGGAGGAGGATGGCTCATGTGGAAGAAATATCTGCTCTTCCAGATGACAGG	2580
QY	2615	GTAGTCAAGCCATGTGTCTTAACTCCAGAGGCTCTCTAGAGGCTCTTAGTGCCCATGAAGACTCCA	2674



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Db 2581 GTAGCTCAGCCATGTGTCTTAATCTCAGAGGCTCTAGTGGCCATGAAGACTCCA 2640
Qy 2675 GGCATTTCAGGGGATATACAGTAGACACCAAAATTTATCTTTTAAAGAGAGGAATGGG 2734
Db 2641 GGCATTTCAGGGGATATACAGTAGACACCAAAATTTATCTTTTAAAGAGAGG-ATGGG 2699
Qy 2735 CTGGAGAGATGGCTCAGCGGTTTAAAGACACTGACTGCTCTTCCAGAGATCTCTGAGTTCAA 2794
Db 2700 CTGGAGAGATGGCTCAGCGGTTTAAAGACACTGACTGCTCTTCCAGAGATCTCTGAGTTCAA 2759
Qy 2795 TTCCAGCAACACATGGTGGCTCAACACCTCTGTAATGGATTCGATGCCCTTTCTTG 2854
Db 2760 TTCCAGCAACACATGGTGGCTCAACACCTCTGTAATGGATTCGATGCCCTTTCTTG 2819
Qy 2855 GCGTGTCTGAAGACAGCCAGCTGTATGCACATATATAAAATAAAATAAATCTTTAAAAA 2914
Db 2820 GCGTGTCTGAAGACAGCCAGCTGTATGCACATATATAAAATAAATAAATCTTTAAAAA 2879
Qy 2915 CAAAACAGAGAGAGGACATGCTACCATTTCTACCTCACTTCTCAAAGCCACCCCT 2974
Db 2880 CAAAACAGAGAGAGGACATGCTACCATTTCTACCTCACTTCTCAAAGCCACCCCT 2939
Qy 2975 AAAGTGAATTGTAACACAGTCCCTTTTGCAGAGAGTTAGAGATATTTCTCAAACTCTA 3034
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Db 3000 ATACCTTCACATCTAAATTCATTTTCAATTCCAAATTCCAAATTTTATATACACTCTC 3059
Qy 3095 CAGTTTGGTGGTGAGGGGTGTTTTTTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTT 3154
Db 3060 CAGTTTGGTGGTGAGGGGTGTTTTTTTGGTTGGTTGGTTGGTTGGTTGGTTGGTTGGTT 3119
Qy 3155 GTTTTGAATTTGTTTTCTCTGTTTCAGATCCATGACGTTCAATTAATGTCATAAATG 3214
Db 3120 GTTTTGAATTTGTTTTCTCTGTTTCAGATCCATGACGTTCAATTAATGTCATAAATG 3179
Qy 3215 AGTTCATTCC 3224
Db 3180 AGTTCATTCC 3189

RESULT 3
US-10-716-204-3
; Sequence 3, Application US/10716204
; Publication No. US20040137483A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF INVENTIONS: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10716,204
; FILING DATE: 18-Nov-2003
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
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; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3205 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-10-716-204-3

Query Match 98.6%; Score 3178; DB 19; Length 3205;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 35 ATGCGAAATGACGGGTGAGAGTATCCACGGGGGAAAGCCTGTGGGGCTGGCACATGGGAC 94
Db 1 ATGCGAAATGACGGGTGAGAGTATCCACGGGGGAAAGCCTGTGGGGCTGGCACATGGGAC 60
Qy 95 AAAGTGTCTGTACGATCGTGGGAAACCCACGGAGAGACCCCTTTAGTACCTCTGGAACAT 154
Db 61 AAAGTGTCTGTACGATCGTGGGAAACCCACGGAGAGACCCCTTTAGTACCTCTGGAACAT 120
Qy 155 CTGGCAAGAGATTCAGGGCCGGTCTGGAAGAAGACTTCGAGGTGACGCTTCCCCAGGAC 214
Db 121 CTGGCAAGAGATTCAGGGCCGGTCTGGAAGAAGACTTCGAGGTGACGCTTCCCCAGGAC 180
Qy 215 GTAGCACTGTGCTGATGCTGCGAGTCCACAAAGCACCCCGGAAGTGTCCCTCCCGTT 274
Db 181 GTAGCACTGTGCTGATGCTGCGAGTCCACAAAGCACCCCGGAAGTGTCCCTCCCGTT 240
Qy 275 ATGCTTTTCGGTTCTGATGCTGTTTCTGCGCTGGTTTCGAGCTGGAGTGGCTACCTGG 334
Db 241 ATGCTTTTCGGTTCTGATGCTGTTTCTGCGCTGGTTTCGAGCTGGAGTGGCTACCTGG 300
Qy 335 GCTGCATCTCACTTCCCTCTGTTATCAGTGGCTGGAAGGGCGGGGAGCTGGTGTGAGA 394
Db 301 GCTGCATCTCACTTCCCTCTGTTATCAGTGGCTGGAAGGGCGGGGAGCTGGTGTGAGA 360
Qy 395 GAGGAGCAGCAAAAGGTGTCTCTGCAAGACCATCACCTTACACTGCAGGATCAGGCCAG 454
Db 361 GAGGAGCAGCAAAAGGTGTCTCTGCAAGACCATCACCTTACACTGCAGGATCAGGCCAG 420
Qy 455 AAGGAGCTTGAGTCCAGGCAAGATGTACAGCTGGAAGACTTACATTTGAAGTTGGCT 514
Db 421 AAGGAGCTTGAGTCCAGGCAAGATGTACAGCTGGAAGACTTACATTTGAAGTTGGCT 480
Qy 515 CGCTGCTTGAACAGGAGACTGTGAAGACTTGAACCTCAACATCAAGTACTCTCGGATG 574
Db 481 CGCTGCTTGAACAGGAGACTGTGAAGACTTGAACCTCAACATCAAGTACTCTCGGATG 540
Qy 575 AAGATGCCAAACTCTTCTTTAAAGCCCACTCCGCTATACGAGCTCAAGTCAAGGG 634
Db 541 AAGATGCCAAACTCTTCTTTAAAGCCCACTCCGCTATACGAGCTCAAGTCAAGGG 600
Qy 635 CTCCTGGACCGCACAGGACTCTGGAGGAGTCTGAGGGAGATGAGAGGCTGTTTAACTTC 694
Db 601 CTCCTGGACCGCACAGGACTCTGGAGGAGTCTGAGGGAGATGAGAGGCTGTTTAACTTC 660
Qy 695 CGCAAGACTCCAGCAGAGATATGTTTTCACACTGGCAGGAGAGATGCTTCTCGCC 754
Db 661 CGCAAGACTCCAGCAGAGATATGTTTTCACACTGGCAGGAGAGATGCTTCTCGCC 720
Qy 755 TCCAGATTCTTAATGGCATCAACCCGCTCTGATTGGCCGCTGTACAGTCTCCCAAC 814
Db 721 TCCAGATTCTTAATGGCATCAACCCGCTCTGATTGGCCGCTGTACAGTCTCCCAAC 780
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QY	815	AACTTCCCGTCACTGATGAATGATGGGCCCCAGATGCTGGGCCCTGGAAACGATCTGGAG	874
Db	781	AACTTCCCGTCACTGATGAATGATGGGCCCCAGTGTCTGGGCCCTGGAAACGATCTGGAG	840
QY	875	GCTGAGTTCGAGAGAGGCTCCCTGTTCTTGTGGATCATGGCATCTTTCTGGAGTCCAC	934
Db	841	GCTGAGTTCGAGAGAGGCTCCCTGTTCTTGTGGATCATGGCATCTTTCTGGAGTCCAC	900
QY	935	ACCAACATCCTCAATGGAAAGCTCAGTTCTCTGCAGCCCCGATGACCCCTGTTACACCGAC	994
Db	901	ACCAACATCCTCAATGGAAAGCTCAGTTCTCTGCAGCCCCGATGACCCCTGTTACACCGAC	960
QY	995	AGCTCAGGTCGGACCCCTGCTTCCCATTCGCATCCAGCTCAACAGACTCCCGGGCCA	1054
Db	961	AGCTCAGGTCGGACCCCTGCTTCCCATTCGCATCCAGCTCAACAGACTCCCGGGCCA	1020
QY	1055	GACACCCCATCTTCTGCGCCAGCGATGACGTGGGACTGTTGCTGGCCAGACCTGG	1114
Db	1021	GACACCCCATCTTCTGCGCCAGCGATGACGTGGGACTGTTGCTGGCCAGACCTGG	1080
QY	1115	GTTTCGCAATTCGAGTTTACATCCATGAGGCTGTCAACATCTGCTGCATGCCCATCTG	1174
Db	1081	GTTTCGCAATTCGAGTTTACATCCATGAGGCTGTCAACATCTGCTGCATGCCCATCTG	1140
QY	1175	ATTCCAGAACTCTTTGCCCTTGGCCACATTAAGTCAGTCGCCTAGTGTCAACCTCTCTTC	1234
Db	1141	ATTCCAGAACTCTTTGCCCTTGGCCACATTAAGTCAGTCGCCTAGTGTCAACCTCTCTTC	1200
QY	1235	AGCTATTGATTCCTCACAATTCGGTACACATCGACATCAACCGTTGCCCGGAGCTG	1294
Db	1201	AGCTATTGATTCCTCACAATTCGGTACACATCGACATCAACCGTTGCCCGGAGCTG	1260
QY	1295	CTCGTTGCCCTTGGGAAGTTGATAGACAAGTCCACAGGCTTGGCACTGGGGGATCTCT	1354
Db	1261	CTCGTTGCCCTTGGGAAGTTGATAGACAAGTCCACAGGCTTGGCACTGGGGGATCTCT	1320
QY	1355	GAAGCTGATTAAGAGAAACATGAGCAGCTGAATCTCTGTCTGTGTCTCCCTGAAGAT	1414
Db	1321	GAAGCTGATTAAGAGAAACATGAGCAGCTGAATCTCTGTGTCTCCCTGAAGAT	1380
QY	1415	ATCCGAGCCGAGGTGTGGAAGACATCCAGGCTACTATTACGAGATATGGGATGGAG	1474
Db	1381	ATCCGAGCCGAGGTGTGGAAGACATCCAGGCTACTATTACGAGATATGGGATGGAG	1440
QY	1475	ATCTGGGGGCAATAAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCCAAAGTGAC	1534
Db	1441	ATCTGGGGGCAATAAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCCAAAGTGAC	1500
QY	1535	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTGGGTGAGGAGATCTTCTCTGAGGCG	1594
Db	1501	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTGGGTGAGGAGATCTTCTCTGAGGCG	1560
QY	1595	TTCTCTGGCGGAGAAAGCTCAGGTATGCCCTCTTGTGGATACCGGGAAGCCCTGGTC	1654
Db	1561	TTCTCTGGCGGAGAAAGCTCAGGTATGCCCTCTTGTGGATACCGGGAAGCCCTGGTC	1620
QY	1655	CAGTATATCAACCATGGTGATTTTCACTGCTCAGCCAAGCATGCCTGTCAGTTCAGGC	1714
Db	1621	CAGTATATCAACCATGGTGATTTTCACTGCTCAGCCAAGCATGCCTGTCAGTTCAGGC	1680
QY	1715	CAGTTCGACTCTTGTGTTGGATGCCCAATCTGCCACCTACCATGCAGTACCAACACT	1774
Db	1681	CAGTTCGACTCTTGTGTTGGATGCCCAATCTGCCACCTACCATGCAGTACCAACACT	1740
QY	1775	ACTTCCAAAGGCCAGGCCCTGAGTTTTCATAGCCACGCTCCAGCAGTTAATTCG	1834
Db	1741	ACTTCCAAAGGCCAGGCCCTGAGTTTTCATAGCCACGCTCCAGCAGTTAATTCG	1800
QY	1835	TCAAGTTATCACAATCTCTCTGGCTGCTAAGCGCAGAACTCGGGACCAAGGCC	1894
Db	1801	TCAAGTTATCACAATCTCTCTGGCTGCTAAGCGCAGAACTCGGGACCAAGGCC	1860
QY	1895	CTGGGCCACTATCCAGATGAACATTTTCAGAGGATGCCCGCCGGAAGCGTGGCTGCC	1954

Db	1861	CTGGGCCACTATCCAGATGAACACTTTCACAGAGGATGCCCGCCGGAAGCGTGGCTGCC	1920
QY	1955	TTCCAGAGAAAGCTGATCCAGATCTTCCAAAGGCGCATCAGGAGAGGAAACGAGGCCCTGGCA	2014
Db	1921	TTCCAGAGAAAGCTGATCCAGATCTTCCAAAGGCGCATCAGGAGAGGAAACGAGGCCCTGGCA	1980
QY	2015	CTGGCCCTACACTTACCTGGATCTCCCTCTCATTTGAGAAACAGTGTCTCCATCAACATCTT	2074
Db	1981	CTGGCCCTACACTTACCTGGATCTCCCTCTCATTTGAGAAACAGTGTCTCCATCAACATCTT	2040
QY	2075	GGAGAGACAGTCTCTGTGTGATATAGAACTTCTTGACCATGCCCTCTCCAGGCTAAGTCC	2134
Db	2041	GGAGAGACAGTCTCTGTGTGATATAGAACTTCTTGACCATGCCCTCTCCAGGCTAAGTCC	2100
QY	2135	CGGTATGCTTCTCTTGGGCAACCAAGGCCCTCTTTACACACACACACACACACACAC	2194
Db	2101	CGGTATGCTTCTCTTGGGCAACCAAGGCCCTCTTTACACACACACACACACACACAC	2160
QY	2195	TAATAAAATCGAAACAGAAACCTTAACTCCACAGAGGCAAGATCTCACACAGCAGA	2254
Db	2161	TAATAAAATCGAAACAGAAACCTTAACTCCACAGAGGCAAGATCTCACACAGCAGA	2220
QY	2255	GAGCATCCAAATGTTTGGAGACCTGAGCTTTCAGCTCTGATTAAACGCTTTCGCTGTTT	2314
Db	2221	GAGCATCCAAATGTTTGGAGACCTGAGCTTTCAGCTCTGATTAAACGCTTTCGCTGTTT	2280
QY	2315	GCTTTGCTTCTTATTTCCATTAAACATGAGCGGTAAACAGAAAGCAGAAACCTGTTTAC	2374
Db	2281	GCTTTGCTTCTTATTTCCATTAAACATGAGCGGTAAACAGAAAGCAGAAACCTGTTTAC	2340
QY	2375	TGCACAAAGCCACTGAGATCTCACCTCACCTGACACAAAGGCGAGTATCATACAGGCTT	2434
Db	2341	TGCACAAAGCCACTGAGATCTCACCTCACCTGACACAAAGGCGAGTATCATACAGGCTT	2400
QY	2435	ATCAGGAAACAGGAAATTTGCTCAATCAAGCCTACCCACTAGGTCATCTGTCAGCTAGG	2494
Db	2401	ATCAGGAAACAGGAAATTTGCTCAATCAAGCCTACCCACTAGGTCATCTGTCAGCTAGG	2460
QY	2495	ACCTCACACTGGCATCTTTAGCTTTGAGAGGGGATTAAGTGGAGTCAGTACGAAAGAGAA	2554
Db	2461	ACCTCACACTGGCATCTTTAGCTTTGAGAGGGGATTAAGTGGAGTCAGTACGAAAGAGAA	2520
QY	2555	GGACAGGACGAAAGGATCGCTCCATGTGGAAGAAACATATCTGCTCTTCCAGATGACAGG	2614
Db	2521	GGACAGGACGAAAGGATCGCTCCATGTGGAAGAAACATATCTGCTCTTCCAGATGACAGG	2580
QY	2615	GTAGCTCACAGCCATGTGTCTTAACTCCAGAGGTCTCTAGTGGCCATGAGACTCCA	2674
Db	2581	GTAGCTCACAGCCATGTGTCTTAACTCCAGAGGTCTCTAGTGGCCATGAGACTCCA	2640
QY	2675	GGCATTTAGGGGATATACAGTAGACACCAAAATTTATCTTTTAAAGAGAGGAAATGGG	2734
Db	2641	GGCATTTAGGGGATATACAGTAGACACCAAAATTTATCTTTTAAAGAGAGG-ATGGG	2699
QY	2735	CTGGAGAGATGGCTCAGCGGTTAAGAGCACTGACTGCTCTTCCAGAGATCTCTGAGTCAA	2794
Db	2700	CTGGAGAGATGGCTCAGCGGTTAAGAGCACTGACTGCTCTTCCAGAGATCTCTGAGTCAA	2759
QY	2795	TTCCAGAGAAACCATGGTGGCTCACAAACCATCTGTAAATGGGATTCGATGCCCTCTTCTG	2854
Db	2760	TTCCAGAGAAACCATGGTGGCTCACAAACCATCTGTAAATGGGATTCGATGCCCTCTTCTG	2819
QY	2855	GGGTCTCTGAGACAGCGACAGTGTATGACATATATAAAATATAATCTTTTAAAAAA	2914
Db	2820	GGGTCTCTGAGACAGCGACAGTGTATGACATATATAAAATATAATCTTTTAAAAAA	2879
QY	2915	CAAAAACAGAGAGAGGAGCATGCTACCTTTCTACCTCACTTCTTCTCAAGGCCACCT	2974
Db	2880	CAAAAACAGAGAGAGGAGCATGCTACCTTTCTACCTCACTTCTTCTCAAGGCCACCT	2939
QY	2975	AAAGTGAATTTGTAACCAAGGCTCCCTTTTCAGAGAGTATGAAAGATATTTCTCAAACTCTA	3034

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Db 3060 CAGTTTGTGGTGAGGGTGTGTTTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTTT 3119  
QY 3155 GTTTTGTATTTTGTGTTTCTCTGTTTCCAGACTCCATGACAGCTTCATTAATGTCATAAATG 3214  
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QY 3215 AGTTCAATCC 3224  
Db 3180 AGTTCAATCC 3189

## RESULT 4

US-09-764-246-1  
; Sequence 1, Application US/09764246  
; Patent No. US20010046672A1  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; BOEGLIN, WILLIAM E.  
; JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/764,246  
; FILING DATE: 17-Jan-2001  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-764-246-1

Query Match 43.3%; Score 1395.2; DB 9; Length 2685;  
Best Local Similarity 79.8%; Pred. No. 0;  
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;  
QY 7 GCAGTAGAGACTAACT--GGTCAGGAGGATGGGAAATGCAGGTCAGAGTATCCACG 64  
Db 42 GCCGTAGAGACTGACTTAGGCTGGCAGCATGCCGAGTTCCAGGTCAGGCTGTCCACC 101

QY 65 GGGAAAGCCTGTGGGGCTGGCACATGGGACAAAGTGTCTGTACGATCGTGGGAACCCAC 124  
Db 102 GGAAAGCCTTTCGGGGCTGGCACATGGGACAAAGTGTCTGTACGATCGTGGGAACCCGG 161  
QY 125 GGAGAGAGCCCTTATGTACCTCTGGACCATCTGGGCAAGAGTTCAGCGCCGCTGTGAA 184  
Db 162 GGAGAGAGCCCTTATGTACCTCTGGACCATCTCGGCAAGAGTTCAGCTCGGCGCTGAG 221  
QY 185 GAAGACTTCAGAGTGAAGCTTCCAGGACGTAGGCACTGTCTGATGCTCGAGTCCAC 244  
Db 222 GAGGACTTCAGAGTGAAGCTTCCAGGACGTAGGCAAGTGTCTGTGCTGCTCGGCTGCAC 281  
QY 245 AAAGCAAGCCCGGAGAGTGTCCCTCCCGCTTATGTCTTCCGTTCTGTGATGCTGCTGCG 304  
Db 282 AAGCGCCCTCCCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 338  
QY 305 CGCTGGTTTCAGAGTGGAGTGTCTACCTGGGGCTGCACTCCACTTCCCTGTTTATCAGTGG 364  
Db 339 CGCTGGTTTCAGAGTGGAGTGTCTACCTGGGGCTGCACTCCCTTCTTCCCTGCTACCACTGG 398  
QY 365 CTGGAAGGGCGGGGAGTGGTGTCTGAGAGAGGAGAGCAAAAGTGTCTTGGCAAGAC 424  
Db 399 CTGAGAGGGCGGGGAGTGGTGTCTGAGAGAGGAGTGTCTGAGCAAGTGTCTTGGGACAG 458  
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QY 485 AGCTGGAAGACTTACATTTGAAGTGTGGCTCGCTGCTGACACAGAGACTGTGAAAGAC 544  
Db 519 CAGTGGAGGGTTTACAAACAGTGTGGCTTCTGCTGATGAAAGACAGTGTGGAAGAC 578  
QY 545 TTGAGCTTCAACATCAAGTACTCTGCGATGAAGATGCCAAACTCTTTTAAAGCCAC 604  
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QY 725 GCACACTGGCAGGAGTGTCTTCTGCGCTCCAGTTCCTTAAATGGCATCAACCCCGTGC 784  
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QY 785 CTGATTCGCGCTGTGTCAGTCTCCCAAACTTCCTGCGGTCTGATGAAATGGTGTGCTC 844  
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Db 999 TCTGCGGCGCAATGACCTGTATACAGAGCCAGGCTGCGGCGCTGCTGCTGCTC 1058  
QY 1025 GCCATCCAGCTCAAAAGACTCCCGGCGCAGACACCCCATCTTCTGCGCCGAGGAGTAC 1084  
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Db 1179 GGCCTCAGCCAGCAGCTGTGCACTCACTGTGCTGAGGTTTCCACCTGGCTACCCCTG 1238
Qy 1205 CGTACAGCTCCTAGGTGTCACCTCTCTCAAGCTATTGATTCCTCACTTCGGTACACA 1264
Db 1239 CGTACAGCTGCCCACTGCCACCTCTCTTCAAGCTGCTGATCCCGACACACCGATACACC 1298
Qy 1265 CTGCACATCAACACGCTTGCCCGGAGCTGCTGCTGCCCTCGGGAAGTTGATAGACAAG 1324
Db 1299 CTGCACATCAACACACTGCCCGGAGCTGCTTATCGTCCAGGGCAGGTGGTGACAGG 1358
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Db 1359 TCACAGGCTATGGCACTGAAGGCTTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418
Qy 1385 AACTACTCTGCTGCTGCTCTCTGATGATCCGAGCCGAGGTTGGAAGACATCCCA 1444
Db 1419 AACTATTCTCTCTGCTGCTGCTGAGGATATCCCGACCCGAGGATGAAGACATCCCA 1478
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Db 1479 GGCTACTACTACGATGATGGGATGACAGATTTGGGGTGCAATGGGAGCTTTCTCT 1538
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Db 1539 GAAATCATCGGTATCTACTACCAAGTGATGATCTGTCCAAGATCACAGAGAGCTCCAG 1598
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Db 1719 TCAGCCAAAGCATGCGGCTGTCAGTGAGGCGAGTTTGACTCTCTGCTTGGATGCCAAC 1778
Qy 1745 CTGCCACCTTACCATGAGCTACACACCTCTTCCAAAGGCGAGCCCGGCTGAGGT 1804
Db 1779 CTGCCACCTTACCATGAGCTACACACCTTCCAAAGGCGAGCCCGGCTGAGGT 1838
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Db 1839 TTATAGCAGCAGCTCCAGCAGTTAATCGTCAAGTTATCAATCATCTCTCTCTGGCTG 1898
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Qy 1925 GAGGATGCCCCCGGGAAGCGTGGCTTCCAGAGAAAGTATCCAGATCTCCAG 1984
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Qy 1985 GGATCAGGAGAGGAAGCAGGAGCTTGGCACTGACCTTACACCTTACCTGCTCCCTC 2044
Db 2019 GGATCAGGAGAGGAAGCAGGAGCTTGGCTGCTGCTTACCTTACCTTACCTTCCCTC 2078
Qy 2045 ATTGAGAACAGTGTCTTCCATCTTAACATCTTGGAGAGAGAGCTCTCTGTGACAT 2098
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RESULT 5  
US-09-960-706-985  
; Sequence 985, Application US/09960706  
; Publication No. US20030134280A1  
; GENERAL INFORMATION:  
; APPLICANT: Munger, William E.  
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia  
; TITLE OF INVENTION: Gene Expression Profiles  
; FILE REFERENCE: 44921-5029-01US

; CURRENT APPLICATION NUMBER: US/09/960,706  
; CURRENT FILING DATE: 2001-09-24  
; PRIOR APPLICATION NUMBER: 60/223,323  
; PRIOR FILING DATE: 2000-08-07  
; PRIOR APPLICATION NUMBER: 09/873,319  
; PRIOR FILING DATE: 2001-06-05  
; NUMBER OF SEQ ID NOS: 1124  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 985  
; LENGTH: 2685  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 U78294  
US-09-960-706-985

Query Match 43.3%; Score 1395.2; DB 10; Length 2685;  
Best Local Similarity 79.8%; Pred. No. 0;  
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;  
  
Qy 7 GCAGTAGAGAGCTAAACT--GGTCAGAGAGGATGGCGAAATGACGGGTGAGAGTATCCAGG 64  
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Qy 125 GGAGNAGCCCTTAGTACCTCTGGACCATCTGGGCAAGGAGTTCAGGCGCGGCTGTAA 184  
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Db 519 CAGTGGAAAGGCTTACAAACCCAGTTGGCTCTACTGCTGGATGAAAGACAGTGGAAAGAC 578  
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Db 1599 GCCTGGGTGAGAGATCTTCTCTCAAGGGCTTCTTAACAGGAGCTCAGGTATCCCT 1658  
QY 1625 TCCTTTGTTGGATPACCCGGGAAGCCTGTGTCAGTATATCAATGGTGTATTCACCTGC 1684  
Db 1659 TCCTCACTGGAGACCCGGGAAGCCTGTGTGAGTATGTCAACATGGTATATTCACCTGC 1718  
QY 1685 TCAGCCAGCATGCACTGCTGAGTTCAGGCCAGTTCGACTCTTGTGTTGGATGCCCAAT 1744  
Db 1719 TCAGCCAGCATGCGGCTGTGAGTGCAGGGCAGTTTGAATCTCTGTGTTGATGCCCAAC 1778  
QY 1745 CTGCCACCTTACCATGCACTACCAACCTACTCTCAAGGCCAGGCCCGGCTGAGAGT 1804  
Db 1779 CTGCCACCCAGCATGCACTGCCACCAACCACTCTCAAGGGCTGGCAACATGCGAGGCG 1838  
QY 1805 TTCTATAGCCAGCTCCCAAGCAGTTAAATTCGTCAGTTATCAATCATTCCTCTCTGGCTG 1864  
Db 1839 TTCTATAGCCACCTCCCAACCTGTCAATGCCACATGTGATGTCACTCTGTCTCTCTGGTGT 1898  
QY 1865 CTAGCCAGCAACTGGGGACCAAGGCCCTTGGGCCACTATCCAGATGAACATTTCA 1924

Db 1899 CTGACCAAGGACCTGGAGACCAAGGCCCTTGGGCACCTATCCGATGAGCACTTCACA 1958  
QY 1925 GAGGATGCCCCCGCGCAAGCGTGGCTGCTTCCAGAGAAAGCTGATTCAGATTCCTCAAG 1984  
Db 1959 GAGGAGGCCCTCGCGGAGCATGCGCACCTTCCAGAGCGCGCTGCGCCAGATCTCGAGG 2018  
QY 1985 GGCATCAGGAGAGGACCGGAGGCTGGCAGCTGCCCTACACTACCTAGATCTCCCTTC 2044  
Db 2019 GGCATCCAGGAGCGGAACCGGGGCTGTGTGCTTGCCTTACACCTACTAGACCTCCCTTC 2078  
QY 2045 ATTGAGAACAGTGTCTCCATCTTAACATCTTGGAGAAAGACAGTCTCTGTGTGACAT 2098  
Db 2079 ATCGAGAACAGCTCTCCATCTTAATCCAGGGGAACACAGGCCCGAGATGACAT 2132

## RESULT 6

US-09-873-319-642  
; Sequence 642, Application US/09873319A  
; Publication No. US20030134324A1  
; GENERAL INFORMATION:  
; APPLICANT: Munger, William E.  
; APPLICANT: Kulkarni, Prakash  
; APPLICANT: Getzenberg, Robert H.  
; APPLICANT: Waga, Iwao  
; APPLICANT: Yamamoto, Jun  
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic  
; FILE OF INVENTION: Hyperplasia Using Gene Expression Profiles  
; FILE REFERENCE: 44921-5029-US  
; CURRENT APPLICATION NUMBER: US/09/873,319A  
; EARLIER FILING DATE: 2001-06-05  
; EARLIER APPLICATION NUMBER: US 60/223,323  
; EARLIER FILING DATE: 2000-08-07  
; NUMBER OF SEQ ID NOS: 755  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 642  
; LENGTH: 2685  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20030134324A1 U78294  
US-09-873-319-642

Query Match 43.3%; Score 1395.2; DB 10; Length 2685;  
Best Local Similarity 79.8%; Pred. No. 0;  
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;  
QY 7 GCAGTAGAGAGCTAAACT--GGTCAGGAGGATGGCGAAATCAGGGTCAGAGTATCCACG 64  
Db 42 GCCGTAGAGAGCTGAGCTTAGGCTGGCAGCATGGCCGAGTTCAGGGTCAGGGTGTCCACC 101  
QY 65 GGGGAAGCCTGTGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATCGTGGGAACCCAC 124  
Db 102 GGAGAGCCTTCGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATCGTGGGACCCGG 161  
QY 125 GGAGAGAGCCTTGTAGTACCTCTGTGACCATCTGGGCAAGGATTCAGGCCGCGGTGCTGAA 184  
Db 162 GGAGAGAGCCTCCCACTGCCCCCTGGCAAACTCGGCAAGGAGTTCACTCGCGGGCGCTGAG 221  
QY 185 GAACATTCGAGGTGAGCTTCCCGCAGGAGCTAGGCAGTGTGCTGATGATCTGCGAGTCCAC 244  
Db 222 GAGGACTTCAGAGTGAAGCTCCCGGAGAGCGTAGGCCAGTGTCTGCTGCTGCGGTGCAC 281  
QY 245 AAAGCACCCCGGAAGTGTCTCCCGCTTATGTCTTTTCCGTTCTGTGATGCTGTGTTCTGC 304  
Db 282 AAGCGCCCCC---AGTGTGCCCTTGTGGGGCCCCCTGGCCCCCGGATGCTGTGTTCTGC 338  
QY 305 CGCTGGTTTCAGCTGGAGTGGCTACCTTGGGGCTGCATCTCACTTCCCTCTGTATCAGTGG 364  
Db 339 CGCTGGTTTCAGCTGACACCGCGCGGGGCGGCCACCTCTCTTCTCCCTGTCTACAGTGG 398  
QY 365 CTGGAAGGGGGGGAGCTGGTCTGAGAGAGGAGCAGCAAGAGTGTCTCTGGCAAGC 424  
Db 399 CTGAGGGGGGGGGGACCCCTGTGCTGACGAGGGGTACAGCCAGGTGTCTCTGGGACAC 458

QY 425 CATCACTTACATGAGGATCAGGCCAGAAAGGAGCTTGAGTCCAGGCAGAGATGTAC 484  
DB 459 CACCACTTGTCTCCAGCAACAGCGCCAGAGGAGCTTCAGGCCCGGAGAGATGTAC 518  
QY 485 AGCTGGAAGACTTACATTTGAAGGTTGGCCCTCCCTGCTTGACACAGAGACTGTGAAGAC 544  
DB 519 CAGTGAAGGCTTACAAACCCAGGTTGGCTCACTCCCTGGATGAAAGACAGTGAAGAC 578  
QY 545 TTGGACCTCAACATCAAGTACTCTCGATGAAGATGCCAACTCTCTTTAAAGCCAC 604  
DB 579 TTGGAGCTCAATATCAAAATACTTCAAGCAAGAATGCCAACTTTATCTAAGACTGGC 638  
QY 605 TCCGGCTATACCGAGTGAAGCTCAAAAGGCTCCTGGACCGCACAGGACTCTGGAGGAGT 664  
DB 639 TCTGCTTTTGCAGAGATGAANAATCAAGGGTTGCTGGACCGCAAGGGCTCTGGAGGAGT 698  
QY 665 CTGAGGAGATGAGAGGCTGTTTAACTTCCGCAAGACTTCAGAGCAGAGATGTGTTT 724  
DB 699 CTGAATGAGATGAANAAGGATCTTCAACTTCCGAGGAGCCCAAGAGCTGAGCAGCATTT 758  
QY 725 GCACACTGCGAGAGATGCTTCTTCCGCTTCCAGTTCCTAAATGGCATCAACCCGGTC 784  
DB 759 GAGCACTGGCAGAGATGCCCTTCTTCCGCTCCAGTTCCTGAATGGTCTCAACCCGTGC 818  
QY 785 CTGAATTCGCGCTGTCAACAGTCTCCCAACAACTTCCCGGTCACTGATGAATGGTGGC 844  
DB 819 CTGATCCGCGCTGTCACTACCTCCCAAGAACTTCCCGGTCACTGATGCCATGGTGGC 878  
QY 845 CAGTGTCTGGCCCTGGAACCAAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904  
DB 879 TCATTGTTGGTCTTGGGACCAAGTTCGAGGCTGAGCTAGAGAAGGGCTCCCTGTTCTTG 938  
QY 905 GTGGATCATGCGATTTCTTCTGAGTCCACACCACTCTCAATGGAAGCTCAGTTTC 964  
DB 939 GTGGATCATGCGGATCTCTCTGGCATCCAGACCAATGTCAATTAATGGGAAGCCGAGTTC 998  
QY 965 TCTGAGCCCCGATGACCTGTGTACACAGAGCTCAGGGTCCGGACCCCTGCTTCCCAAT 1024  
DB 999 TCTGCGGCCCCAATGACCTGTGTATACAGAGCCAGGCTGCGGGCGCTGCTGCTCTC 1058  
QY 1025 GGCATCCAGCTCAACAGACTCCGCGGCAGACACCCCATCTTCTGCGCCAGCGATGAC 1084  
DB 1059 GGCATCCAGCTCAGCCAGACCCCGGCCCAACAGCCCCATCTTCTGCGCCCATGATGAC 1118  
QY 1085 AGTGGAGCTGTGTCTGCGCAAGACTGCGTTCGCAATTTCTGAGTTTACATCCATGAG 1144  
DB 1119 AAGTGGAGCTGTGTCTGCGCAAGACTGCGTTCGCAATTTCTGAGTTTACATCCATGAG 1178  
QY 1145 GCTGTCCACACATCTGCTGCATGCCATCTGATTTCCAGAAAGTCTTTGCTTGCCCAATTA 1204  
DB 1179 GCGCTCAGCACCTGTCTGCATCCACATCTGCTGCTGAGTCTTCCACCTGGCTACCCCTG 1238  
QY 1205 CGTCACTGCTAGGTGTGACCTCTCTTCAAGCTATTGATTCCTCAGATCTCGGTACACA 1264  
DB 1239 CGTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1298  
QY 1265 CTGCACATCAACAGCTTCCGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1324  
DB 1299 CTGCACATCAACACACTGCGCGCGGAGCTGCTTATCTGTCGAGGGCAGGTGTGGACAGG 1358  
QY 1325 TCCACAGGCTTGGCAGCTGGGGATTTCTGCTGCTGATTAAGAGAAACATGAGCAGCTG 1384  
DB 1359 TCCACAGGCTTGGCAGCTGGGGATTTCTGCTGCTGATTAAGAGAAACATGAGCAGCTG 1418  
QY 1385 AACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1444  
DB 1419 AACTACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1478  
QY 1445 GGTACTATTACCGAGATGAGGATGCGATCTGGGGGCAATAAGAGCTTTGCTCT 1504  
DB 1479 GGCTACTACTACCGATGATGGATGCGATTTGGGGTGCAGTTGGGGTGCAGTGGAAAGCTTTGCTCT 1538

QY 1505 GAAATAGTCAGCATCTACTATCCAAAGTGACACATCCGTCCAAGATGACCAAGAGCTCCAG 1564  
DB 1539 GAAATATCTCGTATCTACTACCAAGTGATGAGTGTGTCCAAAGATGACAGAGCTCCAG 1598  
QY 1565 GCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCGGCCCGAGAAAGCTCAAGGTATGCC 1624  
DB 1599 GCCTGGGTGAGAGAGATCTTCTCCAGGGCTTCTTAACCAAGAGAGCTCAGGTATCCCT 1658  
QY 1625 TCCTTTGTTGGATACCCGGGAAGCCCTGGTCCAGTATATCAACATGGTGTATTTACCTGTC 1684  
DB 1659 TCCTCACTGGAGACCCGGGAAGCCCTGGTGCAGTATGTCAACATGGTGTATTTACCTGTC 1718  
QY 1685 TCAGCAAGCATGACAGCTGTGAGTTCAGGCAGTTCGACTCTTGTGTTGGATGCCAAT 1744  
DB 1719 TCAGCAAGCATGCGGCTGTGAGTGCAGGGCAGTTTGACTCTCTGTGTTGGATGCCAAT 1778  
QY 1745 CTGCCACCTACCATGACGTACCAACCACTTCTTCAAGGCCAGGCCCGGCTCGAGAT 1804  
DB 1779 CTGCCACCAAGTGCAGTGCACCACTTCCAAAGGCCCTGGCAACATGCGAGGGC 1838  
QY 1805 TTCTAGCAGCCTCCAGCAGTTAAATTCGTCAAGTTATCAATCATTTGCTCTCTGGGTG 1864  
DB 1839 TTCTAGCAGCCTCCACCTGTCAATGCCATGTGATGTCACTCTCTGCTCTCTGGTGTG 1898  
QY 1865 CTAGCGCAGAACCTGGGGCAAGGCCCTTGGGCCACTATCCAGATGCAACATTCACA 1924  
DB 1899 CTGAGCAAGGAGCCTGGAGACCAAGGCCCTTGGGCCACTATCCGGATGAGCATTACA 1958  
QY 1925 GAGGATGCCCCCGCGGAAGCGTGTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAG 1984  
DB 1959 GAGGAGGCCCTTGGCGGAGATGCGCACCTTCCAGAGCCGCTGGCCAGATCTCGAGG 2018  
QY 1985 GGCATCAGGAGAGAACCGGAGCCTGGCAGTTCGCTTACACTACCTAGATCTCCCTC 2044  
DB 2019 GGCATCAGGAGAGAACCGGAGCCTGGTGTGCTGCTTACACTACCTAGATCTCCCTC 2078  
QY 2045 ATTGAAGACAGTGTCTCCATCTAATCTTGGAGAGACAGTCTGTGTGACAT 2098  
DB 2079 ATCGAAGACAGCTCTCCATCTAAATCCAGGGGAACACAGGCCCAGATGACAT 2132

## RESULT 7

US-10-716-204-1

; Sequence 1, Application US/10716204

; Publication No. US20040137483A1

; GENERAL INFORMATION:

; APPLICANT: BRASH, ALAN R.

; BOEGLIN, WILLIAM E.

; JISAKA, MITSUO

; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS

; NUMBER OF SEQUENCES: 36

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR.

; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD

; CITY: DURHAM

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage

; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1

; SOFTWARE: WORD PERFECT 6.1 and ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/716,204

; FILING DATE: 18-Nov-2003

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: &lt;Unknown&gt;

; FILING DATE: &lt;Unknown&gt;

; ATTORNEY/AGENT INFORMATION:

; NAME: ARLES A. TAYLOR, JR.

; REGISTRATION NUMBER: 39,395



;	REFERENCE/DOCKET NUMBER: 1242/5	
;	TELECOMMUNICATION INFORMATION:	
;	TELEPHONE: (919) 493-8000	
;	TELEFAX: (919) 419-0383	
;	TELEX: <Unknown>	
;	INFORMATION FOR SEQ ID NO: 1:	
;	SEQUENCE CHARACTERISTICS:	
;	LENGTH: 2685 base pairs	
;	TYPE: nucleic acid	
;	STRANDEDNESS: double	
;	TOPOLOGY: unknown	
;	SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
;	US-10-716-204-1	
	Query Match 43.3%; Score 1395.2; DB 19; Length 2685;	
	Best Local Similarity 79.8%; Pred. No. 0;	
	Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2	
Qy	7 GCAGTAGAGACTAACT--GGTCAGGAGATGGCGAAATGCAGGTTGAGATATCCAGC	644
Db	42 GCCGTAGAGAGCTGAGACTTAGGCTGGCAGCATGGCCGAGTTTCAGGTCACGGGTGTCCACC	101
Qy	65 GGGGAAGCCTGTGGGGCTGGGCACATGGGACAAAGTGTCTGTACAGATCTGTGGGAACCCAC	124
Db	102 GGAGAAGCCTTCGGGGCTGGGCACATGGGACAAAGTGTCTGTACAGATCTGTGGGAGCCCGG	161
Qy	125 GGAGAGAGCCCTTAGTAGTACCTCTGTGACCATCTCTGGGCAAGGAGTTTCAGGCCCGGTGCTGAA	184
Db	162 GGAGAGAGCCCCCACTGCCCTTGACAACTCTCGGCAAGGAGTTTCACTGCGGGCGCTGAG	221
Qy	185 GAAGACTTTCGAGGTGACGCTTCCCGACAGCTPAGGCATGTGCTGATGCTGCGAGTCCAC	244
Db	222 GAGGACTTTCAGGTGACGCTCCCGGAGGACGTAGGCCGAGTGTCTGTCTGCGCGTGCAC	281
Qy	245 AAAGCAGCCCGGAAGTGTCCCTCCCGCTTATGTCTTTCCTTCTGTATGCTCTGGTCTCTGC	304
Db	282 AAGCGGCCCC--AGTCTGCCCTGTCTGGGGCCCCCTGGCCCCGGATGCCCTTCTCTGC	338
Qy	305 CGCTGGTTTCGAGCTGGAGTGGTACTCTGGGGCTGCACCTCCACTTCCCCTGTTTATCAGTGG	364
Db	339 CGCTGGTTTCAGCTGACACCGCGGGGGCGGCACCTTCTTTCCTTCTTACAGTGG	398
Qy	365 CTGGAAGGGCGGGGAGCTGGTGTCTGAGAGAGGAGCAGCAAAAGTGTCTCTGGCAAGAC	424
Db	399 CTGAGGGGGCGGGACCTGGTGTCTGAGGAGGGTTCAGCCAAAGTGTCTCTGGGCAGAC	458
Qy	425 CATCACCTTACATCTGCAGATCAGGCCACAGAGGAGCTTGATCTCAGGCAGAGAAGATGTAC	484
Db	459 CACCACCTGTGTCTCAGCAACAGCGCCAGGAGGAGCTTCAGGCCCGGAGGAGATGTAC	518
Qy	485 AGCTGGAAGACTTACATTTGAAGTTGGCTCGCTGCCCTTGACACAGAGACTGTGAAAGAC	544
Db	519 CAGTGGAAAGGCTTTCACCCAGGTTTGGCTTCACTGCCTGGATGAAAGACAGTGGAAAGAC	578
Qy	545 TTGGAACCTCAACATCAAGTACTCTGCGATGAGAAATGCCAAACTCTTCTTTAAAGCCCAAC	604
Db	579 TTGAGACTCAATATCAAAATACTCCACAGCAAGAATGCCAACTTTTATCTACAAGCTGCG	638
Qy	605 TCCCGGTATACGGAGCTGAAAGTCAAAAGGCTCTCTGGACCGCACAGGACTCTGAGGAGGT	664
Db	639 TCTGCTTTTGAGAGATGAAAATCAAGGGTTTGTCTGGACCGCAAGGGGCTCTCGGAGGAGT	698
Qy	665 CTGAGGGAGATGAGAAGGCTGTTTAACTTCGCGAAGACTTCACAGCAGCAGAGTATGTGTTT	724
Db	699 CTGAATGAGATGAAAGGATCTTTCAACTTCGAGGAGACCCACAGCAGCTGACACGCATTT	758
Qy	725 GCACACTGGCAGGAGATGTCCTTTCGCTCCAGTTCCTTAAATGGCATCAACCCGGTTC	784
Db	759 GAGCACTGGCAGGAGATGTCCTTTCGCTCCAGTTCCTTGAATGGTCTCAACCCCTGTCTC	818
Qy	785 CTGANTCGCCGTGTCAAGTGTCCCAACAACTTCCTCCGGTCACTGATGAATATGTTGGCC	844
Db	819 CTGATCGCCGCTGTCACTACTCTCCAAAGAACTTCCCGTCACTGATGCCATGTTGGCC	878

Qy	845	CGAGTGTGGCCCTTGGAACCAAGTCTGCGAGGTGAGTTGGAGAAGGGCTCCCTGTCTTGTG	904
Db	879	TCATTGTGGGTCTCGGACCAAGCTTTCAGGCTGAGCTAGAGAAGGGCTCCCTGTCTTGTG	938
Qy	905	GTGGATCATGGCAATCTTTCTGAGTCCACCAACATCCTCAATGGAAGCCTCAGTTC	964
Db	939	GTGGATCAGGGCATCTCTCTGGCATCCAGACCAATGTCAATTANTGGAAAGCCGAGTTC	998
Qy	965	TCTGCAGCCCGATGACCCCTGTTTACACAGAGCTCAGGGTCGGAGCCCTCTGTTCCCAAT	1024
Db	999	TCTGCGGCCCAATGACCCCTGCTATACAGAGCCAGGCTGCGGCGCTGTGCTCTC	1058
Qy	1025	GCCATTCAGCTCAAAAGAGTCCCGGGCCAGACAAACCCCATCTTCTGCCCCAGCGATGAC	1084
Db	1059	GCCATTCAGCTCAGCAGAACCCCGGCCCAACAGGCCCATCTTCTCTGCCCACTGATGAC	1118
Qy	1085	ACGTGGAGCTGGTTGCTGGCCAAAGACTGGGTTGCGAAATTCAGTGTTTACATCCATGAG	1144
Db	1119	AAGTGGAGCTGGTTGCTGGCCAAAGACTGGGTGGCAGATGCCGAGTCTCTCTTCCATGAG	1178
Qy	1145	GCTGTCAACATCTGCTGCATGCCCATCTGATTCACAGAAATCTTTGCCTTGGGCCACATTA	1204
Db	1179	GCCTCAGGCACCTGTGCACTCACATCTGTGCCTGAGGTCTTCAACCTGGCTACCCCTG	1238
Qy	1205	CGTCAGCTGGCTAGGTGTCAACCTCTCTTCAAGCTATTGATTCCTCACATTCGGTACACA	1264
Db	1239	CGTCAGCTGCCCACTGCCACCCCTCTCTTCAAGCTCTGTATCCCGCACACCCCGATACACC	1298
Qy	1265	CTGCACATCAACAGCTTGGCCGGGAGCTGCTGTTTGCCTCGGGAAGTTGATAGACAAG	1324
Db	1299	CTGCACATCAACACATCGCCCGGGAGCTGCTTATCTGTGCAGCGCAGGTGGTGGACAGG	1358
Qy	1325	TCCACAGGCTTGGCACTGGGGATTTCTGTGACCTGATAAAGAGAAACATGGAGCAGCTG	1384
Db	1359	TCCACAGGCATCGCATTTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG	1418
Qy	1385	AATCTACTGTCTGTGTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACATCCCA	1444
Db	1419	AACTATTCTCTGTGTCTGTCTGAGGATATCCGACCCGAGGAGTTGAAGACATCCCA	1478
Qy	1445	GGCTACTATTACCGAGATGATGGGATGCAGATCTGGGGGCAATAAAGAGCTTTGTCTCT	1504
Db	1479	GGCTACTACTACCTGATGATGGGATGCAGATTTGGGTGCAGTGGAAACGCTTTGTCTCT	1538
Qy	1505	GAAATAGTCAGCATCTACTATCCAAAGTACATATCCCGTCCAAAGATGACCAAGAGTCCAG	1564
Db	1539	GAAATCATCGGTATCTACTACCCAAAGTATGAGTCTGTCCAGATGACAGAGAGTCCAG	1598
Qy	1565	GCTGGGTGAGGAGATCTTCTGTAGGGCTTCCCTCGGCCGAGAAAGCTCAGGTATGCC	1624
Db	1599	GCCTGGGTACAGAGATCTTCTCAAGGGCTTCTCAAAACCCAGAGAGCTCAGGTATCCCT	1658
Qy	1625	TCCTTGTGGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGATGATATTCACCTGC	1684
Db	1659	TCCTCACTGGAGACCCGGGAGCCCTGGTGCAGTATGTCAACATGATGATATTAACCTGC	1718
Qy	1685	TCAGCAAGCATGCACTGTCACTTTCAGGCGAGTTCGACTCTTGTGTTGGATGCCCAAT	1744
Db	1719	TCAGCAAGCATGCGGCTGTCACTGTCAGGCGAGTTTGTGACTCTGTGTTGGATGCCCAAC	1778
Qy	1745	CTGCGCACTTACCATGAGCTACCAACCTACTTCCAAAGGCCAGGCCCGGCTGAGAGT	1804
Db	1779	CTGCCACCCAGCATGAGCTGCCAACCAACCACTCCAAAGGCTTGGCAACATGCGAGGGC	1838
Qy	1805	TTCATAGCCACGCTCCAGCAGTTAAATTCGTCAAGTTATCACATCAATGCTCTCTGCGCTG	1864
Db	1839	TTCATAGCCACCTCCCACTGTCAATGCCACATGTGATGTCACTCTTGTCTCTGTGTTG	1898
Qy	1865	CTAAGCGCAGAACCTCGGGACCAAGGCCCTCTGGGCCATATCCAGATGAACACTTCACA	1924
Db	1899	CTGAGCAAGAGGCTTGGAGACCAAGGCCCTCTGGGCACTTATCCGNATGAGCACTTCACA	1958

QY 1925 GAGGATGCCCCCGGGAAGAGGTGGTGGCTTCCAGAGAAAAGTGATCCAGATCTCCAAAG 1984  
DB 1959 GAGGAGGCCCTCGGCGGAGCATCGCACTTCCAGAGCGGCTGGCCAGATCTCGAGG 2018  
QY 1985 GCATCAGAGGGAACCGAGGCTGGCACTGGCCCTACACCTACTGATCTCCCTC 2044  
DB 2019 GGATCCAGAGGGAACCGGCGCTGGTGGCTGCGCTACACCTACTGAGCCCTCCCTC 2078  
QY 2045 ATTGAGAACAGTGTCTCCATCTAAACATCTTGAGGAAGACAGTCTGTGTGACAT 2098  
DB 2079 ATCGAGAACGGTCTCGATCTAAATCCAGGGGAACACAGGCCCCAGATGACAT 2132

RESULT 8  
US-09-862-658-1  
; Sequence 1, Application US/09862658  
; Patent No. US20020137101A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; TITLE OF INVENTION: 46638, A NOVEL HUMAN LIPOXYGENASE FAMILY  
; FILE OF INVENTION: MEMBER AND USES THEREOF  
; FILE REFERENCE: 10448-053001  
; CURRENT APPLICATION NUMBER: US/09/862,658  
; CURRENT FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/205,675  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 3320  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (459)...(2591)  
US-09-862-658-1

Query Match 20.5%; Score 659.6; DB 9; Length 3320;  
Best Local Similarity 63.9%; Pred. No. 9.6e-190;  
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

QY 484 CAGCTGGAACTTCAATTAAGAGTTGGCTCGCTCCCTTGACGAGACTGTGAAAGA 543  
DB 1013 CAGTGGAAATCGGTACTCGCCGGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA 1072  
QY 544 CTGGACCTCAACATCAAGTACTCTCGATGAAGATGCCAACTCTCTTTAAAGCCCA 603  
DB 1073 CATGGAGCCCAATGTTTCGATACTCAGCCACCAGACGATCTCGCTCTTCAATGCCAT 1132  
QY 604 CTCGCGGTATACGGAGCTGAAAGTCAAAGGGCTCTCGGACCGCACAGGACTCTGGAGGAG 663  
DB 1133 CCTGGCTCTTGGGAATGAGCTTCGAGGGCTGTTGGATCGCAAGGGCTCTGGAAGAA 1192  
QY 664 TCTGAGGAGATGAGAAGGCTGTTAACTTCGCAAGACTCCAGCAGCAGAGATGTGTT 723  
DB 1193 GCTGGATGATCAGACAAATCTCTCGTGCCATAAGACCTTCACGACAAAGATATGTCAC 1252  
QY 724 TGCACACTGCGAGGAGAGTCCCTTCTCGCTCCCAAGTTCCTAAATGGCATCAACCCGT 783  
DB 1253 AGAGCACTGGTGTGAAGATCACTTCTTGGGTACCAAGTACCTGAATGGTGTCAATCCCT 1312  
QY 784 CTTGATTCGCGCTGTACAGTCTCCCAACAACTTCCCGGTCACTGTGATGAATGGTGGC 843  
DB 1313 CATGCTCCATGATCTCTAGCTTGGCCAGCAGCTGCTGTCAACCAATGACATGTTGGC 1372  
QY 844 CCCAGTCTGGGCCCTCGGAACCAAGTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTT 903  
DB 1373 CCCCTTGTGGGACAGACACATGCTCTGTCAGACAGAGCTAGAGAGGGGAAACATCTTCT 1432  
QY 904 GGTGGATCATGGCATTTCTTCTGGAGTCCACACCAACATCTCAATGGAAAGCCTCAGTT 963  
DB 1433 AGCGGACTACTGGATCCTGGCGGAGGCCCCCACTGCTTAAACGGCGCCGACGAGTA 1492

QY 964 CTCTGCAGCCCCCGATGACCCCTGTTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAT 1023  
DB 1493 CGTGCGCGCCCCACTGTGCTGCTGTGGCTCAGCCCCCAG---GGGGGCGCTGGTGGCTT 1549  
QY 1024 TGCCATCCAGCTCAAAAGACTCCCGGGCCAGAACCCCACTCTTCTCCGCCAGCGATGA 1083  
DB 1550 GGCCATCCAGCTCAGCCAGACCCCGGGCCCTGACAGCCCCATCTTCTGCCCCCATGACTC 1609  
QY 1084 CACGTGGGACTGGTTGCTGGGCCAAGACCTGGGTTCGCAATTCCTGAGTTTATCATCATGA 1143  
DB 1610 CGAATGGGACTGGCTGCTGGCCAGACCGTGGGTGGCAACTCTGAGTTCTTGGTGCACGA 1669  
QY 1144 GGCTGTCAACATCTGCTGCTGATGCCCATCTGATCCAGAGTCTTGGCTTGGCCACATTT 1203  
DB 1670 AAACAACACGCACTTCTGTGCACTGCTGTGCGAGGCTTTCGCCATGGCCACGCT 1729  
QY 1204 AGCTCAGCTGCTAGGTGCTCACCCTCTCTCAAGCTATTGATTCCTCATATTCGGTACAC 1263  
DB 1730 GGCCAGCTGCGCTCTGCCACCCCATCTACAGCTCTCTACTCCCCACACTTCGATACAC 1789  
QY 1264 ACTGCACATCAACACGCTTGGCCGGGAGCTGCTGCTGCCCTGGGAAAGTTGATAGACAA 1323  
DB 1790 GCTGAGGTGAACACCATCGCGAGGGCCACGCTGCTCAACCCCGAGGGCTCTGTGACCA 1849  
QY 1324 GTCCACAGGCTTGGCACTGGGGGATTTCTGTGACCTGATAAAGAGAAACATGGAGCAGCT 1383  
DB 1850 GGTCACTGCTCCTCGGGAGGCAAGGCTCTATCTACCTCATGACACGGGCTTGGCCACTT 1909  
QY 1384 GAACTACTCTGCTGCTGCTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACATCC 1443  
DB 1910 CACCTACACCAATTTCTGCTTCCGGAACGCTGCGGGCCCGGGCTCTGGCTATCCC 1969  
QY 1444 AGGCTACTATTACCAGATGATGGGATGCAGATCTGGGGGGCAATAAAGAGCTTTGTCTC 1503  
DB 1970 CAACTACCACTACCGAGACGCGCTGAAGATCTGGGGGGCCATTGAGAGCTTTGTCTC 2029  
QY 1504 TGAATAGTCAGATCTACTATCAAGTGACACATCCGTCGAAGATGACCAAGAGCTCA 1563  
DB 2030 AGAATTCGTTGGGCTACTATTATCCAGTACGATCTGTGACAGCAGGATTCGAGAGTGA 2089  
QY 1564 GSCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGGTATGCC 1623  
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QY 1624 CTCTCTTGTGGATATCCCGGGAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACCTG 1683  
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Db 2570 CATTGAGAACAGTGTCTCCATCTAAC 2595
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RESULT 9
US-10-175-696-22
; Sequence 22, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 3320
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (459)...(2591)
US-10-175-696-22
Query Match 20.5%; Score 659.6; DB 14; Length 3320;
Best Local Similarity 63.9%; Pred. No. 9.6e-190;
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;
QY 484 CAGCTGGAGACTTACATTGAAGTTGGCTCGCTGCTCCACACGAGACTGTGAAGA 543
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Db 1790 GCTGCAGTGAACACCACTCGCAGGGCCACGCTCTCAACCCCGAGGGCTCTGGTGACCA 1849
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QY 1744 TCTGCCACCTACCATGACGCTACCCACCACTACTTCCAAAGGGCCAGCGCCGCTGAGAG 1803
Db 2270 TGCTCCATCATCCATGAGGAGGCCCCCAACCAAGAGGGGACCAACCCCTGAGAC 2329
QY 1804 TTTTCATAGCCACGCTCCAGCAGTTAATTCGTCAAGTTTATCACAATCATTTGCTCTGCT 1863
Db 2330 TTACTTAGACACCTCCCTGAGGTGACATCAGCTGTAAACAACCTCTCTCTCTTCTGTT 2389
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Qy 2044 CATTGAGAACAGTGTCTCCATCTAAC 2069  
Db 2570 CATTGAGAACAGTGTCTCCATCTAAC 2595

RESULT 10  
US-10-776-871-22  
; Sequence 22, Application US/10776871  
; Publication No. US20040132087A1  
; GENERAL INFORMATION:  
; APPLICANT: Gluckemann, Maria Alexandra  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-193001  
; CURRENT APPLICATION NUMBER: US/10/776,871  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/10/175,696  
; PRIOR FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: 10/067,668  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/823,901  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US01/10720  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 60/193,920  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/862,658  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: PCT/US01/16380  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/205,675  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/882,837  
; PRIOR FILING DATE: 2001-06-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 22  
; LENGTH: 3320  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (459)...(2591)  
US-10-776-871-22

Query Match 20.5%; Score 659.6; DB 19; Length 3320;  
Best Local Similarity 63.9%; Pred. No. 9.6e-190;  
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;  
Qy 484 CAGCTCGAAGACTTACATTGAAGTTGGCTCGCTCGCTTGACACGAGACTGTGAAAGA 543  
Db 1013 CAGTGGGAATCGGTACCTCGCCCGCTTCCCATGAAATTTGACATCCCATCCCTGATGTA 1072  
Qy 544 CTTGGACCTCAACATCAAGTACTCTCGGATGAGATGCCAAACTCTTCTTTAAAGCCCA 603  
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Qy 604 CTCGCGTATACGGAGCTGAAAGTCAAGGGCTCTTGGACCGCACAGGACTCTGGAGGAG 663

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RESULT 11  
US-10-422-264-29  
; Sequence 29, Application US/1042264  
; Publication No. US20030172391A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. US20030172391A1 Lipoxigenase Proteins and Polynucleotides  
; FILE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705.0009-00800  
; CURRENT APPLICATION NUMBER: US/10/422,264  
; CURRENT FILING DATE: 2003-04-23  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 29  
; LENGTH: 3384  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-422-264-29

Query Match 20.5%; Score 659.6; DB 16; Length 3384;  
Best Local Similarity 63.9%; Pred. No. 9,8e-190;  
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

Qy 484 CAGCTGGAAGACTTACATGTAAGGTGGCTCGCTGCTTACACGAGACTGTGAAGA 543  
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Qy 604 CTCGCCGTATACGAGCTGAAAGTCAAGGGCTCTCGACCGCACAGGACTCTGGAGGAG 663  
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QY 1864 GCTAAGCCAGAACCTGGGGACCAAGAGCCCTTGGGCCACTATCCAGATGAACACTTCAC 1923  
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QY 2044 CATTGAGAACAGTGTCTCCATCTAAC 2069  
DB 2610 CATTGAGAACAGTGTCTCCATCTAAC 2635

RESULT 12  
US-09-662-658-3  
; Sequence 3, Application US/09862658  
; Patent No. US20020137101A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyers, Rachel  
; TITLE OF INVENTION: 4638, A NOVEL HUMAN LIPOXYGENASE FAMILY  
; FILE REFERENCE: 10448-053001  
; CURRENT APPLICATION NUMBER: US/09/862,658  
; PRIOR FILING DATE: 2001-05-22  
; PRIOR APPLICATION NUMBER: US 60/205,675  
; PRIOR FILING DATE: 2000-05-19  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2136  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-662-658-3

Query Match 20.4%; Score 658.6; DB 9; Length 2136;  
Best Local Similarity 63.9%; Pred. No. 1.5e-189;  
Matches 1013; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

QY 484 CAGCTGGAAAGACTTACATTGAAGGTGGCTCGCTGCTTGACACGAGACTGTGAAGA 543  
DB 555 CAGTGGGAATCGTACTCGCGGCTTCCCCATGAAAATTGACATCCCATCCCTGATGA 614  
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QY 1624 CTCTTGTGTGATACCGGGAGCCCTGCTCAGTATATCACCATGTGATATCACCTG 1683  
DB 1692 AAGCGGCTGTGACCCCGAGAGAGATGGTGAAGTTCTCACTGCAATCATCTCAATTG 1751  
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QY 1864 GCTAAGCCAGAACCTGGGGACCAAGGCCCTTGGGCCACTATCCAGATGAACACTTCAC 1923  
DB 1932 GGTAGCCAAAGAACCCAGGACAGAGGCCCTTGGGCCACTTACCAGATGAGCACTTCAC 1991  
QY 1924 AGAGATGCCGCCCGCGGAGAGGCTGGCTTCCAGAGAAAGCTGATCCAGATCTCCAA 1983  
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Db 2112 CATTGAGAACAGTGTCTCCATCTAA 2136  
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; Sequence 24, Application US/10175696  
; Publication No. US20030092658A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-193001  
; CURRENT APPLICATION NUMBER: US/10175,696  
; CURRENT FILING DATE: 2002-06-20  
; PRIORITY APPLICATION NUMBER: 10/067,668  
; PRIORITY FILING DATE: 2002-02-04  
; PRIORITY APPLICATION NUMBER: 60/266,140  
; PRIORITY FILING DATE: 2001-02-02  
; PRIORITY APPLICATION NUMBER: 09/823,901  
; PRIORITY FILING DATE: 2001-03-30  
; PRIORITY APPLICATION NUMBER: PCT/US01/10720  
; PRIORITY FILING DATE: 2001-04-02  
; PRIORITY APPLICATION NUMBER: 60/193,920  
; PRIORITY FILING DATE: 2000-03-31  
; PRIORITY APPLICATION NUMBER: 09/862,658  
; PRIORITY FILING DATE: 2001-05-21  
; PRIORITY APPLICATION NUMBER: PCT/US01/16380  
; PRIORITY FILING DATE: 2001-05-21  
; PRIORITY APPLICATION NUMBER: 60/205,675  
; PRIORITY FILING DATE: 2000-05-19  
; PRIORITY APPLICATION NUMBER: 09/882,837  
; PRIORITY FILING DATE: 2001-06-15  
; PRIORITY APPLICATION NUMBER: PCT/US01/19319  
; PRIORITY FILING DATE: 2001-06-15  
; PRIORITY APPLICATION NUMBER: 60/211,727  
; PRIORITY FILING DATE: 2000-06-15  
; NUMBER OF SEQ ID NOS: 31  
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; LENGTH: 2136  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-175-696-24

Query Match 20.4%; Score 658.6; DB 14; Length 2136;  
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Matches 1013; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

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Db 1872 TTACTAGACACCTTCCCTGGAAGTGAACATCAGCTGTAAACCACTCTCTCTCTCTCTCT 1931  
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QY 1864 GCTAAGCGCAGAACTGGGGACCAAGGCCCTCTGGCCACTTATCCAGATGAACACTTCCAC 1923  
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Db 1932 GTTAGCCAGAACCCAAAGGACAGAGGCCCTCTGGGACCTTACCAGATGAGACATTCAC 1991  
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: July 19, 2005, 12:01:37 ; Search time 358.769 Seconds  
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Perfect score: 3224  
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Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3178	98.6	3205	US-09-061-768A-3	Sequence 3, Appli
2	3178	98.6	3205	US-09-764-246-3	Sequence 3, Appli
3	1398.4	43.4	2674	US-09-949-016-3041	Sequence 3041, Ap
4	1395.2	43.3	2685	US-09-061-768A-1	Sequence 1, Appli
5	1395.2	43.3	2685	US-09-764-246-1	Sequence 1, Appli
6	1395.2	43.3	2685	US-09-949-016-156	Sequence 156, App
7	659.6	20.5	3384	US-09-547-435-29	Sequence 29, Appli
8	658	20.4	2236	US-09-547-435-5	Sequence 5, Appli
9	658	20.4	2701	US-09-547-435-1	Sequence 1, Appli
10	657	20.4	2307	US-09-799-451-803	Sequence 803, App
11	657	20.4	2604	US-09-547-435-23	Sequence 23, Appli
12	565.8	17.5	2469	US-09-087-727-1	Sequence 1, Appli
13	565.8	17.5	2469	US-09-853-053-1	Sequence 155, App
14	565.8	17.5	2469	US-09-949-016-155	Sequence 11, Appli
15	466.2	14.5	1383	US-09-547-435-11	Sequence 9, Appli
16	466.2	14.5	1848	US-09-547-435-9	Sequence 27, Appli
17	466.2	14.5	2316	US-09-547-435-27	Sequence 1155, Ap
18	400.6	13.7	2497	US-09-023-655-1155	Sequence 3, Appli
19	400.6	13.7	2497	US-10-071-411A-3	Sequence 109, App
20	400.6	13.7	2497	US-09-949-016-109	Sequence 5821, Ap
21	440.2	13.7	2496	US-09-949-016-5821	Sequence 13, Appli
22	407.2	12.6	1441	US-09-547-435-13	Sequence 652, App
23	335.6	10.4	2343	US-09-641-638-652	Sequence 652, App
24	335.6	10.4	2343	US-10-170-097-652	Sequence 7, Appli
25	308.6	9.6	1005	US-09-547-435-7	Sequence 3, Appli
26	308.6	9.6	1470	US-09-547-435-3	Sequence 25, Appli
27	308.6	9.6	1938	US-09-547-435-25	

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Sequence 3040, Ap  
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Sequence 14783, A  
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41 150.6 4.7 90050 4 US-09-893-238-5  
42 148.6 4.6 14082 4 US-09-949-016-11898  
43 148.6 4.6 14087 4 US-09-949-016-14783  
c 44 147.8 4.6 14707 4 US-09-312-762A-3  
45 146 4.5 5889 3 US-09-402-929-3

ALIGNMENTS

RESULT 1  
US-09-061-768A-3  
; Sequence 3, Application US/09061768A  
; Patent No. 6204037  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; APPLICANT: BOEGLIN, WILLIAM E.  
; APPLICANT: JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/061,768A  
; FILING DATE: APRIL 16, 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: NONE  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3205 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
US-09-061-768A-3

Query Match 98.6%; Score 3178; DB 3; Length 3205;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 3189; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
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QY GACAAACCCATCTTCTGCGCAGGATGACAGTGGGACTGGTGTGCGCAAGACTGG 1114  
Db GACAAACCCATCTTCTGCGCAGGATGACAGTGGGACTGGTGTGCGCAAGACTGG 1080  
QY GTTCGCAATTCGAGTTTATCCATGAGGCTGTCAACATCTGCTGATGCCCATCTG 1174  
|||||

Db 1081 GTTCGCAATTCGAGTTTATACATCCATGAGGCTGTCAACATCTGCTGATGCCCATCTG 1140  
QY 1175 ATTCAGAAAGCTTTTGGCTTGGCCACATTAAGTCTAGCTGCTAGGTGTACACCTCTCTTC 1234  
Db 1141 ATTCAGAAAGCTTTTGGCTTGGCCACATTAAGTCTAGCTGCTAGGTGTACACCTCTCTTC 1200  
QY 1235 AAGCTATTGATTCTCAATTCGCTTACATCTGCTGACATCAACACACGCTTGGCCGAGCTG 1294  
Db 1201 AAGCTATTGATTCTCAATTCGCTTACATCTGCTGACATCAACACACGCTTGGCCGAGCTG 1260  
QY 1295 CTCGTTGGCCCTGGGAAGTTGATAGAACAGTCCAGAGCTTGGCACTGGGGGATCTCT 1354  
Db 1261 CTCGTTGGCCCTGGGAAGTTGATAGAACAGTCCAGAGCTTGGCACTGGGGGATCTCTCT 1320  
QY 1355 GACCTGATAAAGAGAAACATGGAGCAGCTGAACACTCTGCTGCTGTCTCTCTGAAAGT 1414  
Db 1321 GACCTGATAAAGAGAAACATGGAGCAGCTGAACACTCTGCTGCTGTCTCTCTGAAAGT 1380  
QY 1415 ATCCGAGCCCGAGGTGTGGAAAGACATCCAGGCTACTATTACCGAGATGATGGGATGAC 1474  
Db 1381 ATCCGAGCCCGAGGTGTGGAAAGACATCCAGGCTACTATTACCGAGATGATGGGATGAC 1440  
QY 1475 ATCCGAGCCCGAGGTGTGGAAAGACATCCAGGCTACTATTACCGAGATGATGGGATGAC 1534  
Db 1441 ATCCGAGCCCGAGGTGTGGAAAGACATCCAGGCTACTATTACCGAGATGATGGGATGAC 1500  
QY 1535 ACATCCGCTCAAGATGACCAAGAGCTCCAGGCTGGGTGAGGAGATCTTCTCTGAGGCG 1594  
Db 1501 ACATCCGCTCAAGATGACCAAGAGCTCCAGGCTGGGTGAGGAGATCTTCTCTGAGGCG 1560  
QY 1595 TTCTCTCGGCGGAGAAAGCTCAGGTATGCTCTCTTGTGTGGATACCCGGGAAAGCCCTGCT 1654  
Db 1561 TTCTCTCGGCGGAGAAAGCTCAGGTATGCTCTCTTGTGTGGATACCCGGGAAAGCCCTGCT 1620  
QY 1655 CAGTATATCAACATGGTGTATTTCACTGCTCAGGCAAGCATGCAAGTGTCTGATTCAGG 1714  
Db 1621 CAGTATATCAACATGGTGTATTTCACTGCTCAGGCAAGCATGCAAGTGTCTGATTCAGG 1680  
QY 1715 CAGTTTCGACTCTTGTGTTTGGATGCCAATCTGCACTGCACTACCATGAGCTACCAACCT 1774  
Db 1681 CAGTTTCGACTCTTGTGTTTGGATGCCAATCTGCACTGCACTACCATGAGCTACCAACCT 1740  
QY 1775 ACTTCCAAAGCCAGGCCCGCTCGAGATTTATAGCCACGCTCCAGCAGATTAATTCG 1834  
Db 1741 ACTTCCAAAGCCAGGCCCGCTCGAGATTTATAGCCACGCTCCAGCAGATTAATTCG 1800  
QY 1835 TCAAGTTATCACTATTTGCTCTCTGCTGCTTAAGCGGAGAACTGGGACCAAGGCC 1894  
Db 1801 TCAAGTTATCACTATTTGCTCTCTGCTGCTTAAGCGGAGAACTGGGACCAAGGCC 1860  
QY 1895 CTGGGCCACTATCCAGATGAAACACTTTCAGAGGATGCCCGCGGAGCGTGGCTGCC 1954  
Db 1861 CTGGGCCACTATCCAGATGAAACACTTTCAGAGGATGCCCGCGGAGCGTGGCTGCC 1920  
QY 1955 TTCCAGAGAAAGCTGATCCAGATCTTCCAAAGGSCATCAGGAGAGGAACCGAGGCTGGCA 2014  
Db 1921 TTCCAGAGAAAGCTGATCCAGATCTTCCAAAGGSCATCAGGAGAGGAACCGAGGCTGGCA 1980  
QY 2015 CTGGCCCTACACTACTGGATCTCCCTCATTTGAGAACAGTGTCTCATCTTAACATCTT 2074  
Db 1981 CTGGCCCTACACTACTGGATCTCCCTCATTTGAGAACAGTGTCTCATCTTAACATCTT 2040  
QY 2075 GGAGAGAGCAGTCTCTGTGTGACATATAGAACTCTTTGACCATGCTCTCCAGGCTAAGTCC 2134  
Db 2041 GGAGAGAGCAGTCTCTGTGTGACATATAGAACTCTTTGACCATGCTCTCCAGGCTAAGTCC 2100  
QY 2135 CGGTATGCTTCTCTGGAAACCAAGGCCCACTCTTTACACACACACACACACACAC 2194  
Db 2101 CGGTATGCTTCTCTGGAAACCAAGGCCCACTCTTTACACACACACACACACACAC 2160  
QY 2195 TAATTAATTCGAAACAGAAAAAACCCTTAACCTCCACAGAGGCAAGATCTCACACAGCAG 2254  
Db 2161 TAATTAATTCGAAACAGAAAAAACCCTTAACCTCCACAGAGGCAAGATCTCACACAGCAG 2220



Qy	2255	GAGCCATCCAAATGTTTGGAGACCTTGAGCTTCTAGCTCTGATTAA	CGGCTTTTCTGGTTT	23114
Db	2221	GAGCCATCCAAATGTTTGGAGACCTTGAGCTTCTAGCTCTGATTAA	CGGCTTTTCTGGTTT	2280
Qy	2315	GCTTTTGCTTTCTATTCCATTAAACCATGGACGGTTAA	CAGAAAGCACAGAAACCTTGTTTCAC	2374
Db	2281	GCTTTTGCTTTCTATTCCATTAAACCATGGACGGTTAA	CAGAAAGCACAGAAACCTTGTTTCAC	2340
Qy	2375	TGCACAAAGCCACTGAGATCTCACCCTCACTGTACACAAAGGACGCTATCATACAGGCTT	2434	
Db	2341	TGCACAAAGCCACTGAGATCTCACCCTCACTGTACACAAAGGACGCTATCATACAGGCTT	2400	
Qy	2435	ATCAGGAACACAGGAAATTTGTGCCAATCAAAAGCCTTACCACCTAGTGCCTCATCGTCACTTACG	2494	
Db	2401	ATCAGGAACACAGGAAATTTGTGCCAATCAAAAGCCTTACCACCTAGTGCCTCATCGTCACTTACG	2460	
Qy	2495	ACCTCACACTGGCAGTCTTTAGCTTTTGAGAAGGGAATTA	CTGAGTCAAGTACGAAAGAGAA	2554
Db	2461	ACCTCACACTGGCAGTCTTTAGCTTTTGAGAAGGGAATTA	CTGAGTCAAGTACGAAAGAGAA	2520
Qy	2555	GGACAGACCAAGGCATGGCTCCATGTGGGAAGAACATATCTGCTCTTCCAGATGACCGG	2614	
Db	2521	GGACAGACCAAGGCATGGCTCCATGTGGGAAGAACATATCTGCTCTTCCAGATGACCGG	2580	
Qy	2615	GTAGCTCACAGCCATGTGTCTAATCTAACTCCAGAGGTCTCTAGTGGCCATTGAAGACTCCA	2674	
Db	2581	GTAGCTCACAGCCATGTGTCTAATCTAACTCCAGAGGTCTCTAGTGGCCATTGAAGACTCCA	2640	
Qy	2675	GGCATTACAGGGGATATACAGTAGTAGACACCAAAAATTATATCTTTTAAAGAGAGGAATGGG	2734	
Db	2641	GGCATTACAGGGGATATACAGTAGTAGACACCAAAAATTATATCTTTTAAAGAGAGAGG - ATGGG	2699	
Qy	2735	CTGGAGAGATGGCTCAGCGGTTAAGACACTGACTGCTCTTCCAGAGATCCTCAGTTCAA	2794	
Db	2700	CTGGAGAGATGGCTCAGCGGTTAAGACACTGACTGCTCTTCCAGAGATCCTCAGTTCAA	2759	
Qy	2795	TTCCAGCAACCAACATGGTGGCTCACAAACATCTGTAAATGGGAATTCGATGCCCTCTTCTG	2854	
Db	2760	TTCCAGCAACCAACATGGTGGCTCACAAACATCTGTAAATGGGAATTCGATGCCCTCTTCTG	2819	
Qy	2855	GGGTGCTGTAAGACAGCGGACAGTGATGACACATATATAAAATAAAATAAAATCTTTTAAAAAA	2914	
Db	2820	GGGTGCTGTAAGACAGCGGACAGTGATGACACATATATAAAATAAAATAAAATCTTTTAAAAAA	2879	
Qy	2915	CAAAAACAAGAGAGAGGACATGCTACCAATTTCTACCTCACTTCTCTCAAGCCACCCCT	2974	
Db	2880	CAAAAACAAGAGAGAGGACATGCTACCAATTTCTACCTCACTTCTCTCAAGCCACCCCT	2939	
Qy	2975	AAAGTGAATTTGTGNAACAGGTGCCCTTTGACAGAGAGTTAGAGATATTCTCAAACTCTA	3034	
Db	2940	AAAGTGAATTTGTGNAACAGGTGCCCTTTGACAGAGAGTTAGAGATATTCTCAAACTCTA	2999	
Qy	3035	ATACCTTCACATCTAAAAATCCATCTTCAATTCCAAATATCCAAATTTTATACACTCTC	3094	
Db	3000	ATACCTTCACATCTAAAAATCCATCTTCAATTCCAAATTTTATACACTCTC	3059	
Qy	3095	CAGTTTGGTGGGTGAGGGGTGTTTTTGTGTTTGGTTTGGTTGGGTGTTTTGTTTTT	3154	
Db	3060	CAGTTTGGTGGGTGAGGGGTGTTTTTGTGTTTGGTTTGGTTGGGTGTTTTGTTTTT	3119	
Qy	3155	GTTTTTCATATTTGTTTTTCTCTGGTTCAGACTCCATGGAGCTTCATTAAATGTCATAAATG	3214	
Db	3120	GTTTTTCATATTTGTTTTTCTCTGGTTCAGACTCCATGGAGCTTCATTAAATGTCATAAATG	3179	
Qy	3215	AGTTTCATTCC	3224	
Db	3180	AGTTTCATTCC	3189	

Patent No. 6649355  
GENERAL INFORMATION:  
APPLICANT: BRASH, ALAN R.  
BOEGLIN, WILLIAM E.  
JITSUKA, MITSUO  
TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/764,246  
FILING DATE: 17-Jan-2001  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3205 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
US-09-764-246-3

Query Match	98.6%; Score 3178; DB 4; Length 3205;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 3189; Conservative 0; Mismatches 0; Indels 1; Gaps 1	
Qy	35 ATGCGAAATGCAGGCTGAGAGTATCCACGGGGAGCCCTGTGGGCTGGACATGGGAC 94
Db	1 ATGCGAAATGCAGGCTGAGAGTATCCACGGGGAGCCCTGTGGGCTGGACATGGGAC 60
Qy	95 AATGTGCTCTCAGCATCTGTGGGAAACCCACGGAGAGAGCCCTTTAGTACTCTGGACCAT 154
Db	61 AATGTGCTCTCAGCATCTGTGGGAAACCCACGGAGAGAGCCCTTTAGTACTCTGGACCAT 120
Qy	155 CTGGCAAGAGATTACGCCCGGTGCTGAAGAAGACTTTCGAGGTGACGCTTCCCCAGGAC 214
Db	121 CTGGCAAGAGATTACGCCCGGTGCTGAAGAAGACTTTCGAGGTGACGCTTCCCCAGGAC 180
Qy	215 GTAGGCACTGTGCTGATGCTGCGAGTGCAAAAGCACCCCCGGAAGTGTCCCTCCCGCTT 274
Db	181 GTAGGCACTGTGCTGATGCTGCGAGTGCAAAAGCACCCCCGGAAGTGTCCCTCCCGCTT 240
Qy	275 ATGTCCTTCGTTCTGATGCTGCTGTCTGCCGCTGGTTTCGAGCTGGAGTGGCTACTCGG 334
Db	241 ATGTCCTTCGTTCTGATGCTGCTGTCTGCCGCTGGTTTCGAGCTGGAGTGGCTACTCGG 300
Qy	335 GCTGCACTCCACTTCCCTGTTATCAGTGGCTGGAAAGGGCGGGGAGCTGGTGTCTAGA 394
Db	301 GCTGCACTCCACTTCCCTGTTATCAGTGGCTGGAAAGGGCGGGGAGCTGGTGTCTAGA 360
Qy	395 GAGGGAGCAGAAAGGTGTCTGCGAAGACCATCACCCCTACATCTGCAAGTACAGGCCAG 454

RESULT 2  
US-09-764-246-3  
; Sequence 3, Application US/09764246

Db	361	GAGGAGCAGCAAAAGGTGTCTTGGCAAGACCAATCAACCTTCACTGCGAGATCAGCGCCAG	420	QY	1535	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTTGGGTGAGGAGATCTTCTCTGAGGC	1594
QY	455	AAGGAGCTTGAGTCCAGGCAAGAGATGTACAGCTCGAAGACTTACATTTGAGGTGGCT	514	Db	1501	ACATCCGTCCAGATGACCAAGAGCTCCAGGCTTGGGTGAGGAGATCTTCTCTGAGGC	1560
Db	421	AAGGAGCTTGAGTCCAGGCAAGAGATGTACAGCTCGAAGACTTACATTTGAGGTGGCT	480	QY	1595	TTCTCTGGCCGAGAAAGCTCAGGTATGCCCTCTTGTGTGGATACCCGGGAAGCCCTGGTC	1654
QY	515	CGCTGCTTTGACCAACAGAGACTGTGAAGAGCTTGGACCTCAACATCAAGTACTCTGCGATG	574	Db	1561	TTCTCTGGCCGAGAAAGCTCAGGTATGCCCTCTTGTGTGGATACCCGGGAAGCCCTGGTC	1620
Db	481	CGCTGCTTTGACCAACAGAGACTGTGAAGAGCTTGGACCTCAACATCAAGTACTCTGCGATG	540	QY	1655	CAGTATATACCATCGTGTATTTCACTCTGCTCAGCAACCAAGCATGCACTGTCTAGTTTCAGGC	1714
QY	575	AAGATTCGCCAACTCTTTTAAAGCCCACTCGCGTATACGGAGCTGAAAGTCAAGGG	634	Db	1621	CAGTATATACCATCGTGTATTTCACTCTGCTCAGCAACCAAGCATGCACTGTCTAGTTTCAGGC	1680
Db	541	AAGAAATGCCAACTCTTTTAAAGCCCACTCGCGTATACGGAGCTGAAAGTCAAGGG	600	QY	1715	CAGTTTCGACTCTTGTGTGTGGATGCCCAATCTGCCACCTTACCATGCGAGCTACCAACCACT	1774
QY	635	CTCTCGACCGCACAGACTCTCGAGGAGTCTGAGGAGATGAGAAGGTGTTTAACTTC	694	Db	1681	CAGTTTCGACTCTTGTGTGTGGATGCCCAATCTGCCACCTTACCATGCGAGCTACCAACCACT	1740
Db	601	CTCTCGACCGCACAGACTCTCGAGGAGTCTGAGGAGATGAGAAGGTGTTTAACTTC	660	QY	1775	ACTTCAAAGGCGCGCCGCTGAGAGTTTTCATAGCCACGCTCCAGAGCTTAATTTCG	1834
QY	695	CGCAAGACTCCAGCAGCAGATATGTGTTTGCACTCTGGCAGGAAGTGCCTTCTTCGCC	754	Db	1741	ACTTCAAAGGCGCGCCGCTGAGAGTTTTCATAGCCACGCTCCAGAGCTTAATTTCG	1800
Db	661	CGCAAGACTCCAGCAGCAGATATGTGTTTGCACTCTGGCAGGAAGTGCCTTCTTCGCC	720	QY	1835	TCAAGTTATCATCATCTTGTCTCTGCTCTAAGCGCAGACCTGGGACCAAGGCC	1894
QY	755	TCCAGTTCTTAATGGCATCAACCCGGTCTCTGATTTGCGCGCTGTGCAGTCTCCAAAC	814	Db	1801	TCAAGTTATCATCATCTTGTCTCTGCTCTAAGCGCAGACCTGGGACCAAGGCC	1860
Db	721	TCCAGTTCTTAATGGCATCAACCCGGTCTCTGATTTGCGCGCTGTGCAGTCTCCAAAC	780	QY	1895	CTGGGCCACTATCCAGATGAACAATTTCAAGAGGATGCCCCCGGCGAAGCGTGGCTGCC	1954
QY	815	AACCTTCCCGTCACTGATGAATGTGTGGCCCAAGTGTGGGCCCTGGAAACCAAGTCTGCAG	874	Db	1861	CTGGGCCACTATCCAGATGAACAATTTCAAGAGGATGCCCCCGGCGAAGCGTGGCTGCC	1920
Db	781	AACCTTCCCGTCACTGATGAATGTGTGGCCCAAGTGTGGGCCCTGGAAACCAAGTCTGCAG	840	QY	1955	TTTCCAGAGAAAGCTGATCCAGATCTTCAAAGGCGCATCAGGAGAGGAAACCGAGGCTGGCA	2014
QY	875	GCTGAGTTGGAGAGGGCTCCCTGTTCTTGGTGGATCATGGCANCTTTCTGGAGTCCAC	934	Db	1921	TTTCCAGAGAAAGCTGATCCAGATCTTCAAAGGCGCATCAGGAGAGGAAACCGAGGCTGGCA	1980
Db	841	GCTGAGTTGGAGAGGGCTCCCTGTTCTTGGTGGATCATGGCANCTTTCTGGAGTCCAC	900	QY	2015	CTGGCCCTACACTCTCGATCTCCCTCTCATTTGAGAAACAGTGTCTCAATCTAAACATCTT	2074
QY	935	ACCAACATCTCAATGGAAGCCCTCAGTTCTTGCGAGCCCGCATGACCTGTGTACACAG	994	Db	1981	CTGGCCCTACACTCTCGATCTCCCTCTCATTTGAGAAACAGTGTCTCAATCTAAACATCTT	2040
Db	901	ACCAACATCTCAATGGAAGCCCTCAGTTCTTGCGAGCCCGCATGACCTGTGTACACAG	960	QY	2075	GGAGAAAGCAGTCTGTGTGACATATAGAACTCTTTGACCATGCTCTCCAGGCTTAAGTCC	2134
QY	995	AGCTCAGGGTCCGAGCCCTGCTTCCATTTGCCATCCAGTCAACAGACTCCCGGGCCA	1054	Db	2041	GGAGAAAGCAGTCTGTGTGACATATAGAACTCTTTGACCATGCTCTCCAGGCTTAAGTCC	2100
Db	961	AGCTCAGGGTCCGAGCCCTGCTTCCATTTGCCATCCAGTCAACAGACTCCCGGGCCA	1020	QY	2135	CGGTATGTTCTCTGGGCAACCAAGCCCATCTTTACACACACACACACACACAC	2194
QY	1055	GACAAACCCATCTTCTGCGCCAGCGATGACACGTGGGACTGTGTGCGCCAAAGACTCGG	1114	Db	2101	CGGTATGTTCTCTGGGCAACCAAGCCCATCTTTACACACACACACACACACAC	2160
Db	1021	GACAAACCCATCTTCTGCGCCAGCGATGACACGTGGGACTGTGTGCGCCAAAGACTCGG	1080	QY	2195	TAATAAATCGAAACAGAAACCTTAACTCCACAGAGGCAAGATCTCACACAGCAGA	2254
QY	1115	GTTTCGAATTTGAGTTTACATCAATGAGGCTGTGCACATCTGCTGATGCCATCTG	1174	Db	2161	TAATAAATCGAAACAGAAACCTTAACTCCACAGAGGCAAGATCTCACACAGCAGA	2220
Db	1081	GTTTCGAATTTGAGTTTACATCAATGAGGCTGTGCACATCTGCTGATGCCATCTG	1140	QY	2255	GAGCCATCCAAATGTTTGGAGACCTTGAGCTTCACTCTGATTAACGGCTTTTGTGGTTT	2314
QY	1175	ATTCCAGAGTCTTTCCTTGGCCACATTAACGTGAGTGTGACCTCTCTTC	1234	Db	2221	GAGCCATCCAAATGTTTGGAGACCTTGAGCTTCACTCTGATTAACGGCTTTTGTGGTTT	2280
Db	1141	ATTCCAGAGTCTTTCCTTGGCCACATTAACGTGAGTGTGACCTCTCTTC	1200	QY	2315	GCTTGTCTTTCTATTTCCATTAACATGAGCGGTAAACAGAAAGCAGAAACCTTGTTCAC	2374
QY	1235	AAGCTATTGATTTCTCACAATTCGGGTACACATGCGATCAACACGCTTGCCTGGGAGCTG	1294	Db	2281	GCTTGTCTTTCTATTTCCATTAACATGAGCGGTAAACAGAAAGCAGAAACCTTGTTCAC	2340
Db	1201	AAGCTATTGATTTCTCACAATTCGGGTACACATGCGATCAACACGCTTGCCTGGGAGCTG	1260	QY	2375	TGCACAAAGCCACTCAGATCTCACCTCTCACACACAAAGGCGAGTATCATACAGGCTT	2434
QY	1295	CTCGTTGCCCTGGGAAGTTGATAGAACAGTCAAGTCAAGGCTTGGGCTGCGGGGATTTCTCT	1354	Db	2341	TGCACAAAGCCACTCAGATCTCACCTCTCACACAAAGGCGAGTATCATACAGGCTT	2400
Db	1261	CTCGTTGCCCTGGGAAGTTGATAGAACAGTCAAGTCAAGGCTTGGGCTGCGGGGATTTCTCT	1320	QY	2435	ATCAGGAACACAGGAATTTGTCCAATCAAGGCTTACCCACTAGGTCCTCGTGACCTACG	2494
QY	1355	GACCTGATAAGAAACATGAGAGAGCTGAACTACTCTGCTCTGTCTCCCTGAAGAT	1414	Db	2401	ATCAGGAACACAGGAATTTGTCCAATCAAGGCTTACCCACTAGGTCCTCGTGACCTACG	2460
Db	1321	GACCTGATAAGAAACATGAGAGAGCTGAACTACTCTGCTCTGTCTCCCTGAAGAT	1380	QY	2495	ACCTCACACTGCGATGCTTTAGCTTTGAGAAAGGATTTACTGAGTCTAGTACGAGTACGAGAA	2554
QY	1415	ATCCGAGCCGAGGTGTGGAAGACATCCCAAGGCTACTATTACCGAGATGATGGGATGCAG	1474	Db	2461	ACCTCACACTGCGATGCTTTAGCTTTGAGAAAGGATTTACTGAGTCTAGTACGAGTACGAGAA	2520
Db	1381	ATCCGAGCCGAGGTGTGGAAGACATCCCAAGGCTACTATTACCGAGATGATGGGATGCAG	1440	QY	2555	GGACAGGAGGAGGATGCTCATGTGGAAGAAATATCTCTCTTCCAGATGACACAG	2614
QY	1475	ATCTGGGGGCAATAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCAAGTGAC	1534	Db	2521	GGACAGGAGGAGGATGCTCATGTGGAAGAAATATCTCTCTTCCAGATGACACAG	2580
Db	1441	ATCTGGGGGCAATAAGAGCTTTGTCTCTGAAATAGTCAGCATCTACTATCAAGTGAC	1500				

Qy	2615	GTAGCTCACAGGCCATGTGTCTAATCTTAAGTCTCAGAGGCTCTCTAGTGGCCATGAAGACTCCA	2674
Db	2581	GTAGCTCACAGGCCATGTGTCTAATCTTAAGTCTCAGAGGCTCTCTAGTGGCCATGAAGACTCCA	2640
Qy	2675	GGCAATTCAGGGGATATACCACTAGACACCAAATTTATACTTTTTAAAGAGAGAGGAATGGG	2734
Db	2641	GGCAATTCAGGGGATATACCACTAGACACCAAATTTATACTTTTTAAAGAGAGAGG-ATGGG	2699
Qy	2735	CTGAGAGATGGCTCAGCGGTTAAGAGCACTGCTCTTTCAGAGATCCTGAGTTCAA	2794
Db	2700	CTGAGAGATGGCTCAGCGGTTAAGAGCACTGCTCTTTCAGAGATCCTGAGTTCAA	2759
Qy	2795	TTCCCGACCAACCATGSGTGCCTCACAAACCATCTGTAATGGGATTTCGATGCCCTCTTCTG	2854
Db	2760	TTCCCGACCAACCATGSGTGCCTCACAAACCATCTGTAATGGGATTTCGATGCCCTCTTCTG	2819
Qy	2855	GCGTGCTCTGAAGACAGCGACAGTGTATGCACATATATAAAATAAAATAATCTTTAAAAAA	2914
Db	2820	GCGTGCTCTGAAGACAGCGACAGTGTATGCACATATATAAAATAAAATAATCTTTAAAAAA	2879
Qy	2915	CAAAACAAGAGAGAGGACATGCTACCAATTTCTACCTCACTTCTTCTCAAGCGACCCCT	2974
Db	2880	CNAACAAGAGAGAGGACATGCTACCAATTTCTACCTCACTTCTTCTCAAGCGACCCCT	2939
Qy	2975	AAAGTGAATTTGTGAACCAAGTCCCTCTTCAGAGAGTTAGAGATATTTCTCAAACTCTA	3034
Db	2940	AAAGTGAATTTGTGAACCAAGTCCCTCTTCAGAGAGTTAGAGATATTTCTCAAACTCTA	2999
Qy	3035	ATACCTTCACATCTAAAATCCATCTTCATTCCAAAATTCCAATATTTATATACACTCTC	3094
Db	3000	ATACCTTCACATCTAAAATCCATCTTCATTCCAAAATTCCAATATTTATATACACTCTC	3059
Qy	3095	CAGTTTGGTGGGTGAGGGGTGTTTTTGGTTGGTTGGTTGGTTGGTGGGGTTTTGTTTTT	3154
Db	3060	CAGTTTGGTGGGTGAGGGGTGTTTTTGGTTGGTTGGTTGGTTGGTGGGGTTTTGTTTTT	3119
Qy	3155	GTTTTTTCATTTTGTTTTTTCTCTGGTTCAGACTCCAATGGAGCTTCATTAATGTCATAAATG	3214
Db	3120	GTTTTTTCATTTTGTTTTTTCTCTGGTTCAGACTCCAATGGAGCTTCATTAATGTCATAAATG	3179
Qy	3215	AGTTTCATTC	3224
Db	3180	AGTTTCATTC	3189

RESULT 3  
US-09-949-016-3041  
Sequence 3041, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3041  
LENGTH: 2674  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-3041

Query Match 43.4%; Score 1398.4; DB 4; Length 2674;  
Best Local Similarity 79.9%; Pred. NO. 0;  
Matches 1673; Conservative 0; Mismatches 416; Indels 5; Gaps 2;

Qy	7	GCAGTAGAGAGCTAAACT--GGTCAGAGAGATGGCGAAATGCAAGGTGAGAGATATCCACG	64
Db	43	GCCGTAGAGAGCTGGACTTAGCTTAGCTGGCAGCATGGCCGAGTTTCAGGGTTCAGGGGTGTCACAC	102
Qy	65	GGGAAGCCCTGTGGGCTGGACATGGGACAAAGTGTCTGTCAAGCATGCTGGGAACCCAC	124
Db	103	GGGAAGCCCTTGGGGCTGGCAATGGGACAAAGTGTCTGTCAAGCATGCTGGGAGCCCGG	162
Qy	125	GGAGAGAGCCCTTAGTAGTACCTCTGGACCATCTGGGCAAGGAGTTTCAAGCGCGGTGCTGAA	184
Db	163	GGAGAGAGCCCCCACTGCCCTGGACAACTCTGGCAAGGAGTTTCACTGGGCGCTGAG	222
Qy	185	GAAGACTTCAGAGTGAAGCTTCCCAAGGACGTGAGGCACTGTGTGTGATGCTGCGAGTCCAC	244
Db	223	GAGGACTTCAGAGTGAAGCTTCCGGAAGGACGTGAGGCGAGTGTGTGTGCTGCGGTGCAC	282
Qy	245	AAAGCACCCCGGAAGTGTCCCTCCGCTTATGTCTTCCGTTCTGATGCTGGTTCGTCG	304
Db	283	AAGCGGCCCC--AGTGTGCCCCCTGCTGGGGCCCTGGCCCCGGATGCTGTGTCTGTC	333
Qy	305	CGCTGTGTTTCAGAGTGGAGTGGCTACTTGGGGCTGCACTCCACTTCCCCTGTATACAGTGG	364
Db	340	CGCTGTGTTTCAGCTGACACCGCCGGGGGGCGGCACTCTCTTCTCCCTGTCTACAGTGG	399
Qy	365	CTGGAAGGGCGGGGAGTGGTGTCTGAGAGAGGGAGCAGCAAGGTGTCTCTGCAAGAC	424
Db	400	CTGGAGGGGGGGGACCCCTGGTGTCTGCAGGAGGGTACAGCCAAGGTGTCTTGGGCAGAC	459
Qy	425	CATCACCTTACATGACAGGATCAGCGCCAGAGGAGCTTGAGTCCAGGCGAAGATGTATC	484
Db	460	CACCACCTTGTCTCCAGCAACAGCGCCAGGAGGAGCTTCAGGCGCCGCGAGGAGATGTAC	519
Qy	485	AGCTTGAAGACTTACATTTGAAGGTGGCGCTCGCTTCCACACAGAGACTGTGTAAGAC	544
Db	520	CAGTGAAGGCTTACAAACCAGGTGGCCCTACTGCTGTGATGAAGAAGCAGTGAAGAC	579
Qy	545	TTGAGCCTCAACATCAAGTACTCTGGGATGAAGAATGCCAAACTCTTCTTAAAGCCAC	604
Db	580	TTGGAGCTCAATATCAATACTCCACAGCCAAAGATGCCAACTTTATCTACAGGCTGGC	639
Qy	605	TCCGCTATACGGAGCTGAAAGTCAAAGGCTCCTGGACCGCAACAGACTCTCTGGAGAGT	664
Db	640	TCTGCTTTTCAGAGATGAATAACAAGGGTTGCTGGACCGCAAGGGGCTCTGGAGAGT	699
Qy	665	CTGAGGAGATGAGAGGCTGTTTAATCTCCGAAGACTCCAGCAGCAGAGTATGTGTTT	724
Db	700	CTGAATGAGATGAAGAGATCTTCAACTTCGGAGGACCCAGAGCTGAGCAGCAATTT	759
Qy	725	GCACATGGCAGGAAGTGCCTTCTTCGCTCCAGTTCTTAATAGCATCAACCCGGTC	784
Db	760	GAGCATGGCAGGAGATGCTTCTTCGCTCCAGTTCTGTGATGGTCTCAACCTGTC	819
Qy	785	CTGATTCGCGCTGTCAAGTCTCCAAACAACTTCCCGGTCACTGATGAATGGTGGCC	844
Db	820	CTGATCCGCGCTGTCACTACCTCCAAAGAACTTCCCGCTCATGATGCCATGGTGGCC	879
Qy	845	CCAGTGTGGGCGCTTGAACCACTGTGAGGCTGAGTTGGAGAAGGGCTCCCTGTTCTTG	904
Db	880	TCAGTGTGTGGTCTCTGGGACACGTTTGAGGCTGAGCTAGAGAAGGGCTCCCTGTTCTTG	939
Qy	905	GTGATCATGGCATCTTTCTGTGAGTCCACCAACATCTCTCAATGGAAAGCCTCAGTTC	964
Db	940	GTGATCACGGCATCTCTCTGGCAATCCAGACCAATGTCTAATGGGAAGCCTCAGTTC	999
Qy	965	TCTGCGCCCGATGACCTTGTATACACAGAGCTCAGGGTCCGGAACCCCTGTCTCCCAT	1024
Db	1000	TCTGCGCCCAATGACCTGTCTATACGAGGCCAGGCTGCGGGCGCTGCTGCTCTC	1059
Qy	1025	GCCATCAGCTCAACAGACTCCCGGGCGAGACAAACCCCATCTTCTGCGCCAGGATGAC	1084
Db	1060	GCCATCAGCTCAGCAGACCCCGGCCCAACAGGCCCATCTTCTGTGCGCACTGATGAC	1119

1085 ACGTGGGACTGTTGCTGGCCAGACCTGGGTTGCAATTTCTGAGTTTACATCCATGAG 1144  
1120 AAGTGGGACTGTTGCTGGCCAGACCTGGGTTGCAATTTCTGAGTTTACATCCATGAG 1179  
1145 GCTGTACACATCTGCTGTGATGCCCATCTGATTCAGAAAGTCTTTGGCTTGGCCACATTA 1204  
1180 GGCCTCAGCCACTGCTGCACTCACTGCTGCTGCTGAGTCTTCCACCTGGCTACCTG 1239  
1205 GGTGAGCTGCTAGTGTGATCCCTCTCTCAAGCTATTGATTTCTCACATTCGGTACACA 1264  
1240 CGTCAAGTCCGCCACTGCCACCTCTCTTCAAGCTGCTGATCCGACACCCGATACACC 1299  
1265 CTGCAATCAACACGCTTCCCGGGAGCTGCTGTTGCCCTTGGAAAGTTGATAGACAAG 1324  
1300 CTGCAATCAACACACTGCCCGGGAGCTGCTTATCGTGCAGGCGAGGTGGTGGACAGG 1359  
1325 TCACAGGCTTGGCACTGGGGGATTTCTCTGACCTGATTAAGAGAAAATGAGAGAGCTG 1384  
1360 TCACAGGCTTGGCACTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1419  
1385 AACTACTCTGCTGCTGCTCCCTGAAGATATCCGAGCCGAGGTTGGAAGACATCCCA 1444  
1420 AACTATTTCTCTGCTGCTGCTGAGGATATCCGAGCCGAGGAGTTGAAGACATCCCA 1479  
1445 GGTCTACTATTACCGAGATGATGGGATGACAGATCTGGGGGCAATAAGAGCTTTGTCTCT 1504  
1480 GGTCTACTACTACGTTGATGGGATGACAGATTTGGGGTGCATGGAAACGCTTTGTCTCT 1539  
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1540 GAAATCATCGGTATCTACTACCAAGTATGATGCTGTCCAAGATGACAGAGAGCTCCAG 1599  
1565 GCTGGGTGAGGAGATCTTCTCTGAGGCTTCCTCGGCGGAGAAAGCTCAGGTATGCC 1624  
1600 GCTGGGTGAGAGAGATCTTCTTCAAGGGCTTCCTTAAACAGAGAGCTCAGGTATGCC 1659  
1625 TCCTTGTGGATACCCGGGAGCCCTGGTCCAGTATATCACCATGATGATATTCACCTGC 1684  
1660 TCCTCACTGGAGACCCGGGAGCCCTGGTGCAGTATGTCACCATGATATTCACCTGC 1719  
1685 TCAGCAAGATGACAGCTGTCAGTTCAGGCGAGTTGCACTCTTGTGTTTGGATGCCAAT 1744  
1720 TCAGCAAGATGACAGCTGTCAGTTCAGGCGAGTTTGAATCTCTGTTGGATGCCAAT 1779  
1745 CTGCACTTACCATGACAGTACACCACTTCTTCAAGGGCTTCCTTAAACAGAGAGCTCAG 1804  
1780 CTGCACTTACCATGACAGTACACCACTTCTTCAAGGGCTTCCTTAAACAGAGAGCTCAG 1839  
1805 TTCTATAGCCACGCTCCAGCAGTTAATTCGTCAAGTTTATCACAATCTTCTCTGCTG 1864  
1840 TTCTATAGCCACCTCCCACTGTCATGCAATGCCATGTCATCTTCTCTGCTGTTG 1899  
1865 CTAAGCGCAGAACTCTGGGACCAAGGCGCTGGGCACTATCCAGATGAACTTTCACA 1924  
1900 CTGAGCAAGGAGCTGAGAGCAAAAGGCGCTGGGCACTTATCCGATGAGCACTTTCACA 1959  
1925 GAGGATGCCCCCGGCGAGAGCTGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAG 1984  
1960 GAGGAGGCGCTTCCGGGAGGATCGCCACCTTCCAGAGCGCTGGCGGAGATCTCGAG 2019  
1985 GGCATCAGGAGAGGAAACGAGGCGCTGGCACTGCCCTTACACCTTACCTGATCTCCCTC 2044  
2020 GGCATCAGGAGGAGAAACGAGGCGCTGGTGTGCTGCTTACCTTACCTTACCTTCCCTC 2079  
2045 ATTGAGAACAGTGTCTCCATCTTAACTTTTGGAGAAAGAGTCTCTGTGTGACAT 2098  
2080 ATCGAGAACAGCTCTCCATCTTAAATCCAGGGGAAACACAGGGCCAGATGACAT 2133

RESULT 4  
US-09-061-768A-1  
; Sequence 1, Application US/09061768A  
; Patent No. 6204037

GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; APPLICANT: BOEGLIN, WILLIAM E.  
; APPLICANT: JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/061.768A  
; FILING DATE: APRIL 16, 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: NONE  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2685 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: unknown  
; US-09-061-768A-1

Query Match 43.3%; Score 1395.2; DB 3; Length 2685;  
Best Local Similarity 79.8%; Pred. No. 0;  
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

QY 7 GCAGTAGAGAGCTAAACT--GGTCAGGAGATGGGCAAAATGCAGGCTGAGAGTATCCAG 64  
DB 42 GCCGTAGAGAGCTGGACTTAGCTGGCAGCATGGCCGAGTTGAGGTGAGGTGTCACC 101  
QY 65 GGGGAAGCCTGTGGGCTGGCACATGGGACAAAGTGTCTGTGAGCATCTGGGAACCCAC 124  
DB 102 GGAGAAGCCTTCGGGCTGGCACATGGGACAAAGTGTCTGTGAGCATCTGGGAGACCCG 161  
QY 125 GGAGAGAGCCCTTAGTACCTCTGGACCATCTGGGCAAGAGTTGAGCCCGTGTGAA 184  
DB 162 GGAGAGAGCCCCCACTGCCCCCTGGGCAATCTCGGCAAGAGTTCACTGGCGGCTGAG 221  
QY 185 GAAGACTTCGAGTGCAGCTTCCCAAGACGCTAGGACATGCTGCTGATGCTGCGAGTCCAC 244  
DB 222 GAGGACTTCAGGTGACGCTCCCGGAGACGTTAGCCGAGTGTGCTGCTGCGCGTGCAC 281  
QY 245 AAAGCACCCCGGAGAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCTGCTGTGC 304  
DB 282 AAGGCGCCCC--AGTGTGCCCCCTGTGGGCCCCCTGGCCCCGATGCTGCTGTGCTGC 338  
QY 305 CGCTGTTGAGCTGAGTGGCTTACCTGGGCTGCACTCCACTTCCCTGTTATTCAGTGG 364  
DB 339 CGTGTGTTCCAGCTGACACCGCGCGGGCGGCCACTCTCTTCTCCCTGCTACCACTGG 398  
QY 365 CTGGAAGGCGCGGGGAGCTGGTGTCTGAGAGGAGGAGCAGAAAGTGTCTCTGGCAAGAC 424  
DB 399 CTGGAGGGGGCGGGGAGCCCTGTGTGCTGTCAGAGGGGTACAGCCAGAGTGTCTCTGGCAGAC 458



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;
; TELSCOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2685 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-764-246-1

Query Match      43.3%; Score 1395.2; DB 4; Length 2685;
Best Local Similarity 79.8%; Pred. No. 0;
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

QY      7 GCAGTAGAGCTAACT--GGTCAGGAGTGGCCGAATGCAGGGTGAGATGCCAG 64
DB      42 GCGGTAGAGAGCTGGACTTAGGTGCGCAGCATGGCCGAGTTGAGGGTCAAGGTGCCACC 101
QY      65 GGGGAAGCCTGTGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATCGTGGGAACCCAC 124
DB      102 GGNAGAGCCTTCGGGGCTGGCAGCATGGGACAAAGTGTCTGTGAGCATCGTGGGGACCCGG 161
QY      125 GGAGAGAGCCCTTAGTACTCTGGGACCATCTGGGCAAGGATTCAGCCGCCGGTGTGAA 184
DB      162 GGAGAGAGCCCCCACTGCGCCCTTGGACAATCTCGGCAAGAGATTCACTCGGGCGCTGAG 221
QY      185 GAAGACTTCAGGTGAGCGCTTCCCGAGGACGTAGGCACTGTGCTGATGCTGCGATGCCAC 244
DB      222 GAGGACTTCAGGTGAGCGCTTCCCGAGGACGTAGGCGGAGTGTGCTGCTGCGCGTGCAC 281
QY      245 AAAGCACCCTCGGAAGTGTCCCTCCCGCTTATGTCTTTCCGTTCTGATGCTGCTGCTGC 304
DB      282 AAGCGCGCCCC--AGTGTGCCCCCTGTGGGGCCCCCTGGCCCCGATGCCCTGTTCTGC 338
QY      305 CGCTGTTTCAGCTGAGTGGTACTCTGGGGTGTGCACTCCACTTCCCTTGTATCAGTGG 364
DB      339 CGCTGTTTCAGCTGAGCAACCGCGCGGGCGGCCACTCTCTTCCCTGCTACCACTGG 398
QY      365 CTGGAGGGCGGGGAGCTGTGCTGAGAGGGAGCAGCAAGGTGCTTGGCAAGAC 424
DB      399 CTGGAGGGGGCGGGGACCCCTGTGCTGCTGAGGGGTACAGCCAAAGTGTCTTGGGCAGAC 458
QY      425 CATCACCTACACTGCAGGATCAGCCAGAGAGGCTTGAATCCAGGCAAGATGTATC 484
DB      459 CACCACCTGTGCTCAGCAACAGCGCCAGGAGGACTTCAGGCCCGGCGAGGATGTATC 518
QY      485 AGCTGGAAGACTTACATTGAAGGTTGGCTTGGCTTGAACCAAGACTGTGAAGAC 544
DB      519 CAGTGGAAAGGCTTACAAACCCAGGTTGGCTCACTGCTGGATGAAAGACAGTGAAGAC 578
QY      545 TTGGACCTCAACATCAAGTACTCTGCGATGAAGATGCCAACTCTCTTTAAGCCCA 604
DB      579 TTGGAGCTCAATATCAAAATCTCCAAGCCCAAGAAATGCCAACTTTTATCTAAGCTGGC 638
QY      605 TCCGCTATACGAGCTGAAAGTCAAAAGGCTCTCGACCGCACAGACTCTTGGAGGAGT 664
DB      639 TCTGCTTTGCAGAGATGAATAATCAAGGGTGTCTGGAACCGAGGGGCTCTGGAGGAGT 698
QY      665 CTGAGGGAGATGAAGAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGTATGTGTTT 724
DB      699 CTGAATGAGATGAAGAGGATCTTCAACTTCGAGGAGACCCAGCAGCTGAGCAGCGATTT 758
QY      725 GCACACTGGCAGGAAGATGCTCTTTCGCTCCAGTTCCTAATGGCATCAACCCGGTC 784
DB      759 GAGCACTGGCAGGAGATGCTCTTTCGCTCCAGTTCCTGAATGCTCTCAACCCCTGTC 818
QY      785 CTGATTGCGCGTGTCAACAGTCTCCCAACAACTTCCCGGTCACTCATGAATGGTGGCC 844
DB      819 CTGATTCGCGCGCTGTCACTACCTCCCAAGAACTTCCCCGTCACTGATGCCATGGTGGCC 878
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QY      845 CCAGTGTGGGCGCTGGAAACCAAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTTCTTG 904
DB      879 TCATTGTTGGGTCTCTGGGACCAAGCTTGAGGCTGAGCTAGAGAGGGCTCCCTGTTCTTG 938
QY      905 GTGATCATGTCATTTCTTTCTGGAGTCCACACCAATCCTCAATGGAAGGCTCAGTTTC 964
DB      939 GTGGATCAGGCATCTCTCTGGCATCCAGACCAATGTCATTAATGGGAGCCGAGTTTC 998
QY      965 TGTGAGCCCCGATGAGCCCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGTTGCCATT 1024
DB      999 TCTGGGCCCCAAATGACCTTGTATATCCAGAGCCAGGCTGCGGGCGCTGTGCTCTCTC 1058
QY      1025 GCCATCCAGCTCAACACAGACTCCCGGGCGACACACCCATCTTCTCCGCCAGCATGAC 1084
DB      1059 GCCATCCAGCTCAGCAGACACCCCGGCCAAACAGCCCAATCTTCTCGCCCACTGATGAC 1118
QY      1085 ACGTGGGACTGGTGTCTGGCCAAAGACCTGGGTTCCCAATTTCTGAGTTTTATCATCCATGAG 1144
DB      1119 AAGTGGGACTGGTGTCTGGCCAAAGACCTGGGTGCGCAATGCCAGTTTCTCTTCCATGAG 1178
QY      1145 GTGTTCACACATCTGCTGCATGCCCATCTGATTCAGAAAGTCTTTGGCTTGGCCACATTA 1204
DB      1179 GCGCTCAGCAGCTGCTGCATCTCACTCATCTGCTGCTGAGGTCTTCACTGCTGCTACCTCTG 1238
QY      1205 GGTGAGCTGCTAGGTGTCACTCTCTTCAAGCTATTGATTTCTCTCACTTCCGTGACACA 1264
DB      1239 GGTGAGCTGCCCCACTGCGCACTCTCTTCAAGCTGTGATCCCCGACACCCGATACACC 1298
QY      1265 CTGCACATCAACACGCTTGGCCGGAGTGTCTGCTTGGCCCTTGGGAAGTTGATAGACAAG 1324
DB      1299 CTGCACATCAACACACTGCGCCGGAGTGTCTTATCTGTCGACAGGCGAGTGTGGACAGG 1358
QY      1325 TCCACAGGCTTGGCACTGGGGGATTTCTGCACTGTATAAAGAGAAACATGAGAGCTG 1384
DB      1359 TCCACAGGCTCGGCATTTGAAGGCTTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418
QY      1385 AACTACTCTGCTGCTGTCTCCCTGAAATATCCAGAGCCGAGGTGTGGAGACATCCCA 1444
DB      1419 AACTATTCTCTCTGTCTGCTGAGGATATCCCGACCCGAGGAGTTGAAGACATCCCA 1478
QY      1445 GGTACTATTACCGAGATGATGGGATGAGATCTCGGGGGCAATAAAGAGCTTTGCTCTCT 1504
DB      1479 GGTACTACTACCGTGTATGGGATGAGATTTGGGGTGCAGTGGAGCGCTTTGCTCTCT 1538
QY      1505 GAAATAGTCAGCATCTATCTCAAGTGACACATCCGCTCCAAAGATGACCAAGAGCTCCAG 1564
DB      1539 GAAATCATCGGTATCTACTACCCAAAGTGTAGTCTGTCCAAGATGACAGAGAGCTCCAG 1598
QY      1565 GCTGGGTGAGGGAGATCTTCTGAGGGCTTCTCGGCGGCAAGAGCTCAGGTATGCC 1624
DB      1599 GCTGGGTGAGAGAGATCTTCTCAAGGGCTTCTTAAACAGGAGGCTCAGGTATCCCT 1658
QY      1625 TCTTTGTTGGATPACCGGGAAGCCCTGTGTCCAGTATATCACCATGTGTATATTCACCTGC 1684
DB      1659 TCTCACTTGGAGACCCGGAGCCCTGTGTGAGTATGTCAACATGGTGTATTCACCTGC 1718
QY      1685 TCAGCCAAAGCATGACAGCTGTCTCAGTTCAGGCCAGTTCGACTTGTGTTTGGATGCCAAT 1744
DB      1719 TCAGCCAAAGCATGCGGCTGTCACTGTCAGGGCAGTTTGACTCTGCTGTGGATGCCAAC 1778
QY      1745 CTGCCAACCTACATGACAGCTACCACTCTTCCAAAGGCGAGCCCGGCTGAGAGT 1804
DB      1779 CTGCCAACCGATGACAGCTGCGCACCCACCTCCAAAGGGCTGGCAACATGCGAGGGC 1838
QY      1805 TTCTAGCCAGCCTCCAGCAGTTAATTGTCAGAGTTATCACTCATTTGCTCTCTGGCTG 1864
DB      1839 TTCTAGCCACCTCCACCTGTCAATGGCATGTGATGTCTCTCTGCTCTCTGCTGTTG 1898
QY      1865 CTAAAGCGAGAACCTGGGGACCAAGGGCCCTGGGCCACTATCCAGATGAACACTTCA 1924
DB      1899 CTGAGCAAGGAGCCTGGAGACCAAGGGCCCTGGGCCACTATCCGATGAGCACTTCA 1958
QY      1925 GAGGATGCCCCCGGGGAAGCGTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAG 1984
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Db 1959 GAGGAGGCCCCCTCGGGGAGCATCGCCACTTCCAGAGCCGCTGGCCAGCATCTCGAGG 2018  
Qy 1985 GGCATCAGGAGAGAACCGAGCCTGCGCATCGCCCTACACTACTGATCCTCCCTC 2044  
Db 2019 GGCATCCAGGAGCGGAACCGGGGCTGGTGCTGCCCTACACCTACTAGACCTCCCTC 2078  
Qy 2045 ATTGAGACAGTGTCTCCATCTTAACATCTTGAGAGACAGTCTGTGTGACAT 2098  
Db 2079 ATCGAGACAGCGTCTCCATCTTAATCCAGGGGACACAGGCCCCAGATGACAT 2132

## RESULT 6

US-09-949-016-156  
; Sequence 156, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 156  
; LENGTH: 2685  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-156

Query Match 43.3%; Score 1395.2; DB 4; Length 2685;  
Best Local Similarity 79.8%; Pred. No. 0;  
Matches 1671; Conservative 0; Mismatches 418; Indels 5; Gaps 2;

Qy 7 GCAGTAGAGAGCTAACT--GGTCAGGAGGATGGGCAATGCAAGGTGAGATATCCACG 64  
Db 42 GCCGTAGAGAGCTGAGCTAGGCTGGCAGCATGGCGAGTTCAGGGTCAGGTGTCCACC 101  
Qy 65 GGGGAAGCCTGTGGGCTGGCAGCATGGGCAAAAGTGTCTGTCAGCATCGTGGGAACCCAC 124  
Db 102 GGAGAAGCCTTCGGGCTGGGACATGGGCAAAAGTGTCTGTCAGCATCGTGGGACCCGG 161  
Qy 125 GGAGAGAGCCCTTAGTACTCTGGACCATCTGGGCAAGGAGTTCAGGCGCGGTGTGAA 184  
Db 162 GGAGAGAGCCCTTACTGCCCCCTGGACATCTCGGCAAGGAGTTCACTGCGGGCGCTGAG 221  
Qy 185 GAAGACTTCAGGTGACGCTTCCGAGGAGCTAGGCACTGTCTGATGCTGAGTCCGAGTCCAC 244  
Db 222 GAGGACTTCAGGTGACGCTTCCGAGGAGCTAGGCGGAGTCTGCTGCTGCGCGCTGAC 281  
Qy 245 AAAGCACCCCGAGGTGCTTCCGCTTATGTCTTTCCGTTCTGATGCTGCTGCTGCTGCTG 304  
Db 282 AAGGCGCCCC--AGTGTGCCCCCTGTGGGGCCCCCTGGCCCCGGATGCCTTGTCTGCTG 338  
Qy 305 CGCTGGTTCAGGTGAGTGGCTACCTGGGGGTGCACTTCCCTTCTGTTATCAGTGG 364  
Db 339 CGCTGGTTCAGGTGACACCGCGCGGGGCGGCCACCTCTCTTCCCCCTGTCTACAGTGG 398  
Qy 365 CTGGAAGGGGGCGGGAGCTGTGTGTGAGAGGGGAGGAGCAAGGTGTCTTGGCAAGAC 424  
Db 399 CTGGAGGGGGCGGGACCCCTGGTGTGTGAGGAGGAGTACAGCAAGGTGTCTTGGGACAG 458  
Qy 425 CATCACTTACATGAGGATCAGGCGCAGAGAGGAGCTTGTGTCAGGCGAGAGATGTAC 484  
Db 459 CACCACCTTGTCTCCAGCAACAGGCGCCAGGAGGAGCTTTCAGGCCCGGAGAGATGTAC 518

Qy 485 AGCTGGAGAGCTTACATTTGAGGTTGGCTCGCTCGCTTGACCCAGAGACTGTGAAAGAC 544  
Db 519 CAGTGGAGAGGCTTACACACCCAGGTTGGCTCAGCTCCCTGGATGAAAGACAGTGGAAAGAC 578  
Qy 545 TTGACCTTCAACATCAAGTACTCTGCGATGAAGATGCCAAACTCTTCTTTAAAGCCAC 604  
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Qy 665 CTGAGGAGATGAGAAGGCTGTTTAACTTCGCAAGACTCCAGCAGCAGAGATATGTGTTT 724  
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Qy 905 GTGATCATGGCATTTCTTTCTGGAGTCCACACCAACATCTCAATGGAAAGCCTCAGTTC 964  
Db 939 GTGATCAGGCATCTCTCTGGCATCCAGACCAATGTCTTATATGGGAAGCGCAGTTC 998  
Qy 965 TCTGAGCGCGGATGACCTGTTTACACAGAGCTCAGGCTCCGAGCCCTGCTTCCCATTT 1024  
Db 999 TCTGCGGCCCAATGACCTGCTATACAGAGCCAGGCTCGGGCCGCTGTGCTCTCTC 1058  
Qy 1025 GCCATCCAGCTCAACAGACTCCCGGGCCAGACACCCCTCTCTCCGCCAGCGATGAC 1084  
Db 1059 GCCATCCAGCTCAGCAGAGACCCCGGGCCAAACAGCCCCATCTCTCCGCCACTGATGAC 1118  
Qy 1085 ACGTGGGAGCTGTTGCTGGCCAAAGACCTTGGGTTGGCAATCTGAGTTTTTACATCCATGAG 1144  
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Db 1179 GCGCTCAGCAGCTGCTGACTCATCTGCTGCTGAGGTCTTCCACCTGGCTACCTGTG 1238  
Qy 1205 GCTCAGCTGCTAGGTGTCACTCTCTTCAAGCTATTGATTCCTCACAATTCGGTACACA 1264  
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Db 1359 TCCACAGGCATCGGCATTTGAAGGCTTCTCTGAGTTGATACAGAGGAACATGAAGCAGCTG 1418  
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Db 1419 AACTATTTCTCTGTGTGTGTGCTTCCAGTATCCCGACCCCGAGGAGTTGAAAGACATCCCA 1478  
Qy 1445 GGCTACTATTACCGAGATGATGGGATGAGATCTGGGGGGCAATAAAGAGCTTTTCTCTCT 1504  
Db 1479 GGCTACTACTACCGTATGATGGGATGAGATTTGGGGTGCAGTGGAAAGCTTTTCTCTCT 1538  
Qy 1505 GAAATAGTTCAGCATCTACTATCCAAAGTGAACATCCGCTCCAAAGATGACCAAGAGCTCCAG 1564  
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Qy 1565 GCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTTCGGCCGAGAAAGCTCAGGTATGCC 1624

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Db 1599 GCCTGGGTACAGAGATCTTCTCAAGGGTCTCTAAACAGAGAGCTCAGGTATCCCT 1658
Qy 1625 TCCTTGTGTGATACCGGGAAGCCCTGGTCCAGTATATCACCATGTGATATTCACCTGC 1684
Db 1659 TCCTCACTGGAGACCGGGAGCCCTGGTCCAGTATGTCAACATGTGATATTCACCTGC 1718
Qy 1685 TCAGCAAGCATCGAGCTGTCAAGTCCAGGCCAGTTCGATCTTGTGTTGGATGCCAAT 1744
Db 1719 TCAGCCAAAGCATCGCGCTGTCAAGTCCAGGCCAGTTCGATCTTGTGTTGGATGCCAAT 1778
Qy 1745 CTGCGACCTACCATGAGCTACCAACACCTACTTCCAAAGGCCAGGCCCGGCTGAGAT 1804
Db 1779 CTGCCACCCAGCATGAGCTGCCACCAACCAACCTCCAAAGGCCCTGCCAATGCCAGGGC 1838
Qy 1805 TTCAATAGCCACGCTCCAGCAGTAAATGTCTCAAGTTATCAATCATTTCTCTGCGTG 1864
Db 1839 TTCAATAGCCACCTCCACCTGTCAATGCCATGTGATGTCAATCTTCTCTGTTG 1898
Qy 1865 CTAAGCGCAGAACTCGGGACCAAGCCCTGGGCCACTATCCAGATGAACATTCACA 1924
Db 1899 CTGAGCAAGGAGCTGGAGACCAAGGCCCTGGGCACCTATCCGATGAGCACTTCACA 1958
Qy 1925 GAGGATGCCCCCGGGAAGCTGGCTGCTTCCAGAGAAAGTGAATCCAGATCTCCAG 1984
Db 1959 GAGGAGGCCCTCGGGGAGCATCGCCACCTTCCAGAGCCGCTGGCCAGATCTCGAGG 2018
Qy 1985 GGCAATCAGGAGGAGAACCGAGCCCTGGCACTGCCCTACACCTTACCTGTGATCTCCCTC 2044
Db 2019 GGGATCAGGAGCGGAACCGGGGCCCTGTGTGCTGCTTACCTTACCTAGACCTCCCTC 2078
Qy 2045 ATTGAGAAGCTGTCTCCATCTAACATCTTGGAGAGAGACAGTCTGTGTGACAT 2098
Db 2079 ATCGAGAACAGCGTCTCCATCTAAATCCAGGGGGAACACAGGCCAGATGACAT 2132

RESULT 7
US-09-547-435-29
; Sequence 29, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides
; FILE REFERENCE: Encoding the Same
; CURRENT APPLICATION NUMBER: US/09/547,435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 3384
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-29

Query Match 20.5%; Score 659.6; DB 4; Length 3384;
Best Local Similarity 63.9%; Pred. No. 2e-187;
Matches 1014; Conservative 0; Mismatches 569; Indels 3; Gaps 1;

Qy 484 CAGCTCGAAGACTTACATTAAGGTGGCTCGCTGCTTGACCAGAGACTGTGAAAGA 543
Db 1053 CAGTGGGAATCGGTACTCTGCCCGGCTTCCCCATGAAAAATGACATCCCATCCCTGATGTA 1112
Qy 544 CTTGGACCTCAACATCAAGTACTCTCGGATGAAGATGCCAAACTCTTCTTTAAAGCCCA 603
Db 1113 CATGGAGCCCAATGTTTCGATCTACGCCACCAAGACGATCTCGCTGCTTCTCAATGCCAT 1172
Qy 604 CTCGCGGTATACGAGAGCTGAAGTCAAAAGGCTCTCGACCGGACAGGACTCTGGAGGAG 663
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Db 1173 CCCTCGCTCCTTGGGAATGAAGCTTCGAGGGCTGTTGGATCGCAAGGGCTCCTGGAAGAA 1232
Qy 664 TCTGAGGAGATGAGAAGGCTGTTTAACTTCGCAAGACTCCAGACGACGAGATATGTGTT 723
Db 1233 GCTGATGACATGCGAAGACATCTTCTGTGTCATTAAGACCTTTCACGACAAAGTATGTAC 1292
Qy 724 TGCACACTGGCAGGAAGATGCTTTCGCTCCAGTTCCTAAATGGCATCAACCCGGT 783
Db 1293 AGAGCACTGGTGAAGATCACTTCTTTGGGTACCAGTACTCTGAATGGTGTCAATCCCGT 1352
Qy 784 CCTGATTCGCGCTGTCAAGTCTCCCAAAACAACTTCGCGGTCACTGATGAATGTTGTCG 843
Db 1353 CATGCTCAGTCATCTCTAGCTTCCCAAGCTGCTGTCAATGATGATGTTGTCG 1412
Qy 844 CCCAGTGTGGGCCCTTGGAAACCACTGTCAGGCTGAGTTGGAGAAAGGGTCTCCTGTTCT 903
Db 1413 CCCCTGTCTGGGACAGGACACATGCTGACAGACAGCTAGAGAGGGGAAACATCTTCT 1472
Qy 904 GGTGATCATGGCATCTTCTTGGAGTCCAACCAACATCTCTCAATGGAAGACCTCATGTT 963
Db 1473 AGCGGACTACTGGATCTCTGGGGAGGCCCCCAACCACTGCTTAAACGCGCCGACAGTA 1532
Qy 964 CTCTCAGCGCCGATGACCTGTTTACACAGAGCTCAGGCTCCGACCCCTGCTTCCCAT 1023
Db 1533 CGTGGCCGCCCACTGTGCTGCTGAGCTCAGCCCCCAG---GGGGCGCTGGTGCCCTT 1589
Qy 1024 TGCCATCCAGCTCAAAAGACTTCCCGGGCCAGACAAACCCCATCTTCTCGCCAGGATGA 1083
Db 1590 GGCATCCAGCTCAGCAGAGACCCCGGGCTGACAGCCCCCATCTTCTGCCCACATGACTC 1649
Qy 1084 CACGTGGGACTGTGTTGCTGGCCAGAACCTGGGTTGCGAAATCTTGAGTTTATCATCATGA 1143
Db 1650 CGAATGGGACTGGCTGTGGCCAGACGCTGGGTGGCAACTCTGAGTTCTCTGGTCAAGA 1709
Qy 1144 GGCTGTCAACATCTGCTGCATGCCCATCTGATCCAGAGTCTTGTGCTTGGCCACAT 1203
Db 1710 AAACAACACGCACTTCTGTGCAAGCTTGTGCGAGGCTTTCGCGCATGGCCACGCT 1769
Qy 1204 AGTCAAGTCTGCTAGGCTGTCACCTCTCTTCAAGCTATTGATTCTCAATTCGGTACAC 1263
Db 1770 GCGCAGCTGCGCTCTGCCACCCCATCTACAGCTCTCTACTCCCCACACATCGATACAC 1829
Qy 1264 ACTGCACATCAACAGCTTGGCCGGGAGTGTCTGTTGCCCTTGGGAAAGTTGATAGACAA 1323
Db 1830 GGTGAGGTGAACACCATCGGAGGGCCACGCTGCTCAACCCGAGGGCTCTGTGGACCA 1889
Qy 1324 GTCACAGCCCTTGGCACTGGGGATCTCTGACCTGATAAGAGAAACATGGAGACGT 1383
Db 1890 GGTCACTCCATCGGGAGGCAAGGCTCATCTACCTCATGAGACGCGGCTTGGCCACAT 1949
Qy 1384 GAACTACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCC 1443
Db 1950 CACCTACACCAATTTCTGCTTCCGACAGCTGCGGGCCCGCGGCTCTGGCTATGCC 2009
Qy 1444 AGGCTACTATTACCAGATGATGGGATCGAGATCTGGGGGGCAATAAAGAGCTTTGTCTC 1503
Db 2010 CAACTACCCTACCGAGACGCGCTGAAGATCTGGGGGGCCATTGAGAGCTTTGTCTC 2069
Qy 1504 TGAATAGTCAGCATCTACTATCCAAGTGACACATCCGTCAGATGACCAAGACTCCA 1563
Db 2070 AGAAATCGTGGCTACTATTATCCAGGTGACGCATCTGTGACAGCAGGATTCGAGATGCA 2129
Qy 1564 GSCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCGGAGAAAGCTCAGGTATGCC 1623
Db 2130 GSCCTGGACTGGGAGATTTTGTCTCAGCGTCTCTGGCCGGGAAAGCTCAGGTATGCC 2189
Qy 1624 CTCCTTGTGGATACCCCGGAAGCCCTGGTCCAGTATATCACCATGGTGTATTCACCTG 1683
Db 2190 AAGCCGGCTGTGCACCCCGAGGAGAGATGGTGAAGTTCCTCACTGCAATCATCTTCAATTG 2249
Qy 1684 CTCAGCCAGCATGAGCTGTGAGTTGAGCCAGTTCAGCTCTTGTGTTTGGATGCCCA 1743
Db 2250 CTCTGCCAGCAGCTGTCTGTCAACAGTGGGCGATGACTTTGGGGGCTTGGATGCCCA 2309
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Qy	1744	TCTGCCACCTTACCATGCAAGCTTACCAACCACTTCTTCCAAAGGCCGAGGCCCGGCTGTGAGAG	1803
Db	2310	TGCTCCCATCATCTCATGAGCGACGCCCCACCCACAGCAACCAAGGGGACCACCACTCTGAAGAC	2369
Qy	1804	TTTTCATAGCCACGGTCCCCAGCAGTTAATTCGTCAAGTTATCACAATCATTTGCTCTCTCGCT	1863
Db	2370	TTACTTAGACACCTCCCTGAAGTGAACATCAGCTGTAAACAACTCTCTCTTCTTGTT	2429
Qy	1864	GCTAAGCGCAGAACCTGTGGGACCAAAAGSCCCTCGGGCACCTATCCAGATGAACACTTCCAC	1923
Db	2430	GGTTAGCCCAAGAACCCCAAGGACCAAGAGGCCCTCTGGCACCTTACCAGATGAGCACTTCCAC	2489
Qy	1924	AGAGGATGCCCCCGGGGGAACGTGGTGCCTTCCAGAGAAAGCTGATCCAGATCTCCAA	1983
Db	2490	AGAGGAGSCCCCGAGGGCGGAGCATCGCGCCTTCCAGAGCGCGCTGGGCCAGATCTCAAG	2549
Qy	1984	GGGCATCAGGGAGAGGAACCGAGCGCTGGGCATCGCTTACACCTTACCTGGATCTCTCCCT	2043
Db	2550	GGACATCCAGAGGCGGAACCAAGGGTCTGGCACTGCCCTACACCTTACCTGGACCCCTCCCT	2609
Qy	2044	CATTGAGAACAGTCTCTCCATCTTAAC	2069
Db	2610	CATTGAGAACAGTGTCTCCATCTTAAC	2635

## RESULT 8

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US-09-547-435-5
; Sequence 5, Application US/09547435
; Patent No. 6582957
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6582957el Lipoxxygenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/09/547, 435
; CURRENT FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2236
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-547-435-5

```

Query Match 20.4%; Score 658; DB 4; Length 2236;  
Best Local Similarity 63.9%; Pred. No. 4.6e-187;  
Matches 1013; Conservative 0; Mismatches 570; Indels 3; Gaps 1

Qy	484	CAGCTGGAGACTTACATGTGAAGGTTGGCTCGCTGTGACCAAGAGACTGTGAAAGA	543
Db	90	CAGTGGGAATCGGTACCTGCGCGGGCTCCCATGAAATTTGCATCCCATCCCTCATGTA	149
Qy	544	CTTGGACCTCAACATCAAGTACTCTGCGCATGAAGAAATGCAAACTCTCTTTAAAGCCCA	603
Db	150	CATGGAGCCCAATGTTCCGATCTCAGCCACCAGACGATCTCGCTGCTCTTCAATGCCAT	209
Qy	604	CTCCGCGTATACGGAGCTGAAAGTCAAAAGGCTCTTGACCGCA CAGGACTCTGAGGAG	663
Db	210	CCCTGCGCTCTTGGGAATGAAGACTTCGAGGGGCTGTGGATCGCAAGGGCTCCTCGGAAGA	269
Qy	664	TCTCAGGGAGAGATGAGAGGCTGTTTTAACTTCGCGCAAGACTCCAGCAGCAGAGATGTGTGT	723
Db	270	GCTGGATGACATGACGAACATCTTCTGCTGCCATGAACCTTCACGACAAAGTATGTCAAC	329
Qy	724	TGCACACTGGCAGGAAGATGCTCTTTCGCTCCCAAGTTCCTTAATGGGCATCAACCCGGT	783
Db	330	AGAGCACTGGTGTGAAGTCACTCTTTTGGGTACCAAGTACCTGAATGGTGTCAATCCCGT	389

Qy	784	CCTGATTGCGCGCTGTGCACAGTCTCCCAAACAACATCTCCCGGTCTACTGATGAATGATGGTGGC	843
Db	390	CATGCTCCACTGCATCTCTAGCTTTGGCCAGCAAGCTGCCTGTCTACCAATGACATGATGGTGGC	449
Qy	844	CCCAGTCTGGGCCCCGTAACCAAGTCTGCAAGGCTGAGTTGGAGAAAGGCTCCCTGTGTTCTT	903
Db	450	CCCCTTGTGTGGGACAGGACACATGCCCTGCAACACAGAGCTTAGAGAGGGGGAAACATCTTCCT	509
Qy	904	GGTGGATCATGGCATTCTTTCTGGAGTCCACACCAACATCCTCAATGGAAAGCCTCAAGTT	963
Db	510	AGCGGACTACTGGATCTGCGGAGGCCCCCACCCTAGCTGCTTAAGCGCGCCAGCAGTA	569
Qy	964	CTCTGCAGCCCCGATGACCTGTGTTACACAGAGCTCAGGGTCCGGAGCCCTGTGTTCCCAT	1023
Db	570	CGTGGCGCCCCACTGTGCTCTGTGTGGCTCAGCCCCAG--GGGGCGCTGTGTGGTCCCTT	626
Qy	1024	TGCCATCCAGCTCAAAACAGACTCCCGGGCCAGACAACCCCATCTCTGTCGCCACGCGATGA	1083
Db	627	GGCCATCCAGCTCAGCCAGACACCCCGGGCCCTGACAGCCCCATCTTCTTGCCCATGTGACTC	686
Qy	1084	CACGTGGGACTGGTTGCTGGCCAAAGACTGGGTTTCGAAATCTTGAGTTTTTACATCCCATGA	1143
Db	687	CGAATGGGACTGGCTGTGSCCAGACGCTGGGTGCGCAACTCTCTGAGTTCTCTGGTGCA	746
Qy	1144	GGCTGTACACATCTGCTGTGATGCCCATCTGATTCAGAGAGTCTTTTGGCTTTGGGCACATT	1203
Db	747	AAACAACACGCACTTTCTGTGCACGCAATTTGCTGTGCGAGGCCCTTCGCCATGGCCACGGCT	806
Qy	1204	ACGTCAGCTGCCTAGGTGTCAACCTCTCTTTTCAGACTATTGATTTCTCTCACATTTCCGTACAC	1263
Db	807	CGCGCAGCTGCGCGCTGTGCCACACCCCATCTATAAAGCTCTTACTCCCCCACAACCTCGATACAC	866
Qy	1264	ACTGCACATCAACACGCTTGCCCGGGAGCTGCTGTTTGCCCTGGGAAGTTGATAGACAA	1323
Db	867	GCTGCAGGTGAACACATCGGGAGGCCACGCTGCTCAACCCCGAGGGCCTCGTGACCA	926
Qy	1324	GTCCACAGGCTTTGGCATCTGGGGATTTCTCTGACCTGATAAAGAGAAACATGGAGCAGCT	1383
Db	927	GGTCAGCTCATCGGAGGCAAGGCCCTCATCTACTCATGAGCACGGGCTCTGGGCTATCCC	986
Qy	1384	GAACTACTCTGTCTGTCTCTCCCTGAGATATCCGAGCCCGAGGTGTGGAGACATCCC	1443
Db	987	CACCTACACAAATTTCTTGCCCTTCGGACAGCCTCGCGGGCCCGGGCGCTCTGGGCTATCCC	1046
Qy	1444	AGGCTACTATTACCGAGATGATGGGATGCAGATCTCGGGGGGCAATAAAGAGCTTTGTCTC	1503
Db	1047	CAACTACACATACGAGACGACGCTGAAAGATCTTGGGCGGCCATTGAGAGCTTTGTCTC	1106
Qy	1504	TGAAATAGTCAGCATCTACTATCCAAAGTGCACATCCGTCGAAGATGACCAAGAGCTCCA	1563
Db	1107	AGAAATCGTGGGCTACTATTATCCAGTGCAGCATCTGTGCAGCAGGATTCGGAGCTGCA	1166
Qy	1564	GGCCTGGGTAGGGAGATCTTCTGTGAGGCTTCTCTGGCCGAGAAAGCTCAGGTATGCC	1623
Db	1167	GGCCTGAGCATGGCGAGATTTTGTCTCAGGCGTTCTTGCGGCGGGGAAAGCTCAGGTTTCCC	1226
Qy	1624	CTCCTTGTGATACCCGGGAAGCCCTGGTTCAGTATATCACCATGGTGATATTCACTG	1683
Db	1227	AAGCCGCTGTGACCCACAGAGATATGGTGAAGTTCTCTACATGCAATCATCTTCAATTG	1286
Qy	1684	CTCAGCCAAGCATGCAGCTGTGAGTTTCAAGGCCAGTTTCAGCTCTTGTGTTTGGATGCCAA	1743
Db	1287	CTCTGCCACGACGCTGCTGTCAACAGTGGGCGCAGCATGACTTTGGGGCCCTGGATGCCAA	1346
Qy	1744	TCTGCGACCTTACATGACGTACCAACCATCTTCCAAAGGCCAGGCCCGGCCCTGAGAG	1803
Db	1347	TGCTCCATCATCTCATGAGGAGGCCCCACCCACAGACCAAGGGGACCAACCCCTGGAAGAC	1406
Qy	1804	TTTTCATAGCACGCTCCACAGTTAATTCGTCAAGTTATACATCATTTGCTCTCTGSGCT	1863
Db	1407	TTACTTAGACACCCCTCCCTCAAGTGAACATCAGCTGTAAACAACCTCTCTCTTCTGGTT	1466
Qy	1864	GCTAAGCGCAGAACCTGGGACCAAGGGCCCTCTGGGCCACTATCCAGATGAACACTTTCAC	1923

Db 1467 GGTAGCAAGAACCCAGAGACAGAGGCCCTTGGGCACTTACCCAGATGAGCACTTAC 1526  
Qy 1924 AGAGGATGGCCCCCGCGGAGCGTGGCTGCTTCCAGAGAAAAGCTGATCCAGATCTCCAA 1983  
Db 1527 AGAGGAGGCCCGAGGCGGAGCATCGCGCTTCCAGAGCGGCTGGCCCAAGTCTCAAG 1586  
Qy 1984 GGCATCAGGAGAGAGAACCGAGGCTGGCACTGGCCCTACACTAGTGGATCTCCCT 2043  
Db 1587 GGCATCAGGAGGAGAACCGAGGCTGGCACTGGCCCTACACTAGTGGATCTCCCT 1646  
Qy 2044 CATTGAGACAGTGTCTCCATCAAC 2069  
Db 1647 CATTGAGAACAGCGTCTCCATCAAC 1672

RESULT 9  
US-09-547-435-1  
; Sequence 1, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705, 0009-0000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1  
; LENGTH: 2701  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-547-435-1

Query Match 20.4%; Score 658; DB 4; Length 2701;  
Best Local Similarity 63.9%; Pred. No. 5.3e-187;  
Matches 1013; Conservative 0; Mismatches 570; Indels 3; Gaps 1;

Qy 484 CAGCTGGAAAGACTTACATTGAAGGTTGGCTCGCTGCTGTGACCAAGAGACTGTGAAGA 543  
Db 555 CAGTGGAAATCGGTACTCTGCGCGGCTTCCCATGAATAATTGACATCCCATCCCTGATGA 614  
Qy 544 CTTGGACCTCAACATCAAGTACTCTGGGATGAAGATGCGAAACTCTTCTTTAAAGCCCA 603  
Db 615 CATGGAGCCCAATGTTTCGATACTCAGCCACCAAGACGATCTCGCTGCTCTTCAATGCCAT 674  
Qy 604 CTCGCGGTATACGAGCTGAAGCTCAAGGCTCCTGGACCGGACAGGACTCTGGAGGAG 663  
Db 675 CCTGCGTCTTGGGAATGAAGCTTCGAGGAGCTGTTGGATTCGCAAGGGCTCTCTGGAAAGA 734  
Qy 664 TCTGAGGAGATCAGAGGCTGTTTAACTTCCCAAGACTTCCAGCAGCAGAGATATGTGT 723  
Db 735 GCTGGATGATCAGCAACATCTTCTGCTGCCATAGACCTTCCAGCAAGATATGTCAC 794  
Qy 724 TGCACTGTGAGGAGAGAGCTTCTTGGCTCCCAAGTTCCTTAATGGCATCAACCCGGT 783  
Db 795 AGAGCACTGTGTGAAGATCACTTCTTGGTACCAGTACCTGAATGTTGTCAATCCCGT 854  
Qy 784 CTTGATTCGCGCTGTCAAGTCTCCCAACACTTCCCGGTCACTGTGAATGATGATGTTGGC 843  
Db 855 CATGCTCCACTGATCTCTAGCTTGGCCAGCAGCTGCTGTGTCACCAATGACATGATGTCG 914  
Qy 844 CCCAGTGTGGGCGCTTGGAAACAGTCTGAGGCTGAGTTGGAGAGGGCTCTCTGTCTT 903  
Db 915 CCCCTTGTGGGACAGACACATGCTCTGAGACAGAGCTAGAGAGGGGGAACATCTTCT 974  
Qy 904 GTTGGATCATGGCATCTTCTTGGAGTCCACACCAACATCTCTCAATGGAAAGCCTCAGTT 963

Db 975 AGCGACTACTGGATCTGGCGGAGGCCCCACCCACTGCCTTAAAGGGCGGCCAGCAGTA 1034  
Qy 964 CTCTCAGCCCCCGATGACCTCTGTTTACA CAGAGCTCAAGGTCGGAACCCCTGCTTCCCAT 1023  
Db 1035 CGTGGCGGCCCCACTGTGCTGCTGTGGCTCAGCCCCCAG---GGGGGGCTGGTGGCCTT 1091  
Qy 1024 TGCATTCAGCTCAAAACAGACTCCGGGCGCAGAACCCCATCTTCTCTGCCCCAGGATGA 1083  
Db 1092 GSCCATTCAGCTCAGCCAGACCCCGGCGCTGACAGCCCCCATCTTCTCTGCCCATGACTC 1151  
Qy 1084 CACGTGGGACTGTTGCTGGCCAGACCTGGGTTCGCAATTCTGAGTTTATCATCCATGA 1143  
Db 1152 CGAATGGGACTGGCTGCTGGCCAGACGCTGGGTGGCAACTCTGAGTTCTCTGGTGCAG 1211  
Qy 1144 GCGTGTACACATCTGCTGCAATGCCCATCTGATTCAGAAAGTCTTGTGCTTGGCCACAT 1203  
Db 1212 AAACAACACGCACTTTCTGTGCAGCAATTTGCTGTGCGAGGCTTCGCCATGGCCACGCT 1271  
Qy 1204 AGTCACTGCTAGGTGTGACCTCTCTTCAAGTATTTGATTCTCTCAGATTCGGTACAC 1263  
Db 1272 GCGCCAGCTGCGCTCTGCCACCCCATCTACAAGCTCCTACTCCCCCACCACACTCGATAC 1331  
Qy 1264 ACTGCACATCAACACGCTTGGCCGGAGCTGCTGCTGCCCCCTGGGAAAGTTGATAGACA 1323  
Db 1332 GCTGAGGTGAACACCATCGAGGGGCCAGCTGCTCAACCCCGAGGGCTCTGTGACCA 1391  
Qy 1324 GTCCAAGGCTTGGCACTGGGGGATTTCTTGACCTGATAAAGAGAAACATGGAGAGCT 1383  
Db 1392 GGTCAAGTCCATCGGAGGCAAGGCTCATCTACCTCATGAGCAGGGCTTGGCCACTT 1451  
Qy 1384 GAACTACTCTGCTGTGCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAAGACATCCC 1443  
Db 1452 CACCTACACCAATTTCTGCTTCCGAGACGCTGCGGGCCCGCGGCTCTGGCTATCCC 1511  
Qy 1444 AGGCTACTATTACCGAGATGATGGATGCGATCTGGGGGGCAATAAAGAGCTTTGTCTC 1503  
Db 1512 CAACTACCACATCCGAGACGAGCGCTGAAAGATCTGGGGGGCCATTGAGAGCTTTGTCTC 1571  
Qy 1504 TGAATAGTCAAGCATCTACTATCCAAAGTGACACATCCGTCCAAGATGACCAAGAGCTCA 1563  
Db 1572 AGAATCTGGGCTACTATTATCCAGTGACGCACTCTGTGACAGAGGATTCGGAGCTGCA 1631  
Qy 1564 GGCCTGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGGCGCAGAAAGCTCAGGTATGCC 1623  
Db 1632 GGCCTGGACTGCGGAGATTTTGTCTCAGGCGTTCCTGGGCGGGAAGCTCAGGTTTCCC 1691  
Qy 1624 CTCCTTGTGGATACCGGGAGCCCTGTCAGTATATCACTGTTGATATCACCTG 1683  
Db 1692 AAGCGGCTGTGCACCCCGAGGAGATGGTGAAGTTCCTCACTGCAATCATCTTCAATTG 1751  
Qy 1684 CTCAGCCAAAGCATGCACTGTCAAGTTCAGGCGCAGTTCGACTCTTGTGTTGGATGCCCAA 1743  
Db 1752 CTCGCCACAGCCTGCTGTCAAGTGGGAGCATGACTTTGGGGCTTGGATGCCCA 1811  
Qy 1744 TCTGCCACTTACATGCAAGTACCAACCACTATTTCCAAAGGCCAGGCCGCCCTGAGAG 1803  
Db 1812 TGCTCCATCATCATGAGGAGCCGCCACCCAGACCAAGGGGACCAACACCTGAAAGAC 1871  
Qy 1804 TTTCTAGCAGCTCCCGAGCGATTAATTCGTCAGTTATCACTCATTTGCTCTCTGGCT 1863  
Db 1872 TTACCTAGACACCTTCCCTGAGTGAACATCAGCTGTAAACAACTCTCTCTCTTCTGGTT 1931  
Qy 1864 GCTAAGCGCAGAACTGGGGACCAAGGCCCTGGGCCACTATCCAGATGAACACTTTCAC 1923  
Db 1932 GGTAGCCAGAAACCAAGGACAGAGGCCCTGGGACCTTACCAGATGAGCACTTTCAC 1991  
Qy 1924 AGAGGATCCCCCGCGGAGCGTGGCTGCCCTTCCAGAGAAAGTGAATCCAGATCTCCAA 1983  
Db 1992 AGAGGAGGCCCGAGGCGAGCATCGCGCTTCCAGAGCGCCCTGGCCAGATCTCAAG 2051  
Qy 1984 GGGCATCAGGAGAGAACCGGAGGCTGGCACTGGCTACACTACCTACCTGGATCTCCCT 2043  
Db 2052 GGACATCCAGGAGCGGAACACAGGGTCTGGCACTGCCCTACACTACCTACCTGGACCTCCCT 2111

QY 2044 CATTGAGAACAGTGTCTCCATCTAAC 2069  
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Db 2112 CATTGAGAACAGCGTCTCCATCTAAC 2137

## RESULT 10

US-09-799-451-803  
; Sequence 803, Application US/09799451  
; Patent No. 6783969  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Kyle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yungqing  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 803  
; LENGTH: 2307  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (172)..(2304)  
US-09-799-451-803

Query Match 20.4%; Score 657; DB 4; Length 2307;

Best Local Similarity 53.8%; Pred. No. 9.4e-187; Mismatches 570; Indels 3; Gaps 1;

Matches 1012; Conservative 0; Mismatches 570; Indels 3; Gaps 1;

QY 484 CAGCTGGAAGACTTACATTGAAGGTTGGCTCGCTCGCTTGACACGAGACTGTGAAAGA 543  
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Db 726 CAGTGGGAATCGGTACCTGCCCGCTTCCCATGAAATTGACATCCCATCCCTGATGTA 785

QY 544 CTGGAACCTCAACATCAAGTACTCTGCGATGAAGAAATGCCAACTCTCTTTAAAGCCCA 603  
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Db 786 CATGGAGCCCAATGTTTCGATACTACGCCACCAAGACGATCTCGCTGCTCTTCAATGCCAT 845

QY 604 CTCGCGTATACGAGCTGAAGTCAAGGGCTCTCGACCGCACAGGACTCTGGAGGAG 663  
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Db 846 CCCTCGCTCTTGGGAATGAAGCTTCGAGGGCTGTGTGATCGAAGGGCTCTCGGAAGA 905

QY 664 TCTGAGGAGATGAGAAGGCTGTTTAACTTCGCGAAGACTCCAGCAGCAGAGATGTGT 723  
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Db 906 GCTGGATGACATGCAGAACATCTTCTGCTGTCATGAACCTTCACGACAAAGATATGTAC 965

QY 724 TGCACTGTGGCAGGAAGATGCTCTTCTGCTCCAGTTCCTAAATGGCATCAACCCGGT 783  
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Db 966 AGAGCACTGGTGAAGATCACTTCTTGGGTACCACTACCTGAATGTGTCTCAATCCCGT 1025

QY 784 CTGATTCGCGCTGTACAGTCTCCCAAGAACTTCCCGGTCACTGATGAATGGTGGC 843  
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Db 1026 CATGCTCACTGCTCTTAGCTTCCCGCAGCAAGCTGTCTGTCACTCAATGATGATGGC 1085

QY 844 CCCAGTCTGGGCCCTGGAACCACTCTGAGGCTGAGTTGGAGAGGGCTCCCTGTTCTT 903  
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Db 1086 CCCCTTGGACAGACATCGCTGACAGAGAGCTAGAGAGGGGAAACATCTTCTT 1145

QY 904 GGTGATCATGGCATTCTTTCTGAGTCCACACCAATCCTCAATGGAAGACCTCAGTT 963  
|||||  
Db 1146 AGCGGACTACTGGATCTTGGGAGGGCCCCACCACTGCTTAAACGGCCGACGACTA 1205

QY 964 CTCTGACGCCCCGATGACCTGTTTACACAGAGCTCAGGGTCCGGACCCCTGTTCCCAT 1023  
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Db 1206 CGTGGCGCCCCACTGTGCTGCTGTGCTCAGCCCCCAG---GGGGCGCTGGTGGCTT 1262

QY 1024 TGCCATCCAGCTCAAAAGACTCCGGGGCCAGACAAACCCATCTTCTGCGCCAGGATGA 1083  
|||||  
Db 1263 GGCCATCCAGCTCAGCCAGACCCCGGGCTGTGACAGCCCCATCTTCTGCCCCACTGACTC 1322

QY 1084 CACGTGGGACTGTTGCTGGCCAAAGACTGCGGTTCGCAATCTGAGATTTTATCATCATGA 1143  
|||||  
Db 1323 CGAATGGGACTGGCTGTGCGCAAGACGTGGTGGCNACTCTGAGTTCCTGGTGACGA 1382

QY 1144 GGCTGTCAACATCTGCTGCATGCCCATCTGATTCCAGAACTCTTGTGCTTGGCCACATT 1203  
|||||  
Db 1383 AAACAACAGCACTTCTGTGACGCACTTGTGTGCGAGGCTTGGCATGGCCACGCT 1442

QY 1204 AGTCACTGCTAGGTGTCACTCTTCAAGCTATTGATTCCTCACTTCGCTACAC 1263  
|||||  
Db 1443 GCGCAGCTGCGCTCTGCCCCACCCCATCTACAGCTCTCTCTCCCCACACTCGATATAC 1502

QY 1264 ACTGCATCAACAGCTTGGCCGGGAGCTCTGTTGCCCTCGGMAAGTTGATAGACAA 1323  
|||||  
Db 1503 GCTGAGGTGAACACATCGCGAGGGCCACGCTGCTCAACCCGAGGGCTCTGTGACCA 1562

QY 1324 GTCCACAGGCTTGGCCTGCGGGAATCTCTGACCTGATTAAGAGAAACATGGAGCAGCT 1383  
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Db 1563 GGTCACTGCTTCCAGGAGCAAGGCTCATCTACTCATGAGCAGGGCTCTGGCCACTT 1622

QY 1384 GAATCTCTGCTGCTCTTCCCTGAAGATATCGAGCCCGAGGTGTGGAGACATCCC 1443  
|||||  
Db 1623 CACCTACACCAATTTCTGCTTCCGCGACAGCTCTGCGGCGCGCGCTCTGGCTATCCC 1682

QY 1444 AGGCTACTATTACCGAGATGATGGATGACATCTGCGGGGCAATAAAGAGCTTGTCTC 1503  
|||||  
Db 1683 CAATACCACTACCGAGACAGCGCTGAAGATCTGGGCGGCCATTTGAGAGCTTGTCTC 1742

QY 1504 TGAATAGTCAGCATCTACTATCCAAGTGACACATCCGTCCAAGATGACCAAGAGCTCCA 1563  
|||||  
Db 1743 AGAATCGTGGCTACTATTATCCAGTGACGATCTGTGAGCAGGATTCGGAGCTGCA 1802

QY 1564 GGCCTGGGTGAGGAGATCTTCTCTGAGGGTCTCTGCGCCGAGAAAGCTCAGGTATGCC 1623  
|||||  
Db 1803 GGCCTGGACTGGCGAGATTTTGTCTAGGCGTCTCTGCGCGGGGAAAGCTCAGGTTTCCC 1862

QY 1624 CTCCTTGTGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGATGATATTCACCTG 1683  
|||||  
Db 1863 AAGCGGCTGTGACCCCGAGGAGATGTTGAAGTTCCTACTGCAATCATCTTCAATTG 1922

QY 1684 CTCAGCCAAAGCATCAGCTGTGCTCAGTTCAGGCGCAGTTCGACTCTTGTGTTGGATGCCAA 1743  
|||||  
Db 1923 CTCTGCCAGCAGCCTGCTGTCAACAGTGGGAGCATGACTTTGGGGCTTGATGCCCAA 1982

QY 1744 TCTGCCACTTACCATGACGCTACACCACTTCTTCCAAAGCCAGGCGCGGCTGAGAG 1803  
|||||  
Db 1983 TGCTCCATCATCTAGGCGAGCCCCACCCCGACCAAGGGGACCAACCCCTCGAAGAC 2042

QY 1804 TTTTATAGCAGCTCCCGCAGGTTAATTCTGCAAGTTATCAGATTCATTCCTCTGCTGCT 1863  
|||||  
Db 2043 TTACTAGACACCTCTCTGAAAGTGAACATCAGCTGTAAACAACTCTCTCTCTCTGCTG 2102

QY 1864 GCTAAGCGCAGAACTGGGGACCAAGGCCCTCTGGGCACTTATCCAGATGAACACTTCCAC 1923  
|||||  
Db 2103 GGTAGCCAGAACCCAGGACGAGGCGCTCTGGGACCTTACCCAGATGAGCACTTCCAC 2162

QY 1924 AGAGGATGCCCCCGGCGAAGCGTGGCTTCCAGAGAAAGCTGTATCCAGATCTCCAA 1983





RESULT 12  
US-09-087-727-1  
; Sequence 1, Application US/09087727A  
; Patent No. 6103496  
; GENERAL INFORMATION:  
; APPLICANT: Brash, Alan R  
; APPLICANT: Boeglin, William E  
; APPLICANT: Kim, Richard B  
; TITLE OF INVENTION: Isolated and Purified 12R-Lipoxygenase Protein and  
; FILE OF INVENTION: Nucleic Acids  
; FILE REFERENCE: Attorney Docket No. 6103496 1242-7  
; CURRENT APPLICATION NUMBER: US/09/087,727A  
; CURRENT FILING DATE: 1998-05-29  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 2469  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (260)..(2362)  
US-09-087-727-1

Query Match 17.5%; Score 565.8; DB 3; Length 2469;  
Best Local Similarity 60.3%; Pred. No. 3.1e-159;  
Matches 955; Conservative 0; Mismatches 627; Indels 3; Gaps 1;

QY	488	TGGAAGACTTACATGAAGTTGGCTCGCTGCTTGACCGAGGACTGTGAAGACTTG	547
DB	788	TGGAATGGCTATATCCGGGATTCCTCAATTCATCAACTTAAAGGCCACCAAGTTCCTG	847
QY	548	GACCTCAACATCAAGTACTCTGCGATGAAGATGCCAACTCTCTTTAAAGCCCACTCC	607
DB	848	AACCTTAATCTCGCTACTCTCTCTCAAGCGGCTCTCTCTGTCGGCTGGGGGCC	907
QY	608	CGGTACGAGAGCTGAAGTCAAGGGCTCTCGGACCGCAGAGACTCTGGAGGAGTCTG	667
DB	908	ATGGCACTGGCTTTCAAGTCCGGGCTGTGGACTGCAAACTTCGTGGGAAGAGGCTG	967
QY	668	AGGAGATGAGAGGCTGTAACTTCGCGAAGACTCAGCAGAGAGATGTGTTGCA	727
DB	968	AAGGACATTAGGAAATTTTCCCTGGCAAGAAATCTGCTGCTCGAGTACGTGGCCGAG	1027
QY	728	CACGTGGAGGAGATGCTCTTTCGCTCCCAAGTTCTTAAATGGCATCAACCGGTCTG	787
DB	1028	CACGTGGAGGAGACACTTCTTTGGTACCAATACCTCAACGGGCTCAACCCGGCCTG	1087
QY	788	ATTCGCCGCTGTCAAGTCTCCCAACAACTTCCCGGTCACTGATGAATGGTGGCCCA	847
DB	1088	ATCCGCCGCTGACCGGATCCAGCAAGTTCCCGGTCCAGACGACATGGTGGCTCG	1147
QY	848	GTGCTGGGCGCTGGAAACAGTCTGAGGCTGAGTGGAGAGGGCTCCCTGTTCTGGTG	907
DB	1148	TTCTCTGGGCGAGGAAACGTGCTTGAAGCGAGCTGGAGAGGGGAAATTTACCTGGCC	1207
QY	908	GATCATGCAATCTTCTGAGTCCACACCAACATCTCTCAATGGAAAGCTCAGTTCTCT	967
DB	1208	GACTACCGCATCATGGAGGGGATCCCAACCGTGGAGCTCAGCGCGGAAGCAGCAC	1267
QY	968	GCAGCCCGGATGACCTGTATACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCAATGCC	1027
DB	1268	TGCGCCCCCTCTGCTGCTGACATTTGACCCGAG---GGCAAGATGATGCCATCGCC	1324
QY	1028	ATCCAGCTCAACAGATCTCCGGGGCCAGAACCCCATCTTCTTCCGCCAGGATGACAG	1087
DB	1325	ATCCAGCTCAGCAGACCCCTGGGCGAGATTTGCCCATCTTCTTCCGCCAGTATCTGAG	1384
QY	1088	TGGAGCTGGTGGTGGCAAGCTGGGTTGGCAATTTGATTTTACATCATGAGGCT	1147
DB	1385	TGGGACTGGCTGCTAGCCCAAGAGCTGGGTACGCTATGCGGAGTTCTACAGCCAGGCC	1444

QY	1148	GTACACATCTGCTGCATGCCCATCTGATTCAGAGCTTTTGGCTTGGCCACATTAGT	1207
DB	1445	ATGCCCACTGCTGGAGACACACTTATGCTGAGGCTTTTGCCTGGCTTGTGAGG	1504
QY	1208	CAGCTGCTAGTGTACCCCTCTCTTCAAGTATTTGATTTCTCATTTCTGGTACACACTG	1267
DB	1505	AACCTGCCATGTGCCACCCCTCTCAAGTCTCTCATCCCCCATACCCGATACACCGTC	1564
QY	1268	CACATCAACAGCTTGGCCGGAGCTGCTGCTGGCCCTGGGAAGTTGATAGAACGTC	1327
DB	1565	CAGATCAACAGCAATGGCCGGGCGTTCTCTCAATGAGGGGGGCTCTCTGCCAAGGC	1624
QY	1328	ACAGCCTTGGCACTGGGGGATTTCTGACCTGTAAAGAGAAACATGGAGCAGTGAAC	1387
DB	1625	ATGTCCTGGGCGTGGAAAGGCTTTGCTGGGGTGTGTACGGGCTCTGTGCGAGCTACC	1684
QY	1388	TACTCTGTCTGTCTCTCCCTGAAGATATCCGAGCCCGAGGTGTGGAAGACATCCAGGC	1447
DB	1685	TATGACAGCTCTTACCTCCCAATGACTTTGTGAGCGTGGGTCCAGGACTGCTGGA	1744
QY	1448	TACTATTACGAGATGATGGGATGAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAA	1507
DB	1745	TATTACTAGCGGATGACAGCTTGGCGGTGTGGAATGCACCTGGAGAAGTATGTGACGAG	1804
QY	1508	ATAGTACGATCTACTATCCAGTGAACATCCGTCAGATGACATCCGTCAGATGACCAAGCTCCAGGCC	1567
DB	1805	ATCATCACTATTATTATCCCGAGTGACGACCGTGGAGGGTGTATCCGGAATTCAGTCT	1864
QY	1568	TGGGTGAGGAGATCTTCTCTGAGGGCTTCTCGCGCGAGAAAGCTCAGGTATGCCCTCC	1627
DB	1865	TGGGTGAGGAGATTTTAAAGAGTCTCTCGCGCGGAGAGCTCAGGTATGCCCTAGG	1924
QY	1628	TTGTTGATATCCCGGAGCCCTGCTCCAGTATATCACTATGATATTCACCTGTCTCA	1687
DB	1925	TGCTTGGACCGTGGCTGAGCTGATCGATATGTCACTATAGTATCTACACCTGTCT	1984
QY	1688	GCAAGAGTACGCTGCTCAGTTTCAAGGCGAGTTCGACTCTTGTGTTGATGCCAATCTG	1747
DB	1985	GCCAAGCAGCTGCTGTCAACACAGGCGAGATGGAGTTTCCCGCTGGATGCCAACTTC	2044
QY	1748	CCACTACCATGACGATACCAACCTTCTTCCAAAGCCAGGCCCGCTGAGAGTTTC	1807
DB	2045	CCAGCTCATGCGGAATCCACCGATTCAGACTAGGGGCTGACCACTTGGAGACCTTC	2104
QY	1808	ATAGCCAGCTCCAGCAGTTTAAATTCGTCAAGTTTATCACTATTTGCTCTCTGGCTGTA	1867
DB	2105	ATGACAGCTTGGCGGATGTGAACACCACTGTCATCAGCTGCTGGTGTCTCTGGACCTTC	2164
QY	1868	AGCGAGAACTGGGGACCAAGGCCCTTGGGCCACTATCCAGATGAACACTTTCACAGAG	1927
DB	2165	AGCGAGAGCTGACGACGAGCGGCCCTGGGACACTTCCCGGACATTCACCTTCGTGGAG	2224
QY	1928	GATGCCCGCGGAGAGCTGGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAGGC	1987
DB	2225	GAGCCCGCGGAGAGAGATAGAGCGCTTCCGCGAGCGCTTGAACAGATCTCAACAGAC	2284
QY	1988	ATCAGGAGAGAGAACCGAGGCTTGGCTTCCCTTACACTTACCTGGATCTTCCCTCAT	2047
DB	2285	ATCCGCGAGCAACAGTGGCTTCCCATCCCTTACTACTTACCTGGACCGGCTGTGAT	2344
QY	2048	GAGAACAGTGTCTCCATCTAACATC	2072
DB	2345	GAGAACAGCATTTCTATTAGGAGC	2369

RESULT 13  
US-09-853-053-1  
; Sequence 1, Application US/09853053  
; Patent No. 656964  
; GENERAL INFORMATION:  
; APPLICANT: Brash, Alan  
; APPLICANT: Boeglin, William

Query Match	17.5%	Score 565.8	DB 4	Length 2469
Best Local Similarity	60.3%	Pred. No. 3.1e-159		
Matches 955	Conservative 0	Mismatches 627	Indels 3	Gaps 1
Qy	488	TGGAAGACTTTACATTGAAGCTTGGSCCTCGCTGCTTCACACAGAGACTGTGAAGAAGCTTG	547	
Db	788	TGGAATGGCTATATTCCGGGAATTCCTCAATTTCTATCAACTTTAAGGCCACCAAGTTCTTG	847	
Qy	548	GACCTCAACATCAAGTACTCTGCGATGAAGAATGCCAAATCTTTCTTTAAAGCCCACTCC	607	
Db	848	AACTTAAATCTCGCTACTCTTCTCTCAAGACGSCCTCTTCTTCTTGGTCCGCTGGGGCCC	907	
Qy	608	CGGTATACGAGCTGAAGTCAAAAGGCTCTTGACCGCACAGAGACTCTCGAGGAGTCTG	667	
Db	908	ATGGCACTGGCTTTCAAAGTCCGGGCTGTGGAGTGCAAACATTCGTGGAAAGAGGCTG	967	
Qy	668	AGGGAGATGAAGAAGCTGTGTTAACTTCGCAAGAAGCTCCAGCAGCAGAGTATGTGTTGCA	727	
Db	968	AAGGACATTAGGAATAATTTCCCTGGCAAGNAATCTGTCTCTCGAGTACGTGGCCGAG	1027	
Qy	728	CATCGGAGGAAGATGCTTTCTTGCCCTCCAGTTCCTTAAATGGCATCAACCCGGTCTTG	787	
Db	1028	CACCTGGGCAGAGACACTTTCTTTGGGTACGAGTACCTCAACGGCGTCAACCCCGGGCTG	1087	
Qy	788	ATTTCGCGCTGTCAAGCTCTCCAAACAACTTCCCGGTCACTGATGAATGTTGGGCCCA	847	
Db	1088	ATCGCCGCTGACGCGGATCCACAGACAGTTCCCGTCAAGACGACATGGTGGCTCCG	1147	
Qy	848	GTGCTGGGCCCTGGAAACAGTCTGCAGGCTGAGTTGGAGAAGGCTCCCTGTGTTCTGGTG	907	
Db	1148	TTCTGGGCGAGGGAACGTGCTTGCAAGCGAGCTGGAGAAGGGAACATTTACCTGGCC	1207	
Qy	908	GATCATGGCATTTCTTCTGGAGTCCACCAACATCTCTCAATGGAAGACCTCAGTTCTCT	967	
Db	1208	GACTACCGCATCATGGAGGCGATCCCCACCGTGGAGCTCAGCGGCGGGAAGCAGCACAC	1267	
Qy	968	GCAGGCCCGATGACCCCTGTTTACACAGAGCTCAGGGTCCGAGCCCTGCTTCCCATGGCC	1027	
Db	1268	TGCGCCCCCTCTGCTGCTGCTGCACTTTGGACCCGAG--GGCAAGATGATGCCATGCC	1324	
Qy	1028	ATCAGGCTCAAAAGACTCCCGGCGCAGACAAACCCCATCTTCTTGCCACGGAATGACACG	1087	
Db	1325	ATCAGCTCAGCCAGACCCCTGGGCGCAGATTGGCCCATCTTCTCTGCCAGTGATTTCTGAG	1384	
Qy	1088	TGGAGCTGGTTGCTGGCCAGAGACTGGGTTGCGGAATTTCTGAGTTTATCATCCATGAGGCT	1147	
Db	1385	TGGAGCTGGCTGTAGCCCAAGAGTGGGTACGCTATGCGGAGTTCTACAGCCACGAGGCC	1444	
Qy	1148	GTCAACATCTGCTGCAATGCCCATCTGATTTCCAGAAGTCTTTGCTTTGGGCCACATTACGT	1207	
Db	1445	ATCGCCACCTGCTGGAGACACACTTATGCTGAGGCTTCTGCTCTGGCTTGTCTGAGG	1504	
Qy	1208	CAGTCTGCTAGGTGTCAACCTCTCTTCAAGATATTGATTCGTCAATTCGGTACACACTG	1267	
Db	1505	AACTTGCCCATGTGCCACCCCTCTCAAGGCTCCTCATCCCCCATACCCGATACACCGTC	1564	
Qy	1268	CACATCAACAGCTTGCCTGGGAGCTGCTGTTGSCCCCTCGGAAGTTGATAGACAAGTCC	1327	

NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 155  
; LENGTH: 2469  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-155

Query Match 17.5%; Score 565.8; DB 4; Length 2469;  
Best Local Similarity 60.3%; Pred. No. 3.1e-159;  
Matches 955; Conservative 0; Mismatches 627; Indels 3; Gaps 1;

QY 488 TGGAGAGCTTACATGAAAGTTGGCTCGCTCGCTTGACACGACACTGTGAAGACTTG 547  
DB 788 TGGATGCTATATCCGGATTCCTCAATTCATCACTTTAAGGCCACCAAGTTCCTG 847  
QY 548 GACCTCAACATCAAGTACTCTCGATGAAGATGCCAAACTCTCTTTAAAGCCCACTCC 607  
DB 848 AACTTAAATCTCCGCTACTCTCTTCAAGACGGCTCTCTTCTCGTCCGCTGGGGCC 907  
QY 608 GGTATACGGAGCTGAAAGTCAAGGGCTCTGGAACCGACAGGACTCTGGAGGAGTCTG 667  
DB 908 ATGGCACTGGCTTTCAAGAGTCGGCGCTGTGGACTGCAAACTTCGTGGAAGAGGCTG 967  
QY 668 AGGAGATGAGAAGCTGTAACTTCCGCAAGACTCCAGCAGCAGAGTATGTGTTGCA 727  
DB 968 AAGGACATTAGGAATTTTCCCTGGCAAGAAATCTGCTGCGAGTACGTGGCCGAG 1027  
QY 728 CACTGGCAGGAAGTGCCTCTTTCCTCCCTCCAGTTCTTAATGGCATCAACCCGGTCCG 787  
DB 1028 CACTGGCAGGAGACCTCTTTGGGTACAGTACTCAAGGGGTCAAACCCGGCTG 1087  
QY 788 ATTGCGCGCTGTCAGTCTCCCAACAACTTCCGGTCACTGATGAATGGTGGCCCA 847  
DB 1088 ATCCGCGCTGCACGCGATCCAGCAAGTTCCCGTCAAGAGCAGATGTGCTGCTCG 1147  
QY 848 GTGCTGGCCCTGGAGCAGTCTGAGCTGAGTTGGAGAGGGCTCTCTGTTGCTG 907  
DB 1148 TTCTTGGCGAGGAACTGTTTGAAGCGAGCTGGAGAGGGGAACTTTACCTGGCC 1207  
QY 908 GATCATGTCATTTCTTGTGAGTCCACCAACATCTCAATGGAAGCCCTCAGTTCTCT 967  
DB 1208 GACTACCGCATATGGAGGGCATCCCACTGGAGTCAAGCGCGGAGCAGCACCAC 1267  
QY 968 GCAGCCCGCATGACCTGTTTACACAGAGCTGAGGGTCCGACCCCTGCTCCCATGCC 1027  
DB 1268 TGGCGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1324  
QY 1028 ATCCAGCTCAACAGACTCCCGGCGCAGACACCCCATCTTCTGCGCAGCATGACAG 1087  
DB 1325 ATCCAGCTCAGCAGACCCCTGGGCGCATTTGCCCCATCTTCTGCGCAGTATCTGAG 1384  
QY 1088 TGGGACTGTTGCTGGCAGACCTGGGTTGCGAATCTGAGTTTACATCATGAGCT 1147  
DB 1385 TGGGACTGTTGCTAGCAGCAGCTGGGTTGCGAATCTGAGTTTACATCATGAGCT 1444  
QY 1148 GTCACATCTGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1207  
DB 1445 ATGCGCCACCTGCTGAGACACACCTCATTTGAGAGCTTTGCTGCTGCTGCTGCTG 1504  
QY 1208 CAGCTGCTAGTGTACCTCTCTTCAAGCTATTTGATTCCTACATTCGGTACACATG 1267  
DB 1505 AACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1564  
QY 1268 CACATCAACAGCTTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1327  
DB 1565 CAGATCAACAGCTTGGCGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1624  
QY 1328 ACAGGCTTGGCAGCTGGGGGATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1387  
DB 1625 ATGCTGCTGGCGTGAAGGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1684  
QY 1388 TACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1447

DB 1685 TATGACAGCTCTACCTCCCCCAATGACTTTGTGGAGCGTGGGTCCAGGACTGCTGCTGA 1744  
QY 1448 TACTATTACCGAGATGATGGAGTGCAGATCTGGGGGCAATAAAGAGCTTTGTCTCTGAA 1507  
DB 1745 TATTACTACCGGATGACAGCTTGGCGGTGTGGAATGCACTGGAGAGTATGTGACGGAG 1804  
QY 1508 ATAGTACGATCTACTATCCAAAGTGACACATCCCTCCAAAGATGACCAAGAGCTCCAGGCC 1567  
DB 1805 ATCATCACCTATTATTATCCCGAGTGAACGAGCCGTGGAGGTGATCCGGAATTCAGTCT 1864  
QY 1568 TGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGAGTATGCCCTCC 1627  
DB 1865 TGGGTGAGGAAATATTTAAAGAGTGCCTCTCTGGGGCGGAGAGCTCAGGCTTCCCTAGG 1924  
QY 1628 TTGTTGANTACCCGGGAAGCCCTGGTCCAGTATATCACTATGATGATATTCACCTGCTCA 1687  
DB 1925 TGTCTGGAAACCGTGCCTGAGCTGATCCGATATGATATGATATGATATGATATGATAT 1984  
QY 1688 GCCAAGCATGCGCTGCTGCTGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1747  
DB 1985 GCCAAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2044  
QY 1748 CCACCTACCATGAGCTTACCAACCTACTTCCAAAGCCAGGCCCGCTGAGAGTTTC 1807  
DB 2045 CCAGCTGCTCATCGGAATCCACCGATTCAGACTAAGGGGCTGACCACTCTGGAGACCTTC 2104  
QY 1808 ATAGCCAGCTCCAGCAGTAAATTCGTCAAGTTTATCACATCATTCGTCTCTGCGTCTA 1867  
DB 2105 ATGACACGCTTGGCGGATGTGAACACAGCTGATCATCGCTGCTGCTGCTGCTGCTGCTG 2164  
QY 1868 AGCCAGAACTGGGGACAAAGGCCCTTGGGCCACTATCCAGATGAACACTTCCAGAG 1927  
DB 2165 AGCCGAGAGCTGACGACAGCGGCCCTTGGGACACTTCCCGGACATTCACCTTCGTGGAG 2224  
QY 1928 GATCCCCCGGCGAAGCTGCTGCTTCCAGAGAAAGCTGATCCAGATCTCCAAAGGCG 1987  
DB 2225 GAGCCCTCGGAGAGCATAGAGCGCTTCCGCGAGCGCTGACCACTGACCACTCTCACAG 2284  
QY 1988 ATAGGAGAGGAAACCGAGGCTTGGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2047  
DB 2285 ATCCGCGAGCGCAACAAGTGCCTTCCCATCCCTTACTACTGAGCCCGGTGCTGATT 2344  
QY 2048 GAGAACAGTGTCTCATCTAACATC 2072  
DB 2345 GAGAACAGCATTTCTATTAGGAGC 2369

## RESULT 15

US-09-547-435-11  
; Sequence 11, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
; FILE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705.0009-00000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 1383  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-547-435-11

Query Match 14.5%; Score 466.2; DB 4; Length 1383;  
Best Local Similarity 61.4%; Pred. No. 2.2e-129;

Matches		766;	Conservative	0;	Mismatches	478;	Indels	3;	Gaps	1;
QY	484	CAGCTGGAAAGACTTACATTAAGAGTTGGCTCGCTCGCTTGACACAGAGACTGTGAAGA	543							
Db	90	CAGTGGAAATCGGTACTCTCCCGGCTTCCCATGAAATTTGACATCCCATCCTGATGTA	149							
QY	544	CTTGGACCTCAACATCAGTACTCTCGATGAAGAATGCCAAACTCTTCTTAAAGCCCA	603							
Db	150	CATGGAGCCCAATGTTTCGATACTTCAGCCACCAAGACGATCTCGCTCTCTCAATGCCAT	209							
QY	604	CTCCGGTATACGGAGCTCAAAAGTCAAAAGGGCTCTGGAGCCGACAGGACTCTGGAGGAG	663							
Db	210	CCCTGGCTCCTTGGGAATGAAGCTTCGAGGGCTTGTGGATCGAAGGGCTCTGGAAGAA	269							
QY	664	TCTGAGGGAGATGAGAAGCTGTTTAACTTCCGAGAGACTCCAGCAGCAGAGATATGTGT	723							
Db	270	GCTGGATGACATGCAGAACATCTTCTGGTGCATAGACCTTTCACGACAAAGTATGTAC	329							
QY	724	TGACACTGGCAGGAAGATGCCTTCTTCGCCCTCCGAGTTCCTTAATGGCATCAACCCGGT	783							
Db	330	AGAGCACTGGTGTGAAGATCACTTCTTTGGGTACCACTACCTGAATGGTGTCAATCCCGT	389							
QY	784	CTGATTCGCCCTGTACAGTCTCCCAAACAACTTCCGGTCACTGTATGAAATGTTGGC	843							
Db	390	CATGCTCCACTGCATCTCTAGCTTGCCCAAGAGCTGCTGTCACAATGACATGGTGGC	449							
QY	844	CCAGTGTGGGCCCTGGAAACAGTCTGCAGGCTGAGTTGGAGAGGGCTCCCTGTTCTT	903							
Db	450	CCCCCTGTCTGGNACAGGACATCATGCTCTGACAGACAGCTAGAGAGGGGAAACATCTTCT	509							
QY	904	GGTGGATCATGGCAATCTTTCTGGAGTCCACACCAACATCTCTCAATGGAAAGCCTCAGTT	963							
Db	510	AGCGGACTACTGGATCCTGGCGAGGCCCCACCCACTGCCTAAACGGCCGCGCAGCAGTA	569							
QY	964	CTCTCAGCCCCGATGACCTGTTACACAGAGCTCAGGCTCCGGACCCCTGTTCCCAT	1023							
Db	570	CGTGGCCCCCCTCATGTGCTGTGCTCAGCCCCCAG---GGGGCGCTGGTGGCCCTT	626							
QY	1024	TGCCATCCAGCTCAAAACAGACTCCCGGGCAGACACCCCATCTTCTGCCCAGGGATGA	1083							
Db	627	GGCCATCCAGCTCAGCCAGACCCCGGGCTGACAGCCCCCATCTTCTGCCCACTGACTC	686							
QY	1084	CAGTGGGACTGGTTGCTGGCCAAAGACCTGGGTTGCAATTTCTGAGTTTATCATCATGA	1143							
Db	687	CGAATGGGACTGGCTGCTGGCCAAAGACGTGGGTGCGCAACTCTGAGTTCTTGSTGCACGA	746							
QY	1144	GGCTGTACACATCTGCTGCATGCCCATCTGATTCAGAGTCTTTGCTTGGCCACATTT	1203							
Db	747	AAACAAACGCACTTTCTGTGACGCAATTTGTGTGCGAGGGCTTCGCCCATGGCCACGCT	806							
QY	1204	AGCTCAGCTGCCTAGGTGTACCCCTCTCTCAAGCTATTGATTTCTCACAATTCGGTACAC	1263							
Db	807	GGCCAGCTGGCGCTCTGCCACCCCATCTACAGCTCCTACTCCCCCACCACACTGATACAC	866							
QY	1264	ACTGCATCAACACCGCTTCCCGGAGCTGCTGTTGGCCCTGGGAAATTGATAGACAA	1323							
Db	867	GCTGCAGGTGAACACCATCGGAGGGCCACGCTGCTCAACCCCGAGGGGCTCGTGGACCA	926							
QY	1324	GTCCACAGGCTTGGCACTGGGGGATTTCTGACCTGTATAAGAGAAACATGGAGCAGCT	1383							
Db	927	GGTCACTCCATCGGAGGCAAGGGCTCATCTACCTCATGAGCACGGGCTGGCCCACTT	986							
QY	1384	GAACTACTCTGCTGTCTCCCTGAAGATATCCGAGCCGAGGTGTGGAAGACATCCC	1443							
Db	987	CACCTAACCAATTTCTGCTTCCGACAGCCTGCGGGCCCGGGGCTCTTGCTATCCC	1046							
QY	1444	AGGCTACTATTACCGAGATGATGGGATGAGATCTCGGGGGCAATAAAGAGCTTTGTCTC	1503							
Db	1047	CAACTACCACTACCGAGACGACGGCCTGAAGATCTGGGGGCCATTGAGAGCTTTGTCTC	1106							
QY	1504	TGAAATAGTCAGCATCTACTATCCAGTGCACATCCGTCAGATGACCAAGGCTCCA	1563							
Db	1107	AGAAATCGTGGGCTACTATTATCCCACTGACGCACTGTGTGACGAGGATTCGAGCTGCA	1166							

Search completed: July 19, 2005, 21:32:02  
Job time : 364.769 secs

QY	1564	GGCCTGGGTGAGGGAGATCTTCTCTGAGGGCTTCTCGGCCGAGAAAGCTCAGGTATGCC	1623							
Db	1167	GGCCTGGGACTGGCGAGATTTTGTCTCAGGCGTTCTGGGCCGGGAAAGCTCAGGTTTCCC	1226							
QY	1624	CTCCTTGTGTGGATACCCGGGAAGCCCTGGTCCAGTATATCACCATGGTGATATTCACCTG	1683							
Db	1227	AAGCCGCTGTGCACCCCGAGGAGATGTTGAGTTCTCTCACTGCAATCTTCAATTG	1286							
QY	1684	CTCAGCCAAAGCATGTCAGTGTTCAGTTTCAGGCCAGTTTCAGTCTTTGTG	1730							
Db	1287	CTCTGCCCAGCACGCTGTGTCAACAGTGGGCGAGGACGGCAGAGGTG	1333							

GenCore version 5.1.6  
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OM protein - protein search, using sw model  
Run on: July 18, 2005, 21:49:42 ; Search time 28.3348 Seconds  
(without alignment)  
2298.893 Million cell updates/sec

Title: US-10-688-676A-4  
Perfect score: 3604  
Sequence: 1 MAKCRVRVSTGEACGAGTWD.....GLALPYTLDPPLIENSVSI 677

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No., is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1451.5	40.3	674	2	arachidonate 5-lip
2	1442.5	40.0	674	1	arachidonate 5-lip
3	1429	39.7	670	1	arachidonate 5-lip
4	1249	34.7	663	1	arachidonate 12-lip
5	1224	34.0	663	1	arachidonate 12-lip
6	1192	33.1	663	1	arachidonate 12-lip
7	1187	32.9	663	1	arachidonate 12-lip
8	1186.5	32.9	662	1	arachidonate 15-lip
9	1177	32.7	663	1	arachidonate 12-lip
10	1176	32.6	663	1	arachidonate 12-lip
11	1164	32.3	663	1	arachidonate 12-lip
12	1144	31.7	663	1	arachidonate 15-lip
13	1044.5	29.0	1066	2	arachidonate 8-lip
14	592	16.4	685	2	probable lipoxigen
15	555	15.4	914	2	probable lipoxigen
16	541	15.0	862	2	lipoxigenase (EC 1
17	540	15.0	926	2	probable lipoxigen
18	538	14.9	908	2	lipoxigenase (EC 1
19	537.5	14.9	862	2	lipoxigenase (EC 1
20	536	14.9	876	2	probable lipoxigen
21	531	14.7	861	2	lipoxigenase (EC 1
22	523.5	14.5	876	2	lipoxigenase (EC 1
23	521	14.5	839	2	lipoxigenase (EC 1
24	521	14.5	853	2	lipoxigenase (EC 1
25	520	14.4	856	2	lipoxigenase (EC 1
26	519.5	14.4	858	2	lipoxigenase (EC 1
27	519.5	14.4	859	1	lipoxigenase (EC 1
28	518	14.4	853	2	lipoxigenase (EC 1
29	516.5	14.3	864	2	lipoxigenase (EC 1

30	513.5	14.2	857	2	S01864	lipoxigenase (EC 1
31	513	14.2	864	1	S07075	lipoxigenase (EC 1
32	511.5	14.2	599	2	S18612	lipoxigenase (EC 1
33	511.5	14.2	864	2	S13381	lipoxigenase (EC 1
34	509.5	14.1	741	2	S18906	lipoxigenase (EC 1
35	506	14.0	917	2	B96699	probable lipoxigen
36	505.5	14.0	859	2	T06429	lipoxigenase (EC 1
37	505	14.0	517	2	T06274	probable lipoxigen
38	505	14.0	936	2	T06190	lipoxigenase (EC 1
39	503.5	14.0	861	1	S01142	lipoxigenase (EC 1
40	502.5	13.9	877	2	T10085	lipoxigenase (EC 1
41	500.5	13.9	865	2	T11852	lipoxigenase (EC 1
42	498	13.8	868	2	S56655	lipoxigenase (EC 1
43	495.5	13.7	878	2	S74207	lipoxigenase (EC 1
44	495	13.7	862	2	S22153	lipoxigenase (EC 1
45	495	13.7	865	1	DASYL1	lipoxigenase (EC 1

ALIGNMENTS

RESULT 1

149479  
arachidonate 5-lipoxigenase - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C:Accession: I49479  
J:Chen, X.S.; Naumana, T.A.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.  
J: Biol. Chem. 270, 17993-17999, 1995  
A:Title: cDNA cloning, expression, mutagenesis, intracellular localization, and gene chr  
A:Reference number: A57186; MUID:95355399; PMID:7629107  
A:Accession: I49479  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-674 <RES>  
A:Cross-references: UNIPROT:P48999; GB:L42198; PIDN:9886332; PIDN:AAC37673.1; PID:9886333  
C:Genetics:  
A:Gene: Alox5  
C:Superfamily: arachidonate 5-lipoxigenase

Query Match 40.3%; Score 1451.5; DB 2; Length 674;  
Best Local Similarity 42.3%; Pred. No. 3.8e-105; Indels 15; Gaps 6;  
Matches 289; Conservative 133; Mismatches 246;

Qy	1	MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVLDH-LGKSFSAAGEDFEVTL PQ	59
Db	1	MPSYTVVATGSGQWAGTDDYVLSLIGSAGSEKHLDDKAFYNDFERGAVDSYDVTVDE	60
Qy	60	DVGTVMLRVHKAPEVSLPLMSFRSDAFCRWFLEWLPAAALHFPYQWLEGAGELVL	119
Db	61	ELGSIYLVKIEKR-----KYWLHDDWLYKTYTLKTPHGDYIEFFPCYRMTGEIVL	112
Qy	120	REGAAKVSODDHPHTLQDQKQELSESQKMSWKTYIEGWPRCLDHTVTKDLNLKYS	179
Db	113	RDGRAKLARDQDQHILKQHRKLEAKQKQYRWEMWPGFPLSDAKCHKLPDRDIQFDS	172
Qy	180	MNAKLPFAKHSAYTELKVKGLDR-TGLMRSLEMRRLFNFRKTPAAEYVFAHWQEDAF	238
Db	173	EKGVDVFLVNSKAMENLFNRFMFQSSWHDFADEKIFVKISNTISERVKNHWQEDLM	232
Qy	239	PASQFLNGINPVLIRRHCHSLPNPNFPVTDEMVAVPVLGPGTSLQAEKGSLSFLVDHGISG	298
Db	233	FGYQFLNGCNPVLKRCRTALPKPLPVTTEWMEVCSLERQSLSEQVEQGNIFIVDYELDG	292
Qy	299	VHTNILING-KPQFSAAPMTLLHQSSGSPLLPIAQLKQTPGDPNPILPSPDDTWDWLLA	357
Db	293	IDANKTDFCTHQAAPICLLYKRL-ANKIVPIAQLNQTPGESNPILPSPDTSKYDWLLA	351
Qy	358	KTWVRNSEFYTHEAVTHLLHAHLIPEVFALATLQRLPRCHPLFKLLIPHIYTHLINTLA	417
Db	352	KIWRSDSFHVHQIITHLLRTHLVSEVFGIANYQLPAVHPLFKLLVAHVAFTHNTAYKA	411
Qy	418	RELLVAFPKLIDKSTGLGTGFGSDLIKRNMBQLNSVLCPLPEDIRARGV---EDIPGY	474

Db 412 REQLICEYGLFKANATGGGGHVQVQRAVQDLTYSSLCFPEAIRARGMDSTEDMPFFY 471  
QY 475 RDGQMOIGAIKSFVSEIYIYPSDTSVDDQELQAWREIFSBGFLGREGSGMPSLLD 534  
Db 472 RDGLGLWEAIRQSFTEVSVIYENDQVVEEDQELQDFVKDVIYVGMKGKAGSPKSIK 531  
QY 535 TREALVQYITWVITFCSAKHAASVSSQFDSVVMNLPPTMQLPPTSGQARPSFIAT 594  
Db 532 SREKLESLYITVIFTASQAHAANFGQYDWCWIPNAPTMEAPPTAKGVVITISQIVDT 591  
QY 595 LPAVNSSVHIITALLMLLSAEPGDQRPLGHPYDEHFTEDAPRRSVAAPORKLIQISKIRE 654  
Db 592 LPDRGRSCHLGAVALSQFQENELFLGMYPEEHTEKPVKEAMIRFRKNLEAIIISVIAE 651  
QY 655 RNRLGLALPYTLDPLPIENSVS 677  
Db 652 RNKKKKLPYYLSPDRIPNSVAI 674

## RESULT 2

DAHUAL  
arachidonate 5-lipoxygenase (EC 1.13.11.34) [validated] - human  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1989 #sequence revision 03-May-1996 #text\_change 09-Jul-2004  
C:Accession: A28117; A37017; A28397; A32104; A38410  
R:Dixon, R.A.F.; Jones, R.E.; Diehl, R.E.; Bennett, C.D.; Kargman, S.; Rouzer, C.A.  
Proc. Natl. Acad. Sci. U.S.A. 85, 416-420, 1988  
A:Title: Cloning of the cDNA for human 5-lipoxygenase.  
A:Reference number: A28117; MUID:88124852; PMID:3422434  
A:Accession: A28117  
A:Molecule type: mRNA  
A:Residues: 1-674 <DIX>  
A:Cross-references: UNIPROT:P09917; GB:J03600; NID:g187192; PIDN:AAA36183.1; PID:g187193  
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.  
Adv. Prostaglandin Thromboxane Leukot. Res. 19, 466-469, 1989  
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.  
A:Reference number: A37017; MUID:89320027; PMID:2526519  
A:Accession: A37017  
A:Molecule type: mRNA  
A:Residues: 1-674 <WATS>  
R:Matsumoto, T.; Funk, C.D.; Radmark, O.; Hoeseg, J.O.; Joernvall, H.; Samuelsson, B.  
Proc. Natl. Acad. Sci. U.S.A. 85, 26-30, 1988  
A:Title: Molecular cloning and amino acid sequence of human 5-lipoxygenase.  
A:Reference number: A28397; MUID:88124804; PMID:2829172  
A:Accession: A28397  
A:Molecule type: mRNA  
A:Residues: 1-535, 'PVGVDRDLRLRPARRGQLRPVRLVLLDPQCAPHASPATDQ', 581-674 <RF1>  
A:Note: parts of the sequence, including the amino end, were confirmed by protein sequen  
A:Note: this sequence report appears to contain a frameshift error  
R:Funk, C.D.; Hoshiko, S.; Matsumoto, T.; Radmark, O.; Samuelsson, B.  
Proc. Natl. Acad. Sci. U.S.A. 86, 2587-2591, 1989  
A:Title: Characterization of the human 5-lipoxygenase gene.  
A:Reference number: A32104; MUID:89202374; PMID:2565035  
A:Accession: A32104  
A:Molecule type: DNA  
A:Residues: 1-50 <FUN>  
R:Hoshiko, S.; Radmark, O.; Samuelsson, B.  
Proc. Natl. Acad. Sci. U.S.A. 87, 9073-9077, 1990  
A:Title: Characterization of the human 5-lipoxygenase gene promoter.  
A:Reference number: A38410; MUID:91067649; PMID:2251250  
A:Accession: A38410  
A:Molecule type: DNA  
A:Residues: 1-11 <HOS>  
A:Cross-references: GB:M38191  
C:Comment: This calcium- and ATP-requiring enzyme catalyzes the first two steps in the h  
C:Genetics:  
A:Gene: GDB:ALOX5  
A:Cross-references: GDB:132453; OMIM:152390  
A:Map position: 10q11.2-10q11.2  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: iron; leukotriene biosynthesis; metalloprotein; oxidoreductase

F:2-674/Product: arachidonate 5-lipoxygenase #status experimental <MAT>  
F:368,373,551,555,674/Binding site: iron (His, His, His, 11e) #status predicted  
Query Match 40.0%; Score 1442.5; DB 1; Length 674;  
Best Local Similarity 42.6%; Pred. No. 1.9e-104;  
Matches 292; Conservative 126; Mismatches 248; Indels 19; Gaps 7;  
QY 1 MAKCRVRVSTGEACAGTWDKVSIVSVTHGESPLVPLDH-LGKBFSGAGSEDFVETLPQ 59  
Db 1 MPSYTVTVATGSQWFGAGTDDVIYLSLVGSAGCEKHLDDKPFYNDFERGAVDSYDVTVD 60  
QY 60 DVGTVMLRVHKAPPEVSLPLMSFRSDAFCRWFLEWLPGLAALHFPYCWLEGAGELVL 119  
Db 61 ELGEIQLVRIEKR-----KYLNDNDWLYKIITLKTPHGDYIEFFPCYRWITGVEVVL 112  
QY 120 REGAAKVSQDHHPTLQDROKELSRQKMTSWKTYIEGWPRCLDHTVTKDLDLNKKYSA 179  
Db 113 RDGRKLARDQIHLKHRRKELETRQKQYRWENWFGFPLSIDAKCHKDLPRDIQFDS 172  
QY 180 MNAKLFFKAHSAYTELKVGLLDR-TGLWRSLSREMRLEFNPRKTPAAYVYFAHWOEDAF 238  
Db 173 EKVDFVLNYSKAMENLFINRFMHMFQSSWADFDFEKIFVKISNTISERVVMNHQEDLM 232  
QY 239 PASQFLNGINPVLIRCHSLPNPVTDEMVAFLPGTSLQAELEKSLFLVDHGIISG 298  
Db 233 FGYPFLNGCNFVLIRRCTELPEKLPVTTEMVECSLERQLSLEQEQOQGNIFIVDFELLDG 292  
QY 299 VHTNILANGKP--QPSAAPTLLHQSOGSGPLPPIALQIKOTPGDNPFIPLPSDDTDWL 355  
Db 293 IDAN--KTDPCVLQPLAAPICLLYKNL-ANKIVPIALQINQIPGDNFIPLPSDAKYDWL 349  
QY 356 LAKTWVRNSEFYIHBAVTHLLHAHLIPEVVALATLRLQPRCHPLPKLLIPIHRYTLHNT 415  
Db 350 LAKIWRSSDFHVTQITHLRLTHLVSEVFGIAMYRLQPAVHPIFKLLVAHVRFITAIT 409  
QY 416 LARELLVAPGKLIKDSGTGLGTGGSDLIKRWELQYNVSLCLPEDIARGV---EDIPGY 472  
Db 410 KAREQLICEGLDFKANATGGGGHVQVQRAVQDLTYSSLCFPEAIRARGMDSTEDMPFFY 469  
QY 473 YRDDGMOIGAIKSFVSEIYIYPSDTSVDDQELQAWREIFSBGFLGREGSGMPSL 532  
Db 470 FYRDDGLGLWEAIRFTFAEVVDIYIEGQVVEEDPELQDFVNDVYVGMKGKSGSPFKS 529  
QY 533 LDTREALVQYITWVITFCSAKHAASVSSQFDSVVMNLPPTMQLPPTSGQARPSFI 592  
Db 530 VKSRELSEYLTIVIFTASQAHAANFGQYDWCWIPNAPTMEAPPTAKGVVITIEQIV 589  
QY 593 ATLPVNSSVHIITALLMLLSAEPGDQRPLGHPYDEHFTEDAPRRSVAAPORKLIQISKI 652  
Db 590 DTLPRGRSCHLGAVALSQFQENELFLGMYPEEHTEKPVKEAMIRFRKNLEAIVSVI 649  
QY 653 RERNGLALPYTLDPLPIENSVS 677  
Db 650 AERNKKKLPYYLSPDRIPNSVAI 674

## RESULT 3

A30882  
arachidonate 5-lipoxygenase (EC 1.13.11.34) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A30882  
R:Balcarek, J.M.; Theissen, T.W.; Cook, M.N.; Varrichio, A.; Hwang, S.M.; Strohsacker, M.V.  
J. Biol. Chem. 263, 13937-13941, 1988  
A:Title: Isolation and characterization of a cDNA clone encoding rat 5-lipoxygenase.  
A:Reference number: A30882; MUID:86330933; PMID:3417684  
A:Accession: A30882  
A:Molecule type: mRNA  
A:Residues: 1-670 <BAL>  
A:Cross-references: UNIPROT:P12527; GB:J03960; NID:G205228; PIDN:AAA41538.1; PID:G205229  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: oxidoreductase



Query Match 39.7%; Score 1429; DB 1; Length 670;  
Best Local Similarity 42.5%; Pred. No. 2.1e-103;  
Matches 287; Conservative 127; Mismatches 243; Indels 18; Gaps 8;

QY 1 MAKCRVYSTGEACAGTWDKVSIVSIVGTHGESPLVPLDH-LGKEFSAGABEDFEVTLPO 59  
DB 1 MPSYTVTVATGSQWAGTDDYIYLSIGSAGSEKHLDDKAFYNDPERGRSDSYDVTDE 60  
QY 60 DVGTVLMRVHKAPPEVSLPLMSFR-SDAFCRWFELWLPGLAHLFFCYOWLEGAGELV 118  
DB 61 ELGETIYLVKIEK-----RKYRLHDDWLVKYYTLK-TPHDYIEFFCYRWITGEGSIV 110  
QY 119 LREGAAKVSODHHTPLQDQKQKESQKMSYKWTYIEGWPRCLDHTVTDOLDLNKYS 178  
DB 111 LRDCGAKLARDQIHLKHQRKLEKLETKQKQYRMWMPGPPSLSDAKCHKLDPRDIQFD 170  
QY 179 AMKNAKLPFKAHSAYTELKVKGLDLR-TCLWRSLEMERLNFNFRKTPAAEYVFAHWQDA 237  
DB 171 SEKGVDVFLNYSKAMENLFINRFHMFQSSWHDPADEKIFVKISNTISERVKNHWQEDL 230  
QY 238 FASQFLNGINPVLIRRHCHSLPNNPVTDEMVAFLVPGTSLQAELEKGSFLVDHGILS 297  
DB 231 MFGYQFLNGCNPVLIRKTELKPLVTTMVECSLERQLSLEQVQSGNFIYDYEYLLD 290  
QY 298 GVHTNINLNG-KPQESAAPMTLLHQSSGSGPLLPALQKOTGPDNPFLPSDDTDWLL 356  
DB 291 GIDANKTDPCTHQFLAAPICLLYKNL-ANKLVPIAQLNQTGPKNPFLPTDSKYDWLL 349  
QY 357 AKTWVRNSEFYTHEAVTHLLHAHLIPEVPALATLROLPRCHPLPKLLPHIRYTHINTL 416  
DB 350 AKIWRSSDFHIQTHITLRLTHLVSEVFGIYAMVQLPAVHLPLKLLVAHVRFIAINTK 409  
QY 417 ARELLVAPKGLDKSTGLTGSGFSDLIKRNMEQLNYSVLCPEIDIRARGV---EDIPGY 473  
DB 410 AREQLNCEYGLFDKANATGGGHHVQWQRAVQDLTYSSLCFPEALKARGMDNTEIPYF 469  
QY 474 YRDGMQIOWGAIKSVSIVSIYPSDTSVQDDQELQAWVREIFSEGFLGRESSGMPSL 533  
DB 470 YRDGGLLWAEAIQSTTEWVSIIYEDDQVVEDQELQDFVQVYVYVYVYVYVYVYVYV 529  
QY 534 DTREALVOYITWVITFCSAKAAVSSGQFDCSWMPNLPPTMQLPPTTSGKQARPEPIA 593  
DB 530 KSREKLSYLVIVFTASQAHAANVFGQYDWCSPINAPPTWRAPPTAKGVVIEQIVD 589  
QY 594 TLPVAVSSSYHIIALWLSAEPGQDRLGHPYDEHFTEDAPRRSVAAPFQKLIQISKGR 653  
DB 590 TLPDRGRSCWHLGAWALSQFQENELFLGMPYEEHFIEKVPKEAMIRPKNLEAIVSVIA 649  
QY 654 ERNRLGALPYTYLDP 668  
DB 650 ERNKNKKLPYTYLSP 664

RESULT 4  
A54075  
arachidonate 12-lipoxygenase (EC 1.13.11.31), platelet [validated] - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C:Accession: A54075  
R:Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D.  
J. Biol. Chem. 269, 13979-13987, 1994  
A:Title: cDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure  
A:Reference number: A54075; MUID:94245713; PMID:8188678  
A:Accession: A54075  
A:Molecule type: DNA; mRNA  
A:Residues: 1-663 <CHE>  
A:Cross-references: UNIPROT:P39655; GB:U04334; NID:g467220; PIDN:AAA20659.1; PID:g467221  
A:Experimental source: strain C57BL/6, blood platelets  
A:Note: removal or substitution of Ile-663 abolished enzyme activity  
C:Comment: A second arachidonate 12-lipoxygenase from mouse leukocytes is shown in (PIR:  
C:Genetics:  
A:Map position: 11  
C:Superfamily: arachidonate 5-lipoxygenase

C:Keywords: oxidoreductase

Query Match 34.7%; Score 1249; DB 1; Length 663;  
Best Local Similarity 38.8%; Pred. No. 2.4e-89;  
Matches 266; Conservative 117; Mismatches 271; Indels 32; Gaps 9;

QY 1 MAKCRVYSTGEACAGTWDKVSIVSIVGTHGESPLVPLDH-LGKEFSAGABEDFEVTLPOD 60  
DB 1 MGAYRVVVTVGAWLFGSLNLVRLWLVGEHREKX----ELQLRPARKSEBEFDFVDEP 56  
QY 61 VGTVMILRVHKAPPEVSLPLMSFRSDAFCRWFELWLPGLAHL-FFCYOWLEGAGELV 118  
DB 57 LGPQLQFVKLHKQHTVV-----DDAFCNLITVQG-PGTSAAEAVFCYRWVQEGILS 107  
QY 119 LREGAAKVSODHHTPLQDQKQKESQKMSYKWTYIEGWPRCLDHTVTDOLDLNKYS 178  
DB 108 LPEQARLAGNALDVFQKREKELKERQOYCNATWKEGLPQTIAAACKODLPPNMRFH 167  
QY 179 AMKNAKLPFKAHSAYTELKVKGLDLR-TCLWRSLEMERLNFNFRKTPAAEYVFAHWQDAF 238  
DB 168 EEKELDFEWTLKAGVLEWGLKRVVYTLRSWMHLEDFOIFWGQKSALAEKVHQCHQDE 227  
QY 239 FASQFLNGINPVLIRRHCHSLPNNPVTDEMVAFLVPGTSLQAELEK---GSLFLVDHG 294  
DB 228 FGYQFLNGANPMLRRSTSLPSRLVPSGM-----EELQAELEKELKNGSLFEADFI 279  
QY 295 ILSGVHTNINLNGKPFQSAAPMTLLHQSSGSGPLLPALQKOTGPDNP---IFLPSDDT 351  
DB 280 LLDGIPANVIRGEQYLAAPLVMLRMDPG-GKLLPMAIQI-QPNPSSPAPTLFLPSDPP 337  
QY 352 WDMLLAKTWVRNSEFYTHEAVTHLLHAHLIPEVPALATLROLPRCHPLPKLLPHIRYTL 411  
DB 338 LAWLAKIWRNSDFQELQFHLNTHLVAEVIATVATMRCLPGLHPIFKLLVPHIRYTM 397  
QY 412 HINTLARELVAPKGLDKSTGLTGSGFSDLIKRNMEQLNYSVLCPEIDIRARGVEDIPG 471  
DB 398 EINTRTQLISDGIQFQVSTGGGHHVQLLTAVLAQLYHSLCPDDDLNRLGRLIPS 457  
QY 472 YYYRDDGMQIOWGAIKSVSIVSIYPSDTSVQDDQELQAWVREIFSEGFLGRESSGMP 531  
DB 458 ALYARDALQWETVARYVKGWVHLFYQSDDIVRGDPELQAWCRBITEVGLCHAQDRGFPV 517  
QY 532 LLDREALVOYITWVITFCSAKAAVSSGQFDCSWMPNLPPTMQLPPTTSGKQARPEPF 591  
DB 518 SFOSRAQLCHFLTMCVFTCTAQHAANQGLDWTGVPNAPCTMRMPPTSKDDVTMETV 577  
QY 592 IATLPVAVSSSYHIIALWLSAEPGQDRLGHPYDEHFTEDAPRRSVAAPFQKLIQISKG 651  
DB 578 MGSFLVDVQKACLQMTITWHLGRLOQPDVWPLGHHTKTFSDPTKAVLSQFQADLNLEKE 637  
QY 652 IRERNRGLALPYTYLDPPLIENSYSI 677  
DB 638 ITRNEQLDLPEYELKPSRIENSITI 663

RESULT 5

A38283

arachidonate 12-lipoxygenase (EC 1.13.11.31) - human

N:Alternate names: platelet-type 12-lipoxygenase

C:Species: Homo sapiens (man)

C:Date: 31-May-1991 #sequence\_revision 03-May-1996 #text\_change 09-Jul-2004

C:Accession: A38283; A36246; A35953; I51906; I64836; A33091

R:Izumi, T.; Hoshiko, S.; Radmark, O.; Samuelsson, B.

Proc. Natl. Acad. Sci. U.S.A. 87, 7477-7481, 1990

A:Title: Cloning of the cDNA for human 12-lipoxygenase.

A:Reference number: A38283; MUID:91017529; PMID:2217179

A:Accession: A38283

A:Molecule type: mRNA

A:Residues: 1-663 <IU>

A:Cross-references: UNIPROT:P18054; UNIPROT:Q16120; GB:M38192; GB:M58704; NID:

A:Experimental source: platelet mRNA

A:Note: some sequence heterogeneity was found

R:Yoshimoto, T.; Yamamoto, Y.; Arakawa, H.; Yamamoto, S.; Yokoyama, C.; Tanai

Biochem. Biophys. Res. Commun. 172, 1230-1235, 1990  
A;Title: Molecular cloning and expression of human arachidonate 12-lipoxygenase.  
A;Reference number: A36246; PMID:91058562; PMID:2244907  
A;Accession: A36246  
A;Molecule type: mRNA  
A;Residues: 1-188, 'PCLH', 193-260, 'Q', 262-321, 'S', 323-344, 'C', 346-663 <YOS>  
A;Cross-references: GB:M62982; NID:9177106; PIDN:AAA51533.1; PID:9177107  
R;Funk, C.D.; Furci, L.; FitzGerald, G.A.  
Proc. Natl. Acad. Sci. U.S.A. 87, 5638-5642, 1990  
A;Title: Molecular cloning, primary structure, and expression of the human platelet/erythrocyte membrane 12-lipoxygenase.  
A;Reference number: A35953; PMID:90332636; PMID:2377602  
A;Accession: A35953  
A;Molecule type: mRNA  
A;Residues: 1-260, 'Q', 262-321, 'S', 323-388, 'P', 390-663 <FUN>  
A;Cross-references: GB:M35418; NID:9189773; PIDN:AAA60056.1; PID:9189774  
R;Husain, H.; Shornick, L.P.; Shannon, V.R.; Wilson, J.D.; Funk, C.D.; Pentland, A.P.; Am. J. Physiol. 266, C243-C253, 1994  
A;Title: Epidermis contains platelet-type 12-lipoxygenase that is overexpressed in germinal centers.  
A;Reference number: I51906; PMID:94136572; PMID:8304420  
A;Accession: I51906  
A;Status: translation not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 340-427 <RES>  
A;Cross-references: GB:S68587; NID:9545223; PIDN:AAD14020.1; PID:94261720  
A;Experimental source: skin, epidermal cells  
A;Accession: I64836  
A;Status: translation not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 340-396, 'V', 398-427 <RE2>  
A;Cross-references: GB:S68588; NID:9545222; PIDN:AAD14021.1; PID:94261721  
C;Genetics:  
A;Gene: GDB:ALOX12  
A;Cross-references: GDB:127547; OMIM:152391  
A;Map position: 17p13.1-17p13.1  
C;Function:  
A;Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,10E,14Z) - (12S) - 12-HETE  
A;Pathway: leukotriene biosynthesis  
C;Superfamily: arachidonate 5-lipoxygenase  
C;Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidoreductase  
P;360,365,540,544,663/Binding site: iron (His, His, His, Asn, Ile) #status predicted

Query Match 34.0%; Score 1224; DB 1; Length 663;  
Best Local Similarity 37.8%; Pred. No. 2.2e-87;  
Matches 260; Conservative 126; Mismatches 267; Indels 34; Gaps 9;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSPVLPLDLHKGESAGAEEDFEVTLPOD 60  
DB 1 MGRYRIRVATGAWLFGSGNVRVQLVLVGTGRGAEI-----ELQLRPARGEEEFDDHVDAD 56

QY 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFPELWLPGAA--LHFPYQWLEGAGELV 118  
DB 57 LGLLQFVLRKHHLV-----DDMFCDRITVQG-FGACAEVAFPCYRVWQGEDILS 107

QY 119 LREGAAKVSQDHPHTLQDORQKELSRQKMSYKWTYIEGWPCRLDHEVTWKOLDNIKYS 178  
DB 108 LPEGTARLPDGNALDMFQKHREKELDRQIYCWATWKEGLPLTIAADRKDDLPNNRPH 167

QY 179 AMKNAKLFFKAHSAYTELKVGLLDRTGLWRSLEMRRLNFRKTPAAEVVFAHWQEDAF 238  
DB 168 EEKRLDFEWTLLKAGALEMAKRVYITLLSSNCULDFDQIFWGQKSALEKVRQCWQDDEL 227

QY 239 FASQFLNGPVLIRCHSLPNNFPVPTDEMVAFLVPG-----TSLQALEKSGSLFLVH 293  
DB 228 FSVQFLNGANPMLRRSTLSPLR-----VLPFGMEELRAQLEKELQNGSLFEADF 278

QY 294 GILSGVHTNINLKPQFSAAPMTLLHQSGSGPLPIAIOQLKTPGPDNP---IFLPSDD 350  
DB 279 ILDDGIPANVIRGEKQYLAAPLVM-L-KMEPNGKLQPMWQI-QPPNPSPTPTLFLPSDP 336

QY 351 TWDMLAKTVRNSSEYIIEAVTHLHAHLIPEVFAATLRLQPRCHPLFKLLIPIHRYT 410  
DB 337 PLAWLLAKSVNRNSDFQLHEIQYHLLNTHLVAEVIATVNRCLPGLHPIFKLPIHRYT 396

QY 411 LHINTLARELIVAPGKLIKSTGLTGTSGLIKKNMQLNYSVLCLBEDIPARGVEDIP 470  
DB 397 MEINTTRQLTISDGGIFDKAVSTGGGHHVQLRAAAQLTYCSLCPDDLADRLGLLGP 456

QY 471 GYYRDDCQWIGATKSPVSEIVSYTSPDTSVQDDQELQAWVREIFSEGFLGRESSGMP 530  
DB 457 GALYAHDAIRLWEIARIARVEGIVHLFYORDDIVKGDPLQAWCREITEVGLCOADRGP 516

QY 531 SILDTREALVOYITWVIFETCSAKHAAVSSGQFDSVMMNPLPPTMQLPPTPSKGOARPE 590  
DB 517 VSFQSQSLCHFLTMCVFTCTAQHAAINQGLDWAYVPNAPCTWRMPPTTKEDVTWAT 576

QY 591 FIATLPVNSSYHIIALWLLSAEPDORPLGHYPDEHFTEDAPRRSVAAPFORKLIQSK 650  
DB 577 VMGSLPDRVQACLOQWAISSWHLSSRRQDMVPLGHHKERYFSGPKPRAVLNQFRTDLEK 636

QY 651 GIRENRGALPYTYLDPPLIENSYSI 677  
DB 637 EITARNEQDWPYELKFSIENSYSI 663

RESULT 6  
B54075  
Arachidonate 12-lipoxygenase (EC 1.13.11.31), leukocyte [validated] - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 09-Jul-2004  
C;Accession: B54075; I49439  
R;Chen, X.S.; Kurre, U.; Jenkins, N.A.; Copeland, N.G.; Funk, C.D. J. Biol. Chem. 269, 13979-13987, 1994  
A;Title: cDNA cloning, expression, mutagenesis of C-terminal isoleucine, genomic structure and function of mouse arachidonate 12-lipoxygenase.  
A;Reference number: A54075; PMID:94245713; PMID:8188678  
A;Accession: B54075  
A;Molecule type: DNA; mRNA  
A;Residues: 1-663 <CHE>  
A;Cross-references: UNIPROT:P39654; GB:U04331; NID:9467216; PIDN:AAA20658.1; PID:9467217  
A;Experimental source: strains C57BL/6 and ICR, spleen leukocytes  
A;Note: removal or substitution of Ile-663 abolished enzyme activity  
R;Freire-Moar, J.; Alavi-Naseab, A.; Ng, M.; Mulkins, M.; Sigal, E. Biochim. Biophys. Acta 1254, 112-116, 1995  
A;Title: Cloning and characterization of a murine macrophage lipoxygenase.  
A;Reference number: I49439; PMID:95110857; PMID:7811740  
A;Accession: I49439  
A;Status: translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-36, 'N', 38-118, 'Q', 120-396, 'N', 398-663 <RES>  
A;Cross-references: GB:L34570; NID:9509607; PIDN:AAA64930.1; PID:9763530  
C;Comment: A second arachidonate 12-lipoxygenase from mouse platelets is shown in (PIR:A100001)  
C;Genetics:  
A;Map position: 11  
A;Superfamily: arachidonate 5-lipoxygenase  
C;Keywords: oxidoreductase

Query Match 33.1%; Score 1192; DB 1; Length 663;  
Best Local Similarity 37.5%; Pred. No. 6.9e-85;  
Matches 261; Conservative 121; Mismatches 262; Indels 52; Gaps 12;

QY 1 MAKCRVRVSTGACAGTWDKVSIVTGHGSPVLPLDLHKGEP--SAGAEEDFEVTLIP 58  
DB 1 MGVIIRVSTGDSVYVAGSNNEVYLWLGHEA-----SLCKLFRPCRNSEAEFKVDVS 54

QY 59 QDVGVTLMLRVHKAPEVSLPLMSFRSDAWFCRWFPELWLP--PGAALHFPYQWLEGAGE 116  
DB 55 EYLGPLLFVRVQK-----WHYLKEDAWFCNWSIVKGPQDQSGSEYTFPCYRWVQGTSI 106

QY 117 LVLRGAQVSWDHHPTIQDORQKELSRQKMSYKWTYIEGWPCRLDHEVTWKLDLNTIK 176  
DB 107 LMLPGTGTGVVEDSGGLFRNRELEBERRSLYRWGNWKGDTILNVAATISDLFVQDR 166

QY 177 YSAMKNALFFKAHSAYTELKVGLLD-----RTGLWRSLEMRRLNFRKTPAAEY 228  
DB 167 F--REDKRLFEAS-----QVLGTMDTVINFPKNTVTCWKSLLDDPNYVFKSGHTKMAER 218

QY 229 VFAHWQEDAFASQFLNGPVLIRCHSLPNNFPVPTDEMVAFLVPG-----TSLQAL 293



A>Note: there appear to be distinct chromatographic forms, at least one each from reticulor  
r; Izumi, T.; Radmark, O.; Samuelsson, B.  
Adv. Prostaglandin Thromboxane Leukotriene Res. 21, 101-104, 1990  
A:Title: Purification of 15-lipoxygenase from human leukocytes, evidence for the presence  
A:Reference number: A61164  
A:Accession: A61164  
A:Molecule type: protein  
A:Residues: 'X', 3-4, 'X', 6, 'X', 8-12, 'X', 14-19, 'T', 21-22 <123>  
A:Experimental source: leukocyte  
A:Accession: B61164  
A:Molecule type: protein  
A:Residues: 'X', 3-25, 27-31 <123>  
A:Experimental source: leukocyte  
C:Genetics:  
A:Gene: GDB:ALOX15  
A:Cross-references: GDB:132454  
A:Map position: 17pter-17qter  
C:Function:  
A:Description: catalyzes the oxidation of arachidonic acid to (5Z,8Z,11Z,13E)-(15S)-15-H  
A:Pathway: leukotriene biosynthesis  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: fatty acid oxidation; iron; leukotriene biosynthesis; metalloprotein; oxidore  
F:360,365,540,544,662/Binding site: Iron (His, His, His, His, Ile) #status predicted

Query Match 32.9%; Score 1186.5; DB 1; Length 662;  
Best Local Similarity 37.6%; Pred. No. 1.9e-84;  
Matches 259; Conservative 126; Mismatches 266; Indels 37; Gaps 12;

QY 1 MAKCRVRYSTGEACGAGTWDKVSIVSGTHGESPLVPLDHLGKEP--SAGAEDEFEVTL 58  
DB 1 MGLYRIRVSTGASLYAGSNVQLVWVGQHEAA-----LGKRLPARGKETELKVEVP 54

QY 59 QDVGTVMRLVHKAPPEVSLPLMSFRSDAFWCFRWFLEWLPGAA--LHPFCYQWLEGAGE 116  
DB 55 EYLGLPLFVKLR-----HLLKDDAFWFCNWSVQG--PGAGDEVPRPCRWEGNGV 105

QY 117 LVLEGAAKVSWDHHPTLQDQKELSRQKMSYKTYIEGWPRCLDHTETVKDLNLK 176  
DB 106 LSLPEGTGRTVGSDPQGLFKHREELERRKLYRGWGNKDG--LILNAGAKLYDLPLVD 163

QY 177 YSNKNAKLPFFKAHSA--YTELKVKGLDRTGLWRLSLREMRLLFNFRKTPAAEYVPAHWQ 234  
DB 164 ERELEKRDVFEVSLAKGLADLAIDKSLNVLTCWKDLDDFNRFWCGSKLAERVRDSWK 223

QY 235 EDAPFASQFLNGNPVLRCHSLPNF---PVTDEMVAFLPGPSTLQAELEKGSFLV 291  
DB 224 EDALFGYQFLNGANPVVLRSAHLPARLVFPFGMEHLQ-----QLSEKEGGTLFEA 276

QY 292 DHGILSGVHTNINLNGKQPSAAPTMLLHSGSGGLPLPIAQLK--OTPGPNPFLPSD 349  
DB 277 DFLSLDGIRKANVILCSQQHLAAPLVM--KLQPDGKLLPMVQLQLPRTGSPPPFLPTD 335

QY 350 DTWDLAKTWRNSEFYIHEAVTHLLHAHLIPEVPALATLRLQRPCHPLFKLLPHIRY 409  
DB 336 PPMAWLLAKCWRRSSDQLHQLSHLLRGLHMAEIVVATMRCLPSIHPIFKLIIPHLRY 395

QY 410 TLHINTLARELLVAPGKLDKSTGLGTGGSFSLIKRNMEQLNYSVLCLPEDIARARGVEDI 469  
DB 396 TLEINVRARTGLVSDMGIFDQIMSTCGGHHVQLLQKAGAFLYTSSPCPPDDADRLGLV 455

QY 470 PGYYRDDGMQIWAIGKSFVSEIVSYTSPDTSVQDDQELQAVRVEIFSEGFLGREGSQM 529  
DB 456 KSSFYQADALRLWEIIYRVVVEGIVSLHYKTDVAVKDDPELQWCRTBITGLQGAQDRGF 515

QY 530 PSLDTRREALVQVITWVITFCSAKHAASVSGQSDSCVWMPNLPPTTQLPPTTSGOARPE 589  
DB 516 PVSLOARDQVCHVETICTCTGQHASVHLGQDWMYSWPNAPCTMRLPPTTK--DATLE 574

QY 590 SFTATLPVNSSSYHIIALWLSAEPCDQRPGLGHYDEHFTEDAPRPSVAAAFORKLIQIS 649  
DB 575 TVWATLPNFHQSLSQMSITWQLGRRQVAVVVGQHEEYFSGPEPKAVLKFKFREELALD 634

QY 650 KGIRERNRGLALPYTYLDPPLIENSYSI 677  
DB 635 KEIEIRNAKLDMPYEYLRPSVENSVAI 662

RESULT 9  
S30051  
arachidonate 12-lipoxygenase (EC 1.13.11.31) - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: S30051  
R:Watanabe, T.; Medina, J.F.; Haeggstroem, J.Z.; Radmark, O.; Samuelsson, B.  
Eur. J. Biochem. 212, 605-612, 1993  
A:Title: Molecular cloning of a 12-lipoxygenase cDNA from rat brain.  
A:Reference number: S30051; MUID:93185682; PMID:8444196  
A:Accession: S30051  
A:Molecule type: mRNA  
A:Residues: 1-663 <WAT>  
A:Cross-references: UNIPROT:Q02759; EMBL:L06040; NID:g205212; PIDN:AAA41532.1; PID:g205212  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: oxidoreductase

Query Match 32.7%; Score 1177; DB 1; Length 663;  
Best Local Similarity 37.2%; Pred. No. 1e-83;  
Matches 258; Conservative 127; Mismatches 261; Indels 48; Gaps 11;

QY 1 MAKCRVRYSTGEACGAGTWDKVSIVSGTHGESPLVPLDHLGKEFSAGAEDEFEVTLPOD 60  
DB 1 MGVIYRIVSTGDSKYAGSNNEVYLWVGQHEASLGKLLRPCD---SEAEFKVDVSEY 56

QY 61 VGTVMRLVHKAPPEVSLPLMSFRSDAFWCFRWFLEWL--PGAAHLHFCYQWLEGAGELV 118  
DB 57 LGPLLFVRVQK-----WHYLTDDAFWFCNWSYKPGDQGSYMFPCYRVVQGRSILS 108

QY 119 LREGAAKVSWDHHPTLQDQKELSRQKMSYKTYIEGWPRCLDHTETVKDLNLKYS 178  
DB 109 LPEGTGCTVVEDSQGLFRHREELERRSLYRGWGNKDGSLNVAASISDLVDQRP- 167

QY 179 AMKNAKLPFFKAHSAYTELKVAGLLD-----RTGLWRLSLREMRLLFNFRKTPAAEYVF 230  
DB 168 -REDKRIEFAAS-----QVIGVMDTVVFPINTVTCWKSLLDDFNCVFKSGHTKMAEVR 220

QY 231 AHQEDAFAPAQFLNGINPVLRCHSLPNFPVTDENVAPVLGPG-----TSLQAELEK 285  
DB 221 NSWKEDAFPGYQFLNGANPMVLRKSTCLPARL-----VFPGMEKLOQLNKELQK 271

QY 286 GSLFLVDHGILSGVHTNINLNGKQPSAAPTMLLHSGSGGLPLPIAQLK--OTPGPNP 343  
DB 272 GLTFEADFLDGIKANVILCSQQYLAAPLVM--KLMPDGQLLPIAQLQLPRTGSTPTPP 330

QY 344 IFLPSDDTMDLLAKTWRNSEFYIHEAVTHLLHAHLIPEVPALATLRLQRPCHPLFKLL 403  
DB 331 IFTPSDPPMDWLLAKCWRRSSDQLHQLSHLLRGLHMAELFAVATMRCLPSVHPVKLL 390

QY 404 PHIRYTHINTLARELLVAPGKLDKSTGLGTGGSFSLIKRNMEQLNYSVLCLPEDI 463  
DB 391 VPHLLYTMIEINVRASDLISERGFDFKAMSTGGGHLDLLKQAGAFLYTCSLCPDDDLAE 450

QY 464 RVEDIPGYTYRDDGMQIWAIGKSFVSEIVSYTSPDTSVQDDQELQAVRVEIFSEGFLG 523  
DB 451 RGLLDIETCFYAKDAIRLWQIMNRYVVGMPNLYHYTKAVQDDYELQSWCRITDIGLQ 510

QY 524 RESGMPSLDTRREALVQVITWVITFCSAKHAASVSGQSDSCVWMPNLPPTTQLPPTTSG 583  
DB 511 AQDRGFPTSLQSAQACVFTICTCTAQHSSVHLGQDWMYVWPNAPCTMRLPPTTK 570

QY 584 GOARPESTIATLPVNSSSYHIIALWLSAEPCDQRPGLGHYDEHFTEDAPRPSVAAAFOR 643  
DB 571 -EATWKLKMATLPNPNQSTLQINNVVLLGRQVAVVVGQHEEFPNPEAKVLKCKFRE 629

QY 644 KLIQISKGIRERNRGLALPYTYLDPPLIENSYSI 677  
DB 630 ELAALDKJEIRNKSLDIPYEYLRPSVENSVAI 663

## RESULT 10

152462  
arachidonate 12-lipoxygenase (EC 1.13.11.31) - rat  
C:Species: Rattus sp. (rat)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jun-1999  
C:Accession: I52462  
R:Hada, T.; Hagiya, H.; Suzuki, H.; Arakawa, T.; Nakamura, M.; Matsuda, S.; Yoshimoto, T.  
Biochim. Biophys. Acta 1211, 221-228, 1994  
A:Title: Arachidonate 12-lipoxygenase of rat pineal glands: catalytic properties and primary structure  
A:Reference number: I52462; MUID:94162305; PMID:8117750  
A:Accession: I52462  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-663 <RES>  
A:Cross-references: GB:S69383; NID:g545793; PIDN:AAB30132.1; PID:g545794  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: oxidoreductase

Query Match 32.6%; Score 1176; DB 2; Length 663;  
Best Local Similarity 37.3%; Pred. No. 1.2e-83;  
Matches 259; Conservative 125; Mismatches 262; Indels 48; Gaps 11;

QY 1 MAKCRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKEFSAGAEEDFEVTL PQD 60  
DB 1 MGVIKIRVSTGSKYAGNNVYLWLVGQHGSEASLGKLLRPCR-----SEAEFKVDVSGY 56  
QY 61 VGTVMRLVRHKAPEVSLPLMSFRSDAWFCRWFLEWL--PGAALHFFPCYQWLEGAGELV 118  
DB 57 LGPLLFVRVQK-----WHYLTDDANFCNWSVKVGDQGSYFPCYRWQGRSILS 108  
QY 119 LREGAAKVSQDHPHTLQDQKELSRQKYSWKTYIEGWPRCLDHTETVLDLNLKYS 178  
DB 109 LPEGTGCTWEDSQGLFRKHEELEERSLYRWGNKWDGSLNVAASISDL PVDQRF- 167  
QY 179 AMKNAKLPFAKSAATELVKVGLLD-----RTGLWRLSREMRRLNFRKTPAAEVVF 230  
DB 168 -REDKRIEFAS-----QVIGVMDTVVNFPTVTCWKSLDDDFNCVFKSGHTKMAEVR 220  
QY 231 AHQWDAFFAGQFLNGINPVLIRRSCHSPNPFVTDENVAPVLGPG-----TSLOAELEK 285  
DB 221 NSWKEDAFGGYQFLNGANPWLKSTCLPARI-----VFPCKMEKLAQLNKELOK 271  
QY 286 GSLFLVDHGILSGVHTNINLNGKQFSAAPMTLLHQSSGSPLLPIATIQK--QTPGDPNP 343  
DB 272 GTLFEADFFLLDGKIKANVLCSQQYLAAPLVML--KLMPDGQLLPITAIQLELPKTSPTPP 330  
QY 344 IFLPSDDTDWMLLAKTWVRNSEFYIHEAVTHLLHAHLIPEVPALATLRLPCHPLFKL 403  
DB 331 IFTPSDPPMDMLLAKCWRSSDLQLHELQALHRLGHLMAEFVAVATMRCLPSVHPFKLL 390  
QY 404 LPHIRYTHLNTLARELVAPGKLIDKSTGLGTGGFSDLIKRNMEQLNYSVLCPLPEDI 463  
DB 391 VPHLLYTMENINVRARNSDLISERGFDAKWSGTGGGHLDLLQAGAFLYTSLCPDDDLAE 450  
QY 464 RGVEDIPGYRDDQMGQWGAIKSFVSIVSYIPSDTSVQDDQLQAVREIFSEGFLG 523  
DB 451 RGLLDIETCFYAKDALRLQWIMNRYVGMFNHLYKTDKAVQDDYELQSKREITDIGLOG 510  
QY 524 RESSGMPSLDTRREALVQYITWVIFTCSAKHAUVSSGQFSDCVWMPNLPPTWQPLPPTSK 583  
DB 511 AQDRGFPTSLQSAQAQCYITWCIPTCTAQHSSVHLGQDLDFYVWPNAPCTWRLPPTTK 570  
QY 584 GQARPESTIATLPVNSSSYHIIALWLLSAEPGDQRPGLGHYPDEHFTEDAPRRSVAAR 643  
DB 571 -EATMEKLMATLPNPQSTQLNVWMLGRQAVMPLGQHSSEHFFNPENAKAVLKPKFE 629  
QY 644 KLIIQISKGIENRNLGALPYTLDPLPIENSIVI 677  
DB 630 ELAALDKIEIRNKSLLDIPYELRPSMVNSVAI 663

## RESULT 11

A35087  
arachidonate 12-lipoxygenase (EC 1.13.11.31) - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C:Accession: A35087  
R:Yoshimoto, T.; Suzuki, H.; Yamamoto, S.; Takai, T.; Yokoyama, C.; Tanabe, T.  
Proc. Natl. Acad. Sci. U.S.A. 97, 2142-2146, 1990  
A:Title: Cloning and sequence analysis of the cDNA for arachidonate 12-lipoxygenase of pig  
A:Reference number: A35087; MUID:90192763; PMID:2315307  
A:Accession: A35087  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-663 <YOS>  
A:Cross-references: UNIPROT:P16469; GB:M31417  
C:Superfamily: arachidonate 5-lipoxygenase  
C:Keywords: oxidoreductase

Query Match 32.3%; Score 1164; DB 1; Length 663;  
Best Local Similarity 37.9%; Pred. No. 1.1e-82;  
Matches 264; Conservative 119; Mismatches 261; Indels 52; Gaps 15;

QY 1 MAKCRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKEFSAGAEEDFEV 56  
DB 1 MGLYRVSTGSSFYAGSQVQLWVGQHGCEALGWLCLRP-----ARGKETEFSDV 52  
QY 57 LPQDVGTVMRLVRHKAPEVSLPLMSFRSDAWFCRWFLEWLPGA---ALHPFCYQWLEG 113  
DB 53 VSEYLGPLLFFVKLRK-----HLLQDDDAWFCNWSVQG--PGANGDEFRFPFCYRWVEG 103  
QY 114 AGELVLRGAQKVSQDHPHTLQDQKELSRQKYSWKTYIEGWPRCLDHTETVLDL 173  
DB 104 DRILSLPEGTARTVVDPPQGLFKKHEELEERSLYRWGNKWDGSLNVAASISDL PVDQRF- 163  
QY 174 NIKYSAMKNAKLPFAKSA--YTELVKVGLLDRTGLWRLSREMRRLNFRKTPAAEVYFA 231  
DB 164 DERF--LEDKRIDEASLAKGLADLAVKDSNLVMSNLSDFNRIFWCGSKLAEOVRD 221  
QY 232 HWQEDAFAGQFLNGINPVLIRRSCHSPN--NFPVTDENVAPVLGPG--TSLOAELEK--- 285  
DB 222 SKWEDALFGYQFLNGTNPMLLRHVSVPALRKF-----PGMEELQAQLEKBLQ 270  
QY 286 -GSLFLVDHGILSGVHTNINLNGKQFSAAPMTLLHQSSGSPLLPIATIQKTP---CPD 341  
DB 271 GGTLFEADFFLLDGKIKANVLCSQQYLAAPLVML--KLQPDGKLLPMVLIQ--QLPREGSPL 328  
QY 342 NPFLPSDDTDWMLLAKTWVRNSEFYIHEAVTHLLHAHLIPEVPALATLRLPCHPLFK 401  
DB 329 PPLFLPTDPPMWMLLAKCWRSSDFQHLHSHLLRGLHMAEVATATMRCPLSPHPIFK 388  
QY 402 LLPHIRYTHLNTLARELVAPGKLIDKSTGLGTGGFSDLIKRNMEQLNYSVLCPLPEDI 461  
DB 389 LLIPHRYTMENINVRARNSDLISGIFDQVVSTGGGHVLELRRRAALLTYSSFCPPDDL 448  
QY 462 RARVEDIPGYRDDQMGQWGAIKSFVSIVSYIPSDTSVQDDQLQAVREIFSEGFL 521  
DB 449 ADRLGLGVSSFYAQDALRLMEVISRVEGIVSLHYKTDESVKEDFELQACRETFEGL 508  
QY 522 LGRSSGMPSLDTRREALVQYITWVIFTCSAKHAUVSSGQFSDCVWMPNLPPTWQPLPPT 581  
DB 509 LGADRGFPTSLQSKQELCHQFVTWCIPTCTGQHSNHLGQDLDFYVWPNAPCTWRLPPT 568  
QY 582 SKQARPESTIATLPVNSSSYHIIALWLLSAEPGDQRPGLGHYPDEHFTEDAPRRSVAAR 641  
DB 569 TK-DATLETVMATLPNPFHQASLQMSITWQGRCOPTWALGQHEEYFSGPGRAVLTKF 627  
QY 642 QRKLIQISKGIENRNLGALPYTLDPLPIENSIVI 677  
DB 628 REELAALDKIEIRNKSLLDIPYELRPSMVNSVAI 663

## RESULT 12

JQ0018

arachidonate 15-lipoxygenase (EC 1.13.11.33), erythroid-specific - rabbit  
 N:Alternate names: carotene oxidase; lipoxidase  
 N:Contains: lipoxygenase peptides  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
 C:Accession: JQ0018; A61060; A27327; A61568; JCI513  
 R:Fleming, J.; Thiele, B.J.; Chester, J.; O'Prey, J.; Janetzki, S.; Aitken, A.; Anton, I.  
 Gene 79, 181-188, 1989  
 A:Title: The complete sequence of the rabbit erythroid cell-specific 15-lipoxygenase mRNA  
 A:Reference number: JQ0018; MUID:89378774; PMID:2777088  
 A:Accession: JQ0018  
 A:Molecule type: mRNA  
 A:Residues: 1-663 <FLE>  
 A:Cross-references: UNIPROT:P12530; GB:M27214; NID:G2642134; PIDN:AA886978.1; PID:G16490  
 R:Thiele, B.J.; Fleming, J.; Chester, J.; O'Prey, J.; Prehn, S.; Janetzki, S.; Rapoport, B.  
 Biomed. Biochim. Acta 49, s17-s24, 1990  
 A:Title: Structure of the mRNA and of the gene coding for the rabbit erythroid 15-lipoxygenase  
 A:Reference number: A61060; MUID:90351403; PMID:2386503  
 A:Accession: A61060  
 A:Status: not compared with conceptual translation  
 A:Molecule type: mRNA; DNA  
 A:Residues: 2-605, 'F', 607-663 <TH>  
 A:Note: nucleotide sequence is given only for intron/exon boundaries  
 R:Thiele, B.J.; Fleming, J.; Kasuri, K.; O'Prey, J.; Black, E.; Chester, J.; Rapoport, B.  
 Gene 57, 111-119, 1987  
 A:Title: Cloning of a rabbit erythroid-cell-specific lipoxygenase mRNA.  
 A:Reference number: A27327; MUID:88112854; PMID:3123326  
 A:Accession: A27327  
 A:Molecule type: mRNA  
 A:Residues: 1-31 <TH2>  
 A:Cross-references: GB:M33291  
 R:Thiele, B.J.; Black, E.; Fleming, J.; Nack, B.; Rapoport, S.M.; Harrison, P.R.  
 Biomed. Biochim. Acta 46, S120-S123, 1987  
 A:Title: Cloning of reticulocyte lipoxygenase mRNA.  
 A:Reference number: A61568; MUID:87241419; PMID:3109402  
 A:Accession: A61568  
 A:Molecule type: mRNA  
 A:Residues: 1-40, 'SHEH', 540-582, 'S' <TH3>  
 A:Note: this clone was reevaluated in reference JQ0018 and is thought to represent a clone  
 R:O'Prey, J.; Chester, J.; Thiele, B.J.; Janetzki, S.; Prehn, S.; Fleming, J.; Harrison, P.  
 Gene 84, 493-499, 1989  
 A:Title: The promoter structure and complete sequence of the gene encoding the rabbit erythroid 15-lipoxygenase  
 A:Reference number: JCI513; MUID:90128296; PMID:2612916  
 A:Accession: JCI513  
 A:Molecule type: DNA  
 A:Residues: 1-112, 'T', 114-189, 'N', 191-193, 'I', 195-663 <OPR>  
 A:Cross-references: GB:M33291; NID:G164731; PIDN:AAA75014.1; PID:G164732  
 C:Comment: Rabbit reticulocyte lipoxygenase plays a role in the degradation of mitochondria  
 C:Comment: This enzyme catalyzes the dioxygenation of polyenoic fatty acids containing a  
 C:Genetics:  
 A:Gene: 15-lox  
 A:Introns: 45/3; 114/1; 141/2; 182/2; 217/1; 270/3; 318/3; 388/3; 417/3; 474/2; 515/1; 515/2  
 A:Superfamily: arachidonate 5-lipoxygenase  
 C:Keywords: erythrocyte; iron; oxidoreductase

162 PVDERFLEKIDPEASLANGLAELALXDSLNLVAPWKTLDLDFNRIFWGSRSLARRVD 221  
 232 HWQEDAFASQFLNGINPVLIRRHCHSLPNPNFVTDMMVAPVLGPG-TSLQAELEK-----G 286  
 222 SWQEDSLFGYQFLNGANPMLRRSRVQPARL-----VFPFGMEELQAQLEKELKAG 272  
 287 SLFLVDHGILSGVHTNINLNGFQPSAAWTLHQSSGSGPLLPALQIOL---KQTGPDNP 343  
 273 TLFEADFALLDNIRKANVILYCOQYLAAPLVML-KLPDQKLMPMWVLIQLHLPKIGSSPP-P 330  
 344 IFLPSDDTMDWLLAKTWVRNSEFYTHEAVTHLLHAHLIPEVFALATLRLQRPCHPLFKLL 403  
 331 LFLPTDPPMVLAKCWRSSDFQVHLSHLLRGLHMAEVFTVATMRLCLPSIHPVKLI 390  
 404 IPHRYTHLHNTARELIVAPGKLIDKSTGLTGSGFSLIKRNMQLNSVLCLEPIDRA 463  
 391 VPHLYRTLEINVRANGLVSDGIFDQIMSTGGGHHVQLLQOAGAFVRSFPCPDLLAD 450  
 464 RGVEDIPGYRRDDGMQIWAIGKSFVSEIVSYPSDTSVQDDQEOLOAVWREIFSEGFLG 523  
 451 RGLLGVESFYAQDALRLWEIISRYVOGIMGLYKTDRAVRDDELQSGWCREITIGLQG 510  
 524 RESSGMPSLDTRREALVOYITWVIFCSAKAAVSSGQFDSVMMNPPLPPTMQLPPPTSK 583  
 511 AQKGFPTSLQSAQAACHFTWCIFCTGQSSIHGLQLDWFTWVPNAPCTWRLPPPTTK 570  
 584 QARPESFIATLPVNSSYHIIALWLLSAPGQDQPLGHYPDEHFTEDAPRRSVAAPOR 643  
 571 -DATLETVMATLPNLHQSSLQMSIVMQLGRDQIPVPLGQHQEYFSGPEPRAVLEKFE 629  
 644 KLIQISKIGIRNRGLALPYTLDPPLIENSVI 677  
 630 ELAIMDKIEVRNEKLDIPYEYLRPSIVENSVAI 663

RESULT 13  
 T30903  
 arachidonate 8-lipoxygenase (EC 1.13.11.40) / prostaglandin-endoperoxide synthase (EC 1.1.1.6)  
 C:Species: Pterodroma homomalla  
 C:Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004  
 C:Accession: T30903  
 R:Koljak, R.; Boutaud, O.; Shieh, B.H.; Samel, N.; Braash, A.R.  
 Science 277, 1994-1996, 1997  
 A:Title: Identification of a naturally occurring peroxidase-lipoxygenase fusion protein.  
 A:Reference number: Z20930; MUID:97451024; PMID:9302294  
 A:Accession: T30903  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1066 <KOL>  
 A:Cross-references: UNIPROT:O16025; EMBL:AF003692; NID:G2440001; PID:G2440002; PIDN:AAC4;  
 C:Function:  
 A:Description: converts arachidonic acid to an allene oxide with an 8R-hydroperoxide inte  
 C:Keywords: oxidoreductase

Query Match 29.0%; Score 1044.5; DB 2; Length 1066;  
 Best Local Similarity 33.0%; Pred. No. 4.7e-73;  
 Matches 233; Conservative 141; Mismatches 280; Indels 53; Gaps 11;

QY 6 VRVSTGEACGACTWDKVSIVGTHGESPLVPLDH-LGKERSAGAEEDFEVTLPODVGVTV 64  
 378 VEVTGDRHAGTDATITIRITGAKGRDYLDKDKHNDFFAGSKQEQTVQ-GFDVGDI 436  
 65 LMLRVHKAPPEVSLPLMSFRSDA-----WFC-RWFEWMLFGAALHFFCYQWLEGA 114  
 437 QLIELH-----SDGGGVMSGDPMFVNRVLIISSTQDRVYSFPCFRVW--I 480  
 115 GELVIREGAAKVSWDHHPTLQDQKLESRQKMSWTKTYIEGPRCLDHEFTVKDLN 174  
 481 KDWLPFGPEATLPFNEVPAIVSEQRKEQLTKYQMDYVSDMDPMGNKAKTHDPLPD 540  
 175 IKYSAMKNAKLFKKAHSAYTELKVGLLDRTGLWLSRLREMRLEFNFRKTPAAEYFAHWQ 234  
 541 VQFTDEKSRVSQESKAAALVNLIGSLFTMFENWSDYDHYLYRNWILGGTFFNMDRWH 600



Qy 235 EDAPFASQFLNGINPVLIRCHSLPNNFPVTDEMVAFLVPGTSLQAELEKGSFLVDHG 294  
Db 601 EDWFGYQFLNGANPVLIRCDALPSPNFPVNEHVNASLDRGNLDEIKDGHIIYVDFK 660  
Qy 295 ILSGV-----HTNLLNGKQFSAAPMTLLHQSSGSGPLPIALQKQT 337  
Db 661 VLVGAKSVGGVLEDIGYKVPDHLKHDEADIRYCAAPLALFYVK-LGHLMPALQINQE 719  
Qy 338 GPPONPIPLSDDT-WDWLLAKTWVRNSEFIHEAVTHLLHAHLIPEVFALATLRQLPRC 396  
Db 720 GPPENPIWTHNEENHMMMAKFWLGVASNFHQLNTHLLTHLTSTESFALSTWRNLASA 779  
Qy 397 HPLFKLLPIHRYTHINTLARELLVAPGKLDKSTGLTGTFGFSDLIKRNMEOQNSVLC 456  
Db 780 HPVFKLLPHIYGLAIDTIGRKELIGSGGIVDQSLSLGGGGHVTFMKCFKVENLQDYH 839  
Qy 457 LPEDIRARGVED---IPGVYRDDGMQWGAIKSFVSEIYSIYPSDTSVDDOQLOAW 513  
Db 840 LPNALKKRGVDDPSKLPFGYRRDDGLALWEALETFIGSIIAIFYKNDODVDRDNEIQSI 899  
Qy 514 REITSEGFLL---GESSGMPSLDREALVQYITWVIFTCSAKHAAVSSGQFDSQVMPN 570  
Db 900 YDVHKGVRNPGHODHGPASFESEQLKEVITSLVFTSCQHAANVFSQKHVGFPTN 959  
Qy 571 LPPTMQLPPPTSKGOARPESTIATLPVNSSSYHIIALWLLSAEPGDORPLGHVDEHFT 630  
Db 960 APAVLRHPKKKGATLQSLSTLPSKQAALATVYLLTKFSEDERYLGNYSATAWE 1019  
Qy 631 EDAPRSVAARFKLIQISKGIRNRGLALPYTYLDPPLIENSVI 677  
Db 1020 DKDALDAIRNFQDKLEDISKIKQRENLENLEVYIYLLPERIPNGTAI 1066  
RESULT 14  
A:3499  
probable lipoxigenase PA169 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 09-Jul-2004  
C:Accession: AB3499  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; B.  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,  
N.; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: AB2950; MUID:20437337; PMID:10984043  
A:Accession: AB3499  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-685 <STO>  
A:Cross-references: UNIPROT:Q914G8; GB:AE004547; GB:AE004091; NID:g9947089; PIDN:AAG0455  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA169  
Query Match 16.4%; Score 592; DB 2; Length 685;  
Best Local Similarity 33.6%; Pred. No. 5.5e-38;  
Matches 182; Conservative 67; Mismatches 210; Indels 82; Gaps 20;  
Qy 193 YTEL--KVGLLDRTGL-----WRSLEWRRLFNFRKTPAAYVFAH 232  
Db 171 FTELQTRVIALTRVGLLVDDILKSASNLVTRQGQDGLNRPRAVFGTLRLPE---VADS 227  
Qy 233 WQEDAFASQFLNGINPVLIRCHSLPNNFPVTDEMVAFLVPGTSLQAELEKGSFLVD 292  
Db 228 FRDDBAFAWRVAGNPLIRVDALPANFPFGESQFRVRMGADDSLEAAASRLYLID 287  
Qy 293 HGIL-----SGVHTNLLNGKQFSAAPMTLLHQSSGSGPLPIALQKQTPGDPNPIFL- 346  
Db 298 YAELEKLAPEGAVDKLLTG-TGFAVAPIALFALGKDRARLLFVALQCGQDPA-THPMFVR 345  
Qy 347 ----PSDDTWDLAKTWVRNSEFIHEAVTHLLHAHLIPEVFALATLRQLPRCHPLFKL 402

Db 346 PAESDLYWGMQAKTVQVAENYHEMFVHLAQTHLVSEAFCLATQRTLAPSHPLHVL 405  
Qy 403 LIPHRYTHINTLARELLVAPGKLD-----KSTGLTGCGFSDLIKRNMEOQNSVLC 455  
Db 406 LAPFEFTFLNEGAARILLPSAGFIDVMAFAAPTQDTQATAG-----NRLGDFDYRG 458  
Qy 456 CLPEDIARGVED---IPGVYRDDGMQWGAIKSFVSEIYSIYPSDTSVDDOQLOAW 512  
Db 459 MLPESLKARINVDPLAPDPYRDDGLVWNAIKQWAADYVAVYASGDVDTADVELAAM 518  
Qy 513 VREIFSGFLG---RESSGMPSLDREALVQYITWVIFTCSAKHAAVSSGQFDSQVMPN 570  
Db 519 VGEVIGSGKAGFPITG-----RSQLEVLTVWIFTASQAHAANVFPQSPNMTYAPA 571  
Qy 571 LPPTMQLPPPTSKGOA-----RPSFIATLPVNSSSYHIIALWLLSAEPGDORPLG 622  
Db 572 ICAMSAAPADPSGKSEADWLKMPPTLVA-LEKVN--IYHLLGS-VYHRLGLDYRQTG 627  
Qy 623 HYDEHETEDAPRSVAA-----FORKLIQISKGIRNRGLALPYTYLDPPLIENSVS 676  
Db 628 -FPYAPVPSD--RRVTASGGPLERFOARLKEVEATIRNQARRRPVEYLLPSIPASTN 684  
Qy 677 I 677  
Db 685 I 685  
RESULT 15  
T07065  
probable lipoxigenase (EC 1.13.11.12) (clone H3) - potato  
N:Alternate names: 13-lipoxygenase  
C:Species: Solanum tuberosum (potato)  
C:Date: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 09-Jul-2004  
C:Accession: T07065  
R:Royo, J.N.; Vancanneyt, G.; Perez, A.G.; Sanz, C.; Scormann, K.; Rosahl, S.; Sanchez-Se  
J. Biol. Chem. 271, 21012-21019, 1996  
A:Title: Characterization of three potato lipoxigenases with distinct enzymatic activitie  
A:Reference number: Z15894; MUID:96355454; PMID:8702864  
A:Accession: T07065  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-914 <ROY>  
A:Cross-references: UNIPROT:O24371; EMBL:X96406; NID:g1495803; PIDN:CAA65269.1; PID:g149  
A:Experimental source: cv. Desiree; leaf  
C:Function:  
A:Description: catalyzes the hydroperoxidation of specific unsaturated fatty acids  
C:Superfamily: lipoxygenase  
C:Keywords: fatty acid oxidation; oxidoreductase  
Query Match 15.4%; Score 555; DB 2; Length 914;  
Best Local Similarity 26.6%; Pred. No. 6.6e-35;  
Matches 205; Conservative 100; Mismatches 247; Indels 220; Gaps 33;  
Qy 88 WFCWFLEWLPGAALHPCCYQWLEGAGELVREGAKVSWQDHHPTLQDQ-----R 139  
Db 181 FFLESITIEGACGVPVHPPCNSVQPK-----KDHGKRIFFSNQPYLPDETAPAGLSLR 235  
Qy 140 QKELES-----RQKMSWKTYIE-GWP-----RCLDHE 166  
Db 236 ERELRLGDKGVRKLSRIYDYDIYDNLGNPKGIDFARPKLGGDDNVYPRCSRGR 295  
Qy 167 TVKOLDLNI-----KYSAMKNKL----- 185  
Db 296 VPTDITSAESRVEKPNPTVYPRDEQFEESQNTFSTSLKAVLHNLPLSLMASISSNNH 355  
Qy 186 FPKAHSAYTELKVGLLDRTGLWLSLEMRRLFNFRKTPAAYEV----- 229  
Db 356 DFGFSDIDNLYSGLLKLGLQDEV-----LKKLPLPKVSSIKEGDLLKYDTPKI 407  
Qy 230 ----FAHQWQEDAFASQFLNGINPVLIRCHSLPNNFPVTDEMVA-----VLG- 274  
Db 408 LSKOKFA-WLRDDEFARQIAGVNPVSVIEKLFQFPFPPSKLDPEIYGPQESALKKEHILGH 466

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QY 275 -POTSLQAELEKGSFLVDHGILSGVH-----TNILNKPOPSAAPMTLLHQSSGS 324
Db 467 LMGMTVQEALDANKLEIVDH-----HDVYLPFLDRINALDGRKAYATRTIFFL---SDV 517
QY 325 GPLLPITAIOLK--QTGPDN---PIFLP---SDDTWDWLLAKTWVRNSEFYIHEAVTHLL 376
Db 518 GTLKPIAIELSLPQT--GPSRSKRVTTPVCATGNWTQIAKAHVCAKDAGVHQLVNHWL 576
QY 377 HAHLEIPEVFALATRLQPLCHPLFKLLIPIHRYTLHINTLARELLV-----APGK 426
Db 577 RTHASLEPFLAAHRQLSAMHPIYKLLDPHMYTLEINGLARQSLINADGVIEACFTFOR 636
QY 427 LIDKSTGLG-----TGGFSDLIKRNMEOQLNYSVLCLPEDIRAG-----VEDIPGYYY 474
Db 637 YCMEISAAAYKNWRFDEGLPADLIRRG-----AVPDSQPQHGKLLIEDYP---Y 685
QY 475 RDGMOIWAIGAKSFVSEIYSIYPSDTSVQDDOELQAWVREIEFSGFLGREGSGMPSLLD 534
Db 686 AADGLMIWGAIESWVRDYVNHYPSSAQVCSDELQAWYAEITNVGHVDLRNEEWMPTLA 745
QY 535 TREALVOYITWVFTCSAKHAAVSSGQFDSVMMNPLPPTMO--LP-----PPTSKQARP 588
Db 746 TPEDLISILITLWLASAQHAALNFCQPYGGVFNRPPLMRRLIPDENDPEYAVFLADP 805
QY 589 ES-FIATLPAVNSSYHIIALMLLSAEPGDQRPLG--HYPDEHFTEDAPRRSVAAFQR-- 643
Db 806 QKYFFSALPSSLQATKFMVAVDTLSTHSPDEEYLGHERHQPST-WTGDA--EIVEAFYKFS 862
QY 644 -KLIIQISKIRERNRGL-----ALPYTYLDPL-----IENSYSI 677
Db 863 AEIGRIEKIEIDERNANTKLKNRCGAGVLPYELLAPSSGPGVTCRGVPNSVSI 914
```

Search completed: July 18, 2005, 22:02:14  
Job time : 30.3348 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:41:37 ; Search time 114.351 Seconds

(without alignments)

3031.690 Million cell updates/sec

Title: US-10-688-676A-4

Perfect score: 3604

Sequence: 1 MAKCRVRVSTGEACGAGTWD.....GLALPYTLDPPLIENSVSI 677

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	3604	100.0	677	1	LX1B_MOUSE	Q35936 mus musculus
2	3255	90.3	677	2	Q8K4F2	Q8K4F2 rattus norv
3	2883.5	80.0	676	2	Q8IYQ2	Q8IYQ2 homo sapien
4	2880.5	79.9	676	1	LX1B_HUMAN	O15296 homo sapien
5	2767.5	76.8	667	2	Q9XT59	Q9XT59 bos taurus
6	1864	51.7	711	1	LXE3_HUMAN	Q9YJ11 homo sapien
7	1840	51.1	711	1	LXE3_MOUSE	Q9WV07 mus musculus
8	1795	49.8	701	1	LOXR_HUMAN	O75342 homo sapien
9	1770	49.1	701	1	LOXR_MOUSE	O75342 mus musculus
10	1666.5	46.2	686	2	Q66J74	O66J24 xenopus lae
11	1450.5	40.2	673	1	LX05_MOUSE	P48999 mus musculus
12	1447	40.1	672	1	LX05_MESAU	P51399 mesocricetu
13	1447	40.1	672	1	LX05_HUMAN	P12527 rattus norv
14	1441.5	40.0	673	1	LX05_HUMAN	P09917 homo sapien
15	1355	37.8	670	2	Q7T2A9	Q7T2A9 brachydanio
16	1254	34.8	663	2	Q8BHG4	Q8BHG4 m mus muscu
17	1247	34.6	662	1	LX0P_MOUSE	P39655 mus musculus
18	1224	34.0	663	2	Q6ISF8	Q6ISF8 homo sapien
19	1222	33.9	662	1	LX0P_HUMAN	P18054 homo sapien
20	1198	33.2	663	2	Q6PHB2	Q6PHB2 mus musculus
21	1191	33.0	662	1	LX0L_MOUSE	P39654 mus musculus
22	1186	32.9	662	1	LX0P_BOVIN	P27479 bos taurus
23	1185.5	32.9	661	1	LX01_HUMAN	P16050 homo sapien
24	1176	32.6	662	1	LX02_RAT	Q02759 rattus norv
25	1163	32.3	662	1	LX0P_PIG	P16469 sus scrofa
26	1145	31.8	662	1	LX01_RABIT	P12530 oryctolagus
27	1139	31.6	662	1	LX0P_RABIT	O19043 oryctolagus
28	1129.5	31.3	662	1	LX0E_MOUSE	P55249 mus musculus
29	1129.5	31.3	662	2	Q91Y66	Q91Y66 mus musculus
30	1044.5	29.0	1066	1	A0SL_PLEHO	O6025 plexaura ho
31	1030.5	28.6	555	2	Q95103	Q95103 bos taurus

32	847	23.5	430	2	Q9BEG3	Q9BEG3 bos taurus
33	690	19.1	390	2	Q8C587	Q8C587 mus musculus
34	592	16.4	685	1	LOXA_PSEAE	Q3i498 pseudomonas
35	590	16.4	685	1	LOXA_PSEAE	Q8rnt4 pseudomonas
36	561	15.6	896	1	LOX2_HORVU	Q8gam2 hordeum vul
37	555	15.4	914	2	O24371	O24371 solanum tub
38	554	15.4	565	2	Q82V62	Q82V62 nitrosomona
39	553.5	15.4	881	2	O6RSN2	O6ren2 carica papa
40	549.5	15.2	922	2	Q93YA9	Q93ya9 sesbania ro
41	546.5	15.2	881	2	Q9M463	Q9m463 cucumis sat
42	543.5	15.1	860	1	LOXA_LYCES	P38415 lycopersico
43	541	15.0	862	2	Q43191	Q43191 solanum tub
44	540.5	15.0	862	2	Q8W4X6	Q8w4x6 prunus dulc
45	540	15.0	926	2	Q9FNX8	Q9fnx8 arabidopsis

#### ALIGNMENTS

RESULT 1  
LX1B\_MOUSE  
ID LX1B\_MOUSE STANDARD; PRT; 677 AA.  
AC O35936;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Arachidonate 15-lipoxygenase, type II (EC 1.13.11.33) (15-LOX-2) (8S-  
DE lipoxygenase) (8S-LOX).  
GN Name=Alox15b; Synonyms=Alox8;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RC TISSUE=Epidermis;  
RX MEDLINE=97450967; PubMed=9305900; DOI=10.1074/jbc.272.39.24410;  
RA Jieaka M., Kim R.B., Boeglin W.E., Nanney L.B., Brash A.R.;  
RT "Molecular cloning and functional expression of a phorbol ester-  
RT inducible 8S-lipoxygenase from mouse skin";  
RL J. Biol. Chem. 272:24410-24416(1997).  
RN [2]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RC STRAIN=NMRI; TISSUE=Epidermis;  
RX MEDLINE=98186642; PubMed=9518531; DOI=10.1016/S0005-2760(97)00214-2;  
RA Kriegl P., Kinzig A., Heidt M., Marks F., Fuerstenberger G.;  
RT "cDNA cloning of a 8-lipoxygenase and a novel epidermis-type  
RT lipoxygenase from phorbol ester-treated mouse skin";  
RL Biochim. Biophys. Acta 1391:7-12(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Skin;  
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01366;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
RA Nikaudo I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,  
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
RA Balderelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
RA Schriber L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Negashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita K.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Miyazaki A., Sakai K., Sakaki D., Shibata K., Shinagawa A.,  
RA Yasunishi A., Yoshino K., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573(2002).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Kidney;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Strausberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins K.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Munz D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalka U., Smalusz D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -I- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,11Z,13E) - (15S) -  
CC 15-hydroperoxyicoso-5,8,11,13-tetraenoate.  
CC -I- COPACTOR: Iron (By similarity).  
CC -I- PATHWAY: Leukotrienes biosynthesis.  
CC -I- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -I- TISSUE SPECIFICITY: Expressed in epidermis and brain. No  
CC expression found in heart, spleen, liver, skeletal muscle, kidney  
CC or testis.  
CC -I- INDUCTION: By phorbol ester.  
CC -I- SIMILARITY: Belongs to the lipoxigenase family.  
CC -I- SIMILARITY: Contains 1 PLAT domain.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; U93277; AAC53356.1; -;  
DR EMBL; Y14696; CAA75003.1; -;  
DR EMBL; AK028724; BAC26085.1; -;  
DR EMBL; BC015253; AAH15253.1; -;  
DR HSSP; P12530; 1LOX.  
DR MGD; MGI:1098228; Alox15b.  
DR GO; GO:0005622; C:intracellular; ISS.  
DR GO; GO:0006917; P:induction of apoptosis; ISS.  
DR GO; GO:0006629; P:lipid metabolism; ISS.  
DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.  
DR GO; GO:0030336; P:negative regulation of cell migration; ISS.  
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.  
DR GO; GO:0045285; P:negative regulation of growth; ISS.  
DR InterPro; IPR00907; Lipoxigenase.  
DR InterPro; IPR001024; Lipoxigenase LH2.  
DR InterPro; IPR001885; Mam\_lipoxigenase.  
DR InterPro; IPR008976; PLAT\_LH2.  
DR Pfam; PF00305; Lipoxigenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.

DR PRINTS; PR00467; MAMLIPOXGNASE.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00095; PLAT; 1.  
KW Dioxigenase; Iron; Leukotriene biosynthesis; Oxidoreductase;  
KW Polymorphism.  
FT DOMAIN 2 125 PLAT.  
FT METAL 374 374 Iron (By similarity).  
FT METAL 379 379 Iron (By similarity).  
FT METAL 554 554 Iron (By similarity).  
FT METAL 677 677 Iron (By similarity).  
FT VARIANT 32 32 E -> G (in clone K12).  
FT VARIANT 38 38 L -> M (in clone G2).  
FT VARIANT 58 58 P -> R (in clone K12).  
FT VARIANT 76 76 V -> A (in clones G2, G5, G11 and K1).  
FT VARIANT 413 413 I -> V (in clone K7).  
FT VARIANT 536 536 R -> Q (in clones G2, G5 and G11).  
SQ SEQUENCE 677 AA; 76230 MW; 780E1AC9C2F68399 CRC64;  
Query Match 100.0%; Score 3604; DB 1; Length 677;  
Best Local Similarity 100.0%; Pred. No. 1.5e-280;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVSGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60  
DB |||||  
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVSGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60  
DB |||||  
QY 61 VGTVLMLRVHKAPPSVSLPLMSFRSDAWFCRWFLEWLPGAALHPPCQWLEGGAGELVLR 120  
DB |||||  
QY 61 VGTVLMLRVHKAPPSVSLPLMSFRSDAWFCRWFLEWLPGAALHPPCQWLEGGAGELVLR 120  
DB |||||  
QY 121 EGAARVSVQDHHPTLQDQORQKELESQRQWYWKTYIEGMPRLCDHETVKDLDLNKYSAM 180  
DB |||||  
QY 121 EGAARVSVQDHHPTLQDQORQKELESQRQWYWKTYIEGMPRLCDHETVKDLDLNKYSAM 180  
DB |||||  
QY 181 KNAKLFFKAHSAYTELKVGKLLDRTGLWRSREMRLLFNFRKTPAAEYVFAHWQDAPPA 240  
DB |||||  
QY 181 KNAKLFFKAHSAYTELKVGKLLDRTGLWRSREMRLLFNFRKTPAAEYVFAHWQDAPPA 240  
DB |||||  
QY 241 SQFLNGINPLVLRCHSLPNNFPVTVDEMVAIVLPGTSLQAELEKGSFLVDHGLTSGVH 300  
DB |||||  
QY 241 SQFLNGINPLVLRCHSLPNNFPVTVDEMVAIVLPGTSLQAELEKGSFLVDHGLTSGVH 300  
DB |||||  
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQLKQTPGPNPIFLPSDDTWDMLLAKTW 360  
DB |||||  
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQLKQTPGPNPIFLPSDDTWDMLLAKTW 360  
DB |||||  
QY 361 VRNSEFYTHEAVTHLLHAHLIPEVPALATLROLPRCHPLFKLLIPIHRYTLHINTLAREL 420  
DB |||||  
QY 361 VRNSEFYTHEAVTHLLHAHLIPEVPALATLROLPRCHPLFKLLIPIHRYTLHINTLAREL 420  
DB |||||  
QY 421 LVAPGKLIDKSTGLGTGGSFSDLIKENMEQLNYSVLCPLDIRARGVEDIPGYYYRDDGQ 480  
DB |||||  
QY 421 LVAPGKLIDKSTGLGTGGSFSDLIKENMEQLNYSVLCPLDIRARGVEDIPGYYYRDDGQ 480  
DB |||||  
QY 481 IWGAIKSFVSEIVSYIYPDSITSVDQDQELQAWVREIFSEGFSGRESSGMPSLDREALV 540  
DB |||||  
QY 481 IWGAIKSFVSEIVSYIYPDSITSVDQDQELQAWVREIFSEGFSGRESSGMPSLDREALV 540  
DB |||||  
QY 541 QYITWVIFTCSAKHAHVSSGQFDSQVWMPNLPPTTQWLPPPTSKGQARPESFIATLPVNS 600  
DB |||||  
QY 541 QYITWVIFTCSAKHAHVSSGQFDSQVWMPNLPPTTQWLPPPTSKGQARPESFIATLPVNS 600  
DB |||||  
QY 601 SSYHIIALWLLSAEPGDORPLGHYPDEHFTDAPRSVAARFKLIQISKGRERNRGLA 660  
DB |||||  
QY 601 SSYHIIALWLLSAEPGDORPLGHYPDEHFTDAPRSVAARFKLIQISKGRERNRGLA 660  
DB |||||  
QY 661 LPYTYLDPPLENSVSI 677  
DB |||||  
QY 661 LPYTYLDPPLENSVSI 677  
DB |||||

RESULT 2

Q8K4F2  
ID Q8K4F2 PRELIMINARY; PRT; 677 AA.  
AC Q8K4F2;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE 15-lipoxigenase-2.  
GN Name=Alox15b;  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Boeglin W.E., Schneider C., Brash A.R.;  
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- COFACTOR: Iron (By similarity).  
CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
DR EMBL; AF415240; AAN03708.1; -;  
DR HSP; P12530; ILOX.  
DR GO; GO:0005622; C:intracellular; ISS.  
DR GO; GO:0006917; P:induction of apoptosis; ISS.  
DR GO; GO:0006629; P:lipid metabolism; ISS.  
DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.  
DR GO; GO:0030336; P:negative regulation of cell migration; ISS.  
DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.  
DR GO; GO:0045926; P:negative regulation of growth; ISS.  
DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR000907; Lipoxigenase.  
DR InterPro; IPR001024; Lipoxigenase\_LH2.  
DR InterPro; IPR001885; Mam\_lipoxigenase.  
DR InterPro; IPR008976; PLAT\_LH2.  
DR Pfam; PF00305; Lipoxigenase\_1.  
DR Pfam; PF01477; PLAT\_1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR PRINTS; PR00467; MAMLOXGNASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00290; IG\_MHC; UNKNOWN\_1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00095; PLAT; 1.  
KW Dioxigenase; Oxidoreductase.  
SQ SEQUENCE 677 AA; 76145 MW; 49A47B47C491B8B1 CRC64;

Query Match 90.3%; Score 3255; DB 2; Length 677;  
Best Local Similarity 89.2%; Pred. No. 1.7e-252;  
Matches 604; Conservative 32; Mismatches 41; Indels 0; Gaps 0;

Qy 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKPSAGAEDFEVTLPOD 60  
Db 1 MAKFRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKPSAGAEDFEVTLPOD 60  
Qy 61 VGTVMLEVRHKAPEVSVPLMSFRSDAWFCRWFLEWLPGAALHPCCYOWLEGAGELVLR 120  
Db 61 VGTVMLEIRHKAPEVSVPLMSFRSDAWFCRWFLEWLPGAALRPCCYOWLEGAGELVLR 120  
Qy 121 EGAARVSHQDHPHTLQDQKELSRQKXWYKWTYIEGWPRCLDHTETVKDLDLNIKYSAM 180  
Db 121 EGAARVSHQDHPHTLQDQKELSRQKXWYKWTYIEGWPRCLDHTETVKDLDLNIKYSAM 180  
Qy 181 KNAKLFFKAHSAYTELKVGKLLDRTGLWRSIREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240  
Db 181 KNAKLFFKAHSAYTELKVGKLLDRTGLWRSIREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240  
Qy 241 SQFLNGINPVLIIRCHSLPNPFVPTDENVAVPLGPGTSLQAELEKGSFLVDHGLSGVH 300  
Db 241 SQFLNGINPVLIIRCHSLPNPFVPTDENVAVPLGPGTSLQAELEKGSFLVDHGLSGVH 300  
Qy 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQKOTPGDPNPFLPSDDTMDMLLAKTW 360  
Db 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIALQKOTPGDPNPFLPSDDTMDMLLAKTW 360

Qy 361 VRNEFYTHEAVTHLHAHLIPEVFALATLRLQPRCHPLFKLLPHIRYTHINTLAREL 420  
Db 361 VRNEFSIHEALTHLHAHLIPEVFALATLRLQPRCHPLFKLLPHIRYTHINTLAREL 420  
Qy 421 LVAFCKLIDKSTGLTGSGFSDLIKRNMQLNYSVLCPLPEDIRARGVEDIPGYVDDGQV 480  
Db 421 LVAFGVVDKSTGLTGIGGFSGLIKRNMQLNYSVLCPLPEDIRARDVGLPGYVDDGQV 480  
Qy 481 IWGAIKFSVSEIVSIYPSDTSVODDQELQAVWEIIFSEGFLGRESSGMPSLDTRREALV 540  
Db 481 IWSAIRSFVSIYPSDTSVODDQELQAVWEIIFSEGFLGRESSGMPSLDTRREALV 540  
Qy 541 QYITWVFTCSAKHAASVSSQFDCVWMPNLPPTWQLPPTPSKQARPESTIATLPVNS 600  
Db 541 QYITWVFTCSAKHAASVSSQFDCVWMPNLPPTWQLPPTPSKQARPESTIATLPVNS 600  
Qy 601 SSYHIALWLSAEPGDPORPLGHYPDEHFTEDAPRRSVAAPORKLQISKGRNRGLA 660  
Db 601 TCDVIALWLSKEFGDPRPLGHYPDEHFTEDAPRRSVAAPORKLQISKGRNRGLA 660  
Qy 661 LPYTYLDPPLIENSIVI 677  
Db 661 LPYTYLDPPLIENSIVI 677

RESULT 3  
Q8IYQ2  
ID Q8IYQ2 PRELIMINARY; PRT; 676 AA.  
AC Q8IYQ2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Arachidonate 15-lipoxygenase, second type.  
GN Name=ALOX15B;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RN Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Strausberg R.;  
RN Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- COFACTOR: Iron (By similarity).

CC -|- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -|- SIMILARITY: Contains 1 PLAT domain.  
 DR EMBL: BC035217; AAH35217.1; -;  
 DR EMBL: BC063647; AAH63647.1; -;  
 DR HSSP: P25330; ILOX  
 DR GO: GO:0003622; C:intracellular; ISS.  
 DR GO: GO:0006917; P:induction of apoptosis; ISS.  
 DR GO: GO:0006917; P:induction of apoptosis; ISS.  
 DR GO: GO:0006629; P:lipid metabolism; ISS.  
 DR GO: GO:0045786; P:negative regulation of cell cycle; ISS.  
 DR GO: GO:0030336; P:negative regulation of cell migration; ISS.  
 DR GO: GO:0008285; P:negative regulation of cell proliferation; ISS.  
 DR GO: GO:0045926; P:negative regulation of growth; ISS.  
 DR InterPro: IPR003006; IG\_MHC.  
 DR InterPro: IPR000907; Lipoxigenase.  
 DR InterPro: IPR001024; Lipoxigenase LH2.  
 DR InterPro: IPR001885; Mam\_lipoxigenase.  
 DR Pfam: PF00305; Lipoxigenase; 1.  
 DR Pfam: PF01477; PLAT; 1.  
 DR PRINTS: PRO0087; LIPOXYGENASE.  
 DR PRINTS: PRO0467; MAMLIPOXYGENASE.  
 DR SMART: SM00308; LH2; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN 1.  
 DR PROSITE: PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE: PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE: PS00095; PLAT; 1.  
 DR DIOXYGENASE; Oxidoreductase.  
 KW DIOXYGENASE 676 AA; 75884 MW; 4F641DP2FBB902C6 CRC64;  
 SQ SEQUENCE

Query Match 80.0%; Score 2883.5; DB 2; Length 676;  
 Best Local Similarity 78.2%; Pred. No. 1.2e-222;  
 Matches 530; Conservative 68; Mismatches 77; Indels 3; Gaps 2;

QY 1 MAKCRVRVSTGACAGTWDKVSIVTGHGSPVLPLDLHKGFSAGAEEDFEVTLPOD 60  
 DB 1 MAEFVRVSTGAFAGTWDKVSIVTGRGSPPLDLNLKERTAGAEEDFQVTLRED 60  
 QY 61 VGTVMRLRVHKAPEVSVLMS - FRSDAWFCRWFLEWLPGAALHPFCYQWLEGAGELVL 119  
 DB 61 VGRVLLLRVHKAPP - VLPGLGAPADAWFCRWFQLTTPRGGHLLFPCCYQWLEGAGTLVL 118  
 QY 120 REGAAKVSQDHPHTLQDROKELSRQMYKWTYIEGWPCLDHETVKDLDIAIKYSA 179  
 DB 119 QEGTAKVSQADHPVLPQOQBELQARQMYQWKAYNPWCPCLDEKTVEDLELNKYST 178  
 QY 180 MNNAKLPFKAGAYTELKVKGLDRLTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAF 239  
 DB 179 ANNAFYLQAGAPAEKMKGLLDKGLWRSLEMRRLFNFRTPAAEYFAHWQEDAF 238  
 QY 240 ASQFLNGINPVLIRCHSLPNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLISGV 299  
 DB 239 ASQFLNGINPVLIRCHSLPNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLISGI 298  
 QY 300 HTNILNCKQPSAAPTILHQSQSGPILPILAIQLKOTGPDPNPFLPSDDTMDWLLAKT 359  
 DB 299 QTNVINGKQPSAAPTILYQSGCGPFLPILAIQLKOTGPDPNPFLPTDDKMDWLLAKT 358  
 QY 360 WYRNSFYTHAVTHLLHAHLIPEVFALATRLQPRCHPLFKLLIPIHYTHLINTLARE 419  
 DB 359 WYRNEFSFHEATHLHLHLIPEVFTLATLQPRCHPLFKLLIPIHYTHLINTLARE 418  
 QY 420 LIAVAPGLDKSTGLTGTFSDLIKRNMBQLANYSVLCLPEDIARGVEDIPGYVYRDDGM 479  
 DB 419 LLIVPGQVDRSTGIGIEGFSSELIQRMKQLNQLNLLCLPEDITRGVEDIPGYVYRDDGM 478  
 QY 480 QIWGALKSFVSEIVSYIYSDTSVQDDQELQAWREIFEGFLGRSSGMPSLDITREAL 539  
 DB 479 QIWGAVERFVSEIIGIYFSDSVQDDQELQAWREIFSKGFLNQGSSGIPSSLETREAL 538  
 QY 540 VOYITWVITFCSAKHAASVSGQFDSVWPNLPPTTQOLPPPTSKGQARPESTIATLPVYN 599  
 DB 539 VOYITWVITFCSAKHAASVAGQFDSCAWPNLPPTTQOLPPPTSKGLATCEGFIATLPVYN 598  
 QY 600 SSSYHIIALLWLSAEFCQDQRLPHGYDPDEHFTDAPRRSVAAFQKLIQISKGIERNRGL 659

DB 599 ATCDVILLWLSKEPGQRLGTYPDHFTEAPRRSIATFQSRLAQISRGIQERNRGL 658  
 QY 660 ALPYTYLDPPLIENSVS 677  
 DB 659 VLPYTYLDPPLIENSVS 676  
 RESULT 4  
 LX1B HUMAN  
 ID LX1B HUMAN STANDARD; PRT; 676 AA.  
 AC O15296; Q8TEV3; Q8TEV4; Q8TEV5; Q8TEV6; Q9UKM4;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Arachidonate 15-lipoxygenase, type II (EC 1.13.11.33) (15-LOX-2) (15-lipoxygenase 2).  
 GN Name=ALOX15B;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RC TISSUE=Skin;  
 RX MEDLINE=97322340; PubMed=9177185; DOI=10.1073/pnas.94.12.6148;  
 RA Braish A.R., Boeglin W.E., Chang M.S.;  
 RT "Discovery of a second 15S-lipoxygenase in humans.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 94:6148-6152(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM A).  
 RX MEDLINE=21248677; PubMed=11350124; DOI=10.1006/geno.2001.6519;  
 RA Kriegl P., Marks F., Fuerstenberger G.;  
 RT "A gene cluster encoding human epidermis-type lipoxygenases at chromosome 17p13.1: cloning, physical mapping, and expression.";  
 RL Genomics 73:323-330(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS A; B; C AND D).  
 RX MEDLINE=21975171; PubMed=11839751; DOI=10.1074/jbc.M11936200;  
 RA Tang S., Bhatia B., Maldonado C.J., Yang P., Newman R.A., Liu J.,  
 RA Chandra D., Traag J., Klein R.D., Fischer S.M., Chopra D., Shen J.,  
 RA Zhou H.E., Chung L.W.K., Tang D.G.;  
 RT "Evidence that arachidonate 15-lipoxygenase 2 is a negative cell cycle regulator in normal prostate epithelial cells.";  
 RL J. Biol. Chem. 277:16189-16201(2002).  
 RN [4]  
 RP SEQUENCE OF 337-484 FROM N.A. (ISOFORM B).  
 RX MEDLINE=20009393; PubMed=10542053;  
 RA Kilty I., Logan A., Vickers P.J.;  
 RT "Differential characteristics of human 15-lipoxygenase isozymes and a novel splice variant of 15S-lipoxygenase.";  
 RL Eur. J. Biochem. 266:83-93(1999).  
 CC -|- FUNCTION: Converts arachidonic acid exclusively to 15S-hydroperoxyicosatetraenoic acid, while linoleic acid is less well metabolized.  
 CC -|- CATALYTIC ACTIVITY: Arachidonate + O(2) = (5Z,8Z,11Z,13E)-(15S)-15-hydroperoxyicoso-5,8,11,13-tetraenoate.  
 CC -|- COFACTOR: Iron (By similarity).  
 CC -|- PATHWAY: Leukotriene biosynthesis.  
 CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -|- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=A;  
 CC IsoId=O15296-1; Sequence=Displayed;  
 CC Name=B; Synonyms=15-LOX2sv-b;  
 CC IsoId=O15296-2; Sequence=VSP\_003142; VSP\_003143;  
 CC Name=C; Synonyms=15-LOX2sv-c;  
 CC IsoId=O15296-3; Sequence=VSP\_003144; VSP\_003145;  
 CC Name=D; Synonyms=15-LOX2sv-a;  
 CC IsoId=O15296-4; Sequence=VSP\_003142;  
 CC -|- TISSUE SPECIFICITY: Expressed in hair, prostate, lung and cornea.  
 CC -|- SIMILARITY: Belongs to the lipoxygenase family.  
 CC -|- SIMILARITY: Contains 1 PLAT domain.



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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; U78294; AAB61706.1; -  
 DR EMBL; AJ305028; CAC34521.1; -  
 DR EMBL; AJ305029; CAC34521.1; JOINED.  
 DR EMBL; AJ305030; CAC34521.1; JOINED.  
 DR EMBL; AJ305031; CAC34521.1; JOINED.  
 DR EMBL; AF468051; AAL76274.1; -  
 DR EMBL; AF468052; AAL76275.1; -  
 DR EMBL; AF468053; AAL76276.1; -  
 DR EMBL; AF468054; AAL76277.1; -  
 DR EMBL; AF149095; AAD37786.1; ALT\_SEQ.  
 DR HSSP; P12530; ILOX.  
 DR Genew; HGNC:434; ALOX15B.  
 DR MIM; 603697; -  
 DR GO; GO:0005622; C:intracellular; ISS.  
 DR GO; GO:0016165; P:lipoygenase activity; TAS.  
 DR GO; GO:0006631; P:fatty acid metabolism; TAS.  
 DR GO; GO:0006917; P:induction of apoptosis; ISS.  
 DR GO; GO:0045786; P:negative regulation of cell cycle; ISS.  
 DR GO; GO:0030336; P:negative regulation of cell migration; ISS.  
 DR GO; GO:0008285; P:negative regulation of cell proliferation; ISS.  
 DR GO; GO:0045926; P:negative regulation of growth; ISS.  
 DR InterPro; IPR000907; Lipoygenase.  
 DR InterPro; IPR001024; Lipoygenase LH2.  
 DR InterPro; IPR001885; Mam lipoygenase.  
 DR Pfam; PF00305; Lipoygenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00467; MAMLIPOXYGENASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE 1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 DR KW Alternative splicing; dioxygenase; Iron; Leukotriene biosynthesis;  
 KW Oxidoreductase.  
 FT DOMAIN 2 124 PLAT.  
 FT METAL 373 373 Iron (By similarity).  
 FT METAL 378 378 Iron (By similarity).  
 FT METAL 553 553 Iron (By similarity).  
 FT METAL 676 676 Iron (By similarity).  
 FT VARSPPLIC 401 429 Missing (in isoform B and isoform D).  
 FT VARSPPLIC 483 527 Missing (in isoform B).  
 FT VARSPPLIC 561 617 Missing (in isoform B).  
 FT DVLALWLSKEPGQ -> VRKGRPRWQAGGDPAPQPHS  
 FT ALSAFSLTPVIGCTCPACSHPPKAWQAHARAS (in  
 FT isoform C).  
 FT /FTid=VSP\_003144.  
 FT /FTid=VSP\_003143.  
 FT FDSCAWMNLPSPQSLKGLATCEGFIATLPPVNNATC  
 FT DVLALWLSKEPGQ -> VRKGRPRWQAGGDPAPQPHS  
 FT ALSAFSLTPVIGCTCPACSHPPKAWQAHARAS (in  
 FT isoform C).  
 FT /FTid=VSP\_003144.  
 FT /FTid=VSP\_003143.  
 FT VARSPPLIC 618 676 Missing (in isoform C).  
 FT /FTid=VSP\_003145.  
 FT L -> V (in Ref. 3).  
 FT G -> C (in Ref. 4).  
 FT R -> H (in Ref. 3).  
 FT SEQUENCE 676 AA; 75998 MW; 2PF360B2AA03C8AF CRC64;  
 Query March 79.9%; Score 2880.5; DB 1; Length 676;  
 Best Local Similarity 78.0%; Pred. No. 2.1e-222;  
 Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;  
 QY 1 MAKRRVVRVTGACAGTWDKVSIVGTGHSPLVLDHLGKPSAGAEEDFEVTLPOD 60  
 DB 1 MAEFRVRVSTGEAFAGTWDKVSIVGTGHSPLVLDHLGKPSAGAEEDFEVTLPOD 60  
 QY 61 VGTVLMRLVRHKAPPEVSVLPLMS -FRSDAWFCRWFLEWLPGAALHPPCYQWLEGAGELVL 119

Db 61 VGRVLLRVRHKAPP -VPLLGPLAPDANFCRWFQLTTPRGCHLLFCYQWLEGAGTIVL 118  
 QY 120 REGAAKVSQWDDHPTLQDQKELSKQKYSWKTYIEGMPRLCDHETVVDLDLNIKYSA 179  
 Db 119 QEGTAKVSQWDDHPTLQDQKELSKQKYSWKTYIEGMPRLCDHETVVDLDLNIKYSA 178  
 QY 180 MKNAKLFFKHAAYTEUKVGLDRTGLWRSRLRMRLFNFRKTPAAEYVFAHQEDAFF 239  
 Db 179 AKNAFYLOAGSAFENKIKGLDRLKGLWRSRLRMRLFNFRKTPAAEYVFAHQEDAFF 238  
 QY 240 ASQFLNGINPVLRCHSLPNNRPVTDVAPVLPGLTSLQAELEKSLFLVDHGLSGV 299  
 Db 239 ASQFLNGINPVLRCHSLPNNRPVTDVAPVLPGLTSLQAELEKSLFLVDHGLSGV 298  
 QY 300 HTNINLKPQFSAPMTLLHQSQSGSGLPIAQLKQTGPDNPIFLPSDDTDWLLAKT 359  
 Db 299 QTNVINGKPQFSAPMTLLHQSQSGSGLPIAQLKQTGPDNPIFLPSDDTDWLLAKT 358  
 QY 360 WRNSEFYIHEAVTHLHAHLIPVFPALATLRLQPRCHPLFKLLIPHRYTLHINTLARE 419  
 Db 359 WRNABFSFEALTHLHSHLLPEVFTLATLRLQPRCHPLFKLLIPHRYTLHINTLARE 418  
 QY 420 LLVAPGKLIDKSTGLTGSGFSDLIKRNWQLNYSVLCLPDIRARGVEDIPGYRDDGM 479  
 Db 419 LLVPGQVDRSTGIGIEGFSGLIQRNMQLNYSVLCLPDIRARGVEDIPGYRDDGM 478  
 QY 480 QIWGAIKSFVSEIYIYPSDTSVQDDQLQAWREIFSEGFLGREGSGMPSLIDTREAL 539  
 Db 479 QIWGAVERFVSEIYIYPSDESQDDRELQAWREIFSGFLNQESSGIFSSLETREAL 538  
 QY 540 VQYITWVIFTCSAKHAASVSGQFDSVMMNPLPPTMQLPPTPSKGQARPESFIATLPVN 599  
 Db 539 VQYITWVIFTCSAKHAASVSGQFDSVMMNPLPPTMQLPPTPSKGQARPESFIATLPVN 598  
 QY 600 SSSYHIIALWLSAERGDORPLGHYPDEHPTEDAPRSVAFAFKLQISKGIERNRGL 659  
 Db 599 ATCDVILALWLSKSGDQPLGTYPDEHPTEDAPRSVAFAFKLQISKGIERNRGL 658  
 QY 660 ALPYTYLDPLLIENSVSII 677  
 Db 659 VLPYTYLDPLLIENSVSII 676  
 RESULT 5  
 Q9XT59 PRELIMINARY; PRT; 667 AA.  
 ID Q9XT59  
 AC Q9XT59  
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE 15S-lipoxygenase type 2 (Fragment).  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Buthera; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovinae; Bos.  
 OC NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Cornea;  
 RX MEDLINE=99165584; PubMed=10064896; DOI=10.1016/S1388-1981(99)00004-9;  
 RA "Liming M., Oliv E.;  
 RT "cDNA cloning of 15-lipoxygenase type 2 and 12-lipoxygenases of bovine  
 RT corneal epithelium";  
 RL Biochim. Biophys. Acta 1437:124-135 (1999).  
 CC -1- COFACTOR: Iron (By similarity).  
 CC -1- SIMILARITY: Belongs to the lipoxygenase family.  
 CC -1- SIMILARITY: Contains 1 PLAT domain.  
 DR EMBL; AF107263; AAD39096.1; -  
 DR HSSP; P12530; ILOX.  
 DR GO; GO:0005622; C:intracellular; ISS.  
 DR GO; GO:0006917; P:induction of apoptosis; ISS.  
 DR GO; GO:0006629; P:lipid metabolism; ISS.

DR GO: 0045786; P-negative regulation of cell cycle, ISS.  
 DR GO: 0030336; P-negative regulation of cell migration, ISS.  
 DR GO: 0008285; P-negative regulation of cell proliferation, ISS.  
 DR GO: 0045926; P-negative regulation of growth, ISS.  
 DR InterPro: IPR003006; Iq MHC.  
 DR InterPro: IPR000907; Lipoxigenase.  
 DR InterPro: IPR001024; Lipoxigenase\_LH2.  
 DR InterPro: IPR001885; Mam lipoxigenase.  
 DR Pfam: PF00305; Lipoxigenase; 1.  
 DR Pfam: PF01477; PLAT; 1.  
 DR PRINTS: PRO0087; LIPOXYGENASE.  
 DR PRINTS: PRO0467; MAMLIPOXGNASE.  
 DR SMART: SM00308; LH2; 1.  
 DR PROSITE: PS00290; IG MHC; UNKNOWN 1.  
 DR PROSITE: PS00711; LIPOXYGENASE 1; 1.  
 DR PROSITE: PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE: PS00095; PLAT; 1.  
 KW Dioxygenase; Oxidoreductase.  
 FT NON\_TER 1  
 SQ SEQUENCE 667 AA; 75327 MW; B49141C82A0E79C8 CRC64;

Query Match 76.8%; Score 2767.5; DB 2; Length 667;  
 Best Local Similarity 75.3%; Pred. No. 2.5e-213;  
 Matches 503; Conservative 75; Mismatches 89; Indels 1; Gaps 1;

QY 10 TGEACGAGTWDKVSIVGTHGESPLVLDHLGKEFSAGAEDEFVTLPDQVGTVMILRV 69  
 DB 1 TGEAFGVGTWDKISVIVGTRGETPLLDRLGKEFNAGPEEDFEVTPEDVGRVLLVRV 60

QY 70 HKAPPEVSIPLMSFRSDANFCRWFLEWLPAGALHPCHQWLEGAGELVLRGAAKVSWQ 129  
 DB 61 HKAPPAISAP-RALGRDANFCRMLVHTVTPPRGALCFPCYQWLEGRSLVLRGTAKISWE 119

QY 130 DHHTLQDQORQESLRQKMYSKTVIEGWPCRLDHTVTKDLDNLTKYSAMKNALFFKA 189  
 DB 120 DHHTLQDQORQESLRQKMYSKTVIEGWPCRLDHTVTKDLDNLTKYSAMKNALFFKA 179

QY 190 HSAYTELVKGLDRTGLWRSREMRLENFRKTPAAEYVFAHWQDADFASQFLNGINP 249  
 DB 180 GSALAEKLGKLLDRKGLKSKEMRVRNFRKTPAVEVCEHWQDEFAFYQFLNGLNP 239

QY 250 VLIRCHSLPNPPVPTDENVAPVLGPGTSLQAELEKSLFLVDHGLLSGVHNTLNKRPQ 309  
 DB 240 VLIRCHSLPNPPVPTDENVAPVLGPGTSLQAELEKSLFLVDHGLLSGVHNTLNKRPQ 299

QY 310 FSAAPMTLLHQSGLPLPIATOLKQTPGPNPIFLPSDDTMDMLLAKTWVRNSEFYTH 369  
 DB 300 FSTAPMTLLYQRRGRLPLALQLSQTGPGNPIFLPSDDKMDMLLAKTWVRNSEFYTH 359

QY 370 EAVTHLLHAHLIPEVPALATRLQPLCHPLFKLLIPIHYTYLHINTLARELLVAPGKLD 429  
 DB 360 EALTHLLQALHVEVPALATRLQPLCHPLFKLLIPIHYTYLHINTLARELLVAPGQVD 419

QY 430 KSTGLTGFGSGLIKKNMQLNSVLCLPEDIARGVEDIPGVYRDDGMQWGAIKSVF 489  
 DB 420 RSTGLTGFGSGLIKKNMQLNSVLCALPDIDIRARGVEDIPGVYRDDGMQWGAVERVF 479

QY 490 SETVSTVYSDTSQVDDQLQAVVREIFSEGLGREGSSGWPISLDREALVOYITWVFT 549  
 DB 480 SEMIGIYPSDESVRDDELQAVVREIFSEGLGREGSSGWPISLDREALVOYITWVFT 539

QY 550 CSAKHAASVSGQSDSCVWPNPPTTQQLPPPTSKGQARPESTFATLPVNSSSYHIIALW 609  
 DB 540 CSAKHAASVAGQDFDAWPNLPSPPTTQQLPPPTSKGQARLEGFATLPVYNATCDVVIALW 599

QY 610 LLSAEPGDORPLGHYDEHTEFTDAPRSVAAPFORKLIQISKGIERNRGLALPYTVLDPP 669  
 DB 600 LLSKEPDORPLGHYDEHTEFTDAPRSVAAPFORKLIQISKGIERNRGLALPYTVLDPP 659

QY 670 LIENSYSI 677  
 DB 660 LIENSYSI 667

RESULT 6  
 LXE3 HUMAN  
 ID LXE3 HUMAN STANDARD; PRT; 711 AA.  
 AC Q9BYJ1; Q9H4P2; Q9HC22;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Epidermis-type lipoxigenase 3 (EC 1.13.11.-) (e-LOX-3).  
 GN Name=ALOXE3;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21248677; PubMed=11350124; DOI=10.1006/geno.2001.6519;  
 RA Krieg P., Marks P., Fuerstenberger G.;  
 RT "A gene cluster encoding human epidermis-type lipoxigenases at chromosome 17p13.1: cloning, physical mapping, and expression."; Genomics 73:323-330 (2001).  
 RL [2]  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Brash A.R.; Boeglin W.E.;  
 RT "Human epidermal lipoxigenase, ortholog of mouse Alox3."; Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Krieg P., Fuerstenberger G.;  
 RT "cDNA cloning, genomic structure, and chromosomal localization of human epidermis-type lipoxigenase-3."; Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
 RL [4]  
 RN [4]  
 RP VARIANTS NCIE SER-396 AND PHE-500.  
 RX MEDLINE=21634626; PubMed=11773004; DOI=10.1093/hmg/11.1.1107;  
 RA Jobard F., Lefevre C., Karaduman A., Blanchet-Bardon C., Emre S., Weissenbach J., Ozguc M., Lathrop M., Prud'homme J.-F., Fischer J.;  
 RT "Lipoxigenase-3 (ALOXE3) and 12(R)-lipoxigenase (ALOX12B) are mutated in non-bullous congenital ichthyosiform erythroderma (NCIE) linked to chromosome 17p13.1."; Hum. Mol. Genet. 11:1107-113 (2002).  
 RL [5]  
 CC -!- FUNCTION: Introduces molecular oxygen into polyunsaturated fatty acids. Exact substrate is not known.  
 CC -!- COFACTOR: Iron (by similarity).  
 CC -!- PATHWAY: Leukotrienes biosynthesis.  
 CC -!- TISSUE SPECIFICITY: Predominantly expressed in skin.  
 CC -!- DISEASE: Defects in ALOXE3 are a cause of nonbullous congenital ichthyosiform erythroderma (NCIE) [MIM:242100]. NCIE is characterized by prominent erythroderma and fine white, superficial, semiadherent scales. As many as 90% of affected individuals present at birth as collodion babies. Patients suffer from palmoplantar keratoderma, often with painful fissures, digital contractures, and loss of pulp volume. In half of the cases, a nail dystrophy including ridging, subungal hyperkeratosis, or hypoplasia has been described.  
 CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 CC  
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 CC  
 CC -----  
 CC EMBL; AJ305021; CAC34518.1; -  
 CC EMBL; AJ305021; CAC34518.1; JOINED.  
 CC EMBL; AJ305023; CAC34518.1; JOINED.  
 CC EMBL; AJ305025; CAC34518.1; JOINED.  
 CC EMBL; AF182218; AAG16899.1; -  
 CC EMBL; AJ269499; CAC12843.1; -  
 CC HSSP; P12530; ILOX.

DR Genew: HGNC:13743; ALOXE3.  
DR MIM: 607206; --  
DR MIM: 242100; --  
DR InterPro: IPR000907; Lipoxigenase.  
DR InterPro: IPR001024; Lipoxigenase LH2.  
DR InterPro: IPR001885; Mam\_lipoxigenase.  
DR Pfam: PF00305; Lipoxigenase; 1.  
DR Pfam: PF01477; PLAT; 1.  
DR PRINTS: PR00087; LIPOXYGENASE.  
DR PRINTS: PR00467; MAMLIPOXGNASE.  
DR SMART: SM00308; LH2; 1.  
DR PROSITE: PS00711; LIPOXYGENASE 1; 1.  
DR PROSITE: PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE: PS00095; PLAT; 1.  
DR Dioxigenase; Disease mutation; Iron; Leukotriene biosynthesis;  
KW Oxidoreductase.  
FT DOMAIN 2 119 PLAT.  
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FT VARIANT 500 500 V->F (in NCIB).  
FT VARIANT 500 500 V->F (in NCIB).  
FT CONFLICT 155 155 C->R (in Ref. 3).  
FT CONFLICT 194 194 F->L (in Ref. 2).  
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Best Local Similarity 50.1%; Pred. No. 1.1e-140;  
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Db 1 MAVRLCVTTGYSYLRAGLTNLSVLTGTCGSPKQRLDRGRDPAGSVQKYKRCFAE 60  
  
Qy 61 VGTVLMRLVRHKAPPEVSLPLMSFRSDAWFCRWFLEWLPFGAALHPFCYQWLEGAGELVLR 120  
Db 1 LGEILLRLHKE-----RYAFFKDSMYCSRICVTEPDGSGVSHPPCYQWIEGYCTVELR 114  
  
Qy 121 EGAAKVSWQDHHTPTQDORQKELSRQKMYSKWTYIEGWPKCLDHETVKDLDL 173  
Db 115 PGTARTICQDSLPLLDHRTRELRAQRQCYRWKIYAPGFCVVDVNSPQESDKKFAIT 174  
  
Qy 174 -----NIKYSAMKNVAKLFFKAHSAYTELAVK 199  
Db 175 KTTTCVGDGSGNRYLPGFPMKIDIPSLMNEPNRYSATKTSLLFNALPASLGMKLR 234  
  
Qy 200 GLLDRGTGLWRLSREMRRLFNFRKTPAAEYVFAHQEDAFQASQFLNGINPVLIRRSCLP 259  
Db 235 GLLDRKGSWKLLDDMNIFWCHKFTTKYVTEHCEDHFFGQYLVNGVNPVWLHCISLPL 294  
  
Qy 260 NFPVTDVMAVPLGPGTSLQAELEKSLFLVDHGILSGVNTNINLNGKPFQPSAAPMTLLH 319  
Db 295 SKLPVTDVMAVPLGQDTCLQTELERGNIFLADYWLAEAPTHCLNGRQYVVAAPLCLLW 354  
  
Qy 320 QSSGSGPLLPATOLKQTPGDNPTFLSDDTWDLAKTWVRNSEFYIHEAVTHLLHAH 379  
Db 355 LSP-QGALVPLAIQISQTPGDPSPFLPTDSEWDLAKTWVRNSEFVLNTHFLCTH 413  
  
Qy 380 LIPEVFALATLRLQPRCHPLFKLIPHYRYLTHINTLARELLVAPGLKIDKSTGLGTGCF 439  
Db 414 LLCEAFANATLRLQPLCHPIYKLLPHRYTLQVNTIARATLLNPEGLVDQVTSIGRQL 473  
  
Qy 440 SDLIKRNEQLNYSVLCLEPIDRAGVEDIPGYVYRDDGMQIWGAIKFSFVSEIYSIYPS 499  
Db 474 IYLMSTGLAHFTYTNFLPDSLARGVLAIPNHYRVDGLKIWAIESFVSEIVGYIYPS 533  
  
Qy 500 DTSVQDDDELQAWVREISEGFLGREGSGMSLLDTREALVQYITWVTFCSAKHAAYSS 559  
Db 534 DASVQDDSELQAWTGEIFAQAFLEGREGSGFSRLCTPGEMVKFLTAIFNCSAQHAAYNS 593  
  
Qy 560 QOFDSVMPNLPPTMQLPPTTSKQARPESFIATLPVNSSSVYHIALWLLLSAEPQGR 619  
Db 594 QHDFGAWNPAPNSMRQPPQTGKTTTLTKYLTDLTPVNI SCNNLLLFWLVSQEPKQDR 653

Qy 620 PLGHVPDEHFTEDAPRBSVAQFQKLIQISKIGIRNRLGALPYTYLDPPLIENSVS 677  
Db 654 PLGTYPDEHFTEDAPRBSVAQFQKLIQISKIGIRNRLGALPYTYLDPPLIENSVS 711  
  
RESULT 7  
LXE3 MOUSE  
ID LXE3 MOUSE STANDARD; PRT; 711 AA.  
AC Q9WV07;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Epidermis-type lipoxigenase 3 (EC 1.13.11.-) (e-LOX-3).  
GN Name=aloxe3;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NMRI; TISSUE=Skin;  
RX MEDLINE=99296830; PubMed=10366447; DOI=10.1006/geno.1999.5816;  
RA Kizig A., Heidt M., Fuerstenberger G., Marks F., Krieg P.;  
RT "cDNA cloning, genomic structure and chromosomal localization of a  
RT novel epidermis-type lipoxigenase";  
RL Genomics 58:158-164 (1999).  
CC -!- FUNCTION: Introduces molecular oxygen into polyunsaturated fatty  
CC acids. Exact substrate is not known.  
CC -!- COFACTOR: Iron (by similarity).  
CC -!- PATHWAY: Leukotrienes biosynthesis.  
CC -!- TISSUE SPECIFICITY: Skin specific.  
CC -!- SIMILARITY: Belongs to the lipoxigenase family.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
  
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-----  
CC EMBL: Y14695; CAB46101.1; --  
DR HSSP: P12530; ILOX.  
DR MGD: MGI:1345140; Alox3.  
DR InterPro: IPR000907; Lipoxigenase.  
DR InterPro: IPR001024; Lipoxigenase LH2.  
DR InterPro: IPR001885; Mam\_lipoxigenase.  
DR Pfam: PF00305; Lipoxigenase; 1.  
DR Pfam: PF01477; PLAT; 1.  
DR PRINTS: PR00087; LIPOXYGENASE.  
DR PRINTS: PR00467; MAMLIPOXGNASE.  
DR SMART: SM00308; LH2; 1.  
DR PROSITE: PS00711; LIPOXYGENASE 1; 1.  
DR PROSITE: PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE: PS00095; PLAT; 1.  
KW Dioxigenase; Iron; Leukotriene biosynthesis; Oxidoreductase.  
FT DOMAIN 2 119 PLAT.  
SQ SEQUENCE 711 AA; 80578 MW; 6E2183C7C64540E0 CRC64;  
  
Query Match 51.1%; Score 1840; DB 1; Length 711;  
Best Local Similarity 49.7%; Pred. No. 9.4e-139;  
Matches 357; Conservative 113; Mismatches 200; Indels 48; Gaps 3;  
  
Qy 1 MAKCRVRYSTGEACAGTWDKVSIVGTGHSPLVPLDLHLGKFSAGAEDFEVTLPOD 60  
Db 1 MAVRLCVTTGYSYLRAGLTNLSVLTGTCGSPKQRLDRGRDPAGSVQKYKRCFAE 60  
  
Qy 61 VGTVLMRLVRHKAPPEVSLPLMSFRSDAWFCRWFLEWLPFGAALHPFCYQWLEGAGELVLR 120  
Db 1 LGEILLRLHKE-----RYAFFKDSMYCSRICVTEPDGSGVSHPPCYQWIEGYCTVELR 114  
  
Qy 121 EGAAKVSWQDHHTPTQDORQKELSRQKMYSKWTYIEGWPKCLDHETVKDLDL 173  
Db 115 PGTARTICQDSLPLLDHRTRELRAQRQCYRWKIYAPGFCVVDVNSPQESDKKFAIT 174  
  
Qy 174 -----NIKYSAMKNVAKLFFKAHSAYTELAVK 199  
Db 175 KTTTCVGDGSGNRYLPGFPMKIDIPSLMNEPNRYSATKTSLLFNALPASLGMKLR 234  
  
Qy 200 GLLDRGTGLWRLSREMRRLFNFRKTPAAEYVFAHQEDAFQASQFLNGINPVLIRRSCLP 259  
Db 235 GLLDRKGSWKLLDDMNIFWCHKFTTKYVTEHCEDHFFGQYLVNGVNPVWLHCISLPL 294  
  
Qy 260 NFPVTDVMAVPLGPGTSLQAELEKSLFLVDHGILSGVNTNINLNGKPFQPSAAPMTLLH 319  
Db 295 SKLPVTDVMAVPLGQDTCLQTELERGNIFLADYWLAEAPTHCLNGRQYVVAAPLCLLW 354  
  
Qy 320 QSSGSGPLLPATOLKQTPGDNPTFLSDDTWDLAKTWVRNSEFYIHEAVTHLLHAH 379  
Db 355 LSP-QGALVPLAIQISQTPGDPSPFLPTDSEWDLAKTWVRNSEFVLNTHFLCTH 413  
  
Qy 380 LIPEVFALATLRLQPRCHPLFKLIPHYRYLTHINTLARELLVAPGLKIDKSTGLGTGCF 439  
Db 414 LLCEAFANATLRLQPLCHPIYKLLPHRYTLQVNTIARATLLNPEGLVDQVTSIGRQL 473  
  
Qy 440 SDLIKRNEQLNYSVLCLEPIDRAGVEDIPGYVYRDDGMQIWGAIKFSFVSEIYSIYPS 499  
Db 474 IYLMSTGLAHFTYTNFLPDSLARGVLAIPNHYRVDGLKIWAIESFVSEIVGYIYPS 533  
  
Qy 500 DTSVQDDDELQAWVREISEGFLGREGSGMSLLDTREALVQYITWVTFCSAKHAAYSS 559  
Db 534 DASVQDDSELQAWTGEIFAQAFLEGREGSGFSRLCTPGEMVKFLTAIFNCSAQHAAYNS 593  
  
Qy 560 QOFDSVMPNLPPTMQLPPTTSKQARPESFIATLPVNSSSVYHIALWLLLSAEPQGR 619  
Db 594 QHDFGAWNPAPNSMRQPPQTGKTTTLTKYLTDLTPVNI SCNNLLLFWLVSQEPKQDR 653



DR GO:0004052; F:arachidonate 12-lipoxygenase activity; TAS.  
DR GO:0008544; P:epidermal differentiation; TAS.  
DR GO:0006629; P:lipid metabolism; TAS.  
DR InterPro; IPR000907; Lipoxygenase.  
DR InterPro; IPR001024; Lipoxygenase LH2.  
DR InterPro; IPR001885; Mam lipoxygenase.  
DR Pfam; PF00305; Lipoxygenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
DR PROSITE; PS00095; PLAT; 1.  
KW Dioxygenase; Disease mutation; Iron; Leukotriene biosynthesis;  
KW Oxidoreductase.  
FT DOMAIN 2 119 PLAT.  
FT METAL 398 398 Iron (By similarity).  
FT METAL 403 403 Iron (By similarity).  
FT METAL 578 578 Iron (By similarity).  
FT METAL 701 701 Iron (By similarity).  
FT VARIANT 426 426 L -> P (in NCIE).  
FT VARIANT 578 578 /FTID=VAR 015173.  
FT H -> Q (in NCIE).  
FT /FTID=VAR 015174.  
SQ SEQUENCE 701 AA; 80355 MW; C33407575F8B077 CRC64;  
Query Match 49.8%; Score 1795; DB 1; Length 701;  
Best Local Similarity 47.9%; Pred. No. 3.8e-135;  
Matches 339; Conservative 121; Mismatches 210; Indels 38; Gaps 3;  
QY 1 MAKCRVSTGACAGTWDKVSIVGTHGESPLVDHKGKESAGAEDEFVTLPOD 60  
DB 1 MATYKRVATGDLISGTRDSISLTIVGTQGESKQLLNHFRDPATGAVGYTVQCPOD 60  
QY 61 VGTVLMVAVKAPPEVSPLMSFRSDANFCRWFLEWLPALAHPEPCYQWLEGELVLR 120  
DB 61 LGELIIIRLHKE-----RYAFFPKDPWYCNVQICAPNGRIYHPFAYQWMDGYETLALR 114  
QY 121 EGAAKVSWQDHHTTQDQKQESLRQKMYSWKT----- 154  
DB 115 EATGKTADDSPVLLEHKEIRAKQDFYHWRVFLGLPSVHIPSVPVRHRENNR 174  
QY 155 -----YIEGWRCLDHTVTDOLDLNKYSAMQNAKLPFAHSAAYTELKVGLLDRTGLWR 209  
DB 175 PEWNGYIPGFPILINFKATKFLNLNLYSFLKTASFVFLGPMALAFKVRGLDCKHSWK 234  
QY 210 SIREMRLENFRKTPAAEYVFAHWQEDAFASQFLNGINPVLIRCHSLPNFPVTDENV 269  
DB 235 RLKDIRKIPGKSVSYVAEHWAEEDTFGGYLYNGVNPGLIRCTRIPDKFPVTDENV 294  
QY 270 APVLPGTSLQALEKGLFLVDHGILGVHTNLLNGKQPSAAPMTLLHQSOGSGPLLP 329  
DB 295 APFLGEGTCLQALEKGNLYADYRIMGIPVLSGRKHQHCAPCLLH-FGPEGKMP 353  
QY 330 IAIQLKQTPGPNDFPLSPDDTDWLLAKTVWRNSEFYIHEAVTHLHAHLPIPEVALAT 389  
DB 354 IAIQLSQTPGDCPIFLPSDSEWDWLLAKTVWRYAEFYSEAHIAHLLETHLIAEAFCLAL 413  
QY 390 LRQLPRCHPLKLLIPHTRYTHLNTARELLVAPGKLDKSTGLTGCTGSPDSDLRNMEQ 449  
DB 414 LRNLPMCHPLKLLIPHTRYTVQINSIGRAVLLNEGGLSAGKMSLGVEGAGVMVRALSE 473  
QY 450 LNYSLVCLPEDIRAGVEDIPCYYYRDGMQIWLGAIKSVSEIVSYVPSDTSVQDDDEL 509  
DB 474 LTYDSLVLNDFVERGVQDLPGYIYRDDSLAWNALKYIVTEIITYIPSDAAVEGDEL 533  
QY 510 QAWREIFSEGLGREGSSGMPSLDTRALVQYITWVFTCSAKHAAVSSQFQSCVWMP 569  
DB 534 QSWQVEIFKECLLGREGSSGFPRLCTVPELIRYTVIYVTCSAKHAANTQMEFTAWMP 593  
QY 570 NLPTMQLPPTSKQARPESFIATLPANVSSVYHIALWLLSAPPGQRPGLGHPYDHPH 629

DB 594 NFPASMRNPPIQTGKLTTLTFMDTLPDVKTCITLLVLWLSRPPDDRRPLGHFPDIHF 653  
QY 630 TEDAPRSVAARFQKLQISKIGIRNRNGLALPYTLDPLIENSVS 677  
DB 654 VEEAPRSIEAFRQLNQISHDIRQNKCLPIPYLYLDPVLISISI 701  
RESULT 9  
LOXR\_MOUSE STANDARD; PRT; 701 AA.  
AC 070582;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Archadonate 12-lipoxygenase, 12R type (EC 1.13.11.-) (Epidermis-type  
DE lipoxygenase 12) (12R-lipoxygenase) (12R-LOX) (Epidermis-type  
DE lipoxygenase 2) (e-LOX 2).  
GN Name=Alox12b; Synonyms=Aloxe2;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
RC STRAIN=NRI; TISSUE=Epidermis;  
RX MEDLINE=9818642; PubMed=9518531; DOI=10.1016/S0005-2760(97)00214-2;  
RA Krieg P., Kinzig A., Heidt M., Marks F., Fuerstenberger G.;  
RT "cDNA cloning of a 8-lipoxygenase and a novel epidermis-type  
RL Biochim. Biophys. Acta 1391:7-12(1998).  
RN [2]  
RP SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGE.  
RC STRAIN=C57BL/6 X SJL;  
RX MEDLINE=99057919; PubMed=9837935; DOI=10.1074/jbc.273.50.33540;  
RA Sun D., McDonnell M., Chen X.-S., Lakkis M.M., Li H., Isaacs S.N.,  
RA Elsea S.H., Patel P.I., Funk C.D.;  
RT "Human 12(R)-lipoxygenase and the mouse ortholog. Molecular cloning,  
RL J. Biol. Chem. 273:33540-33547(1998).  
CC -!- FUNCTION: Converts arachidonic acid to 12R-  
CC hydroperoxyicosatetraenoic acid (12R-HPETE).  
CC -!- COPACTOR: Iron (By similarity).  
CC -!- PATHWAY: Leukotrienes biosynthesis.  
CC -!- TISSUE SPECIFICITY: Expressed in skin epidermis and other  
CC stratified epithelia including tongue and forestomach. Low levels  
CC of expression are found in trachea, brain and lung. Not expressed  
CC in intestine, liver, kidney, adipose tissue, muscle or  
CC hematopoietic cells.  
CC -!- DEVELOPMENTAL STAGE: In the embryo, expression begins at day 15.5.  
CC -!- SIMILARITY: Belongs to the lipoxygenase family.  
CC -!- SIMILARITY: Contains 1 PLAT domain.  
CC -----  
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CC -----  
CC EMBL; Y14334; CAAT74714.1; -.  
CC EMBL; AF059251; AAC79681.1; -.  
DR HSP; P12530; IL0X.  
DR MGD; MGI:1274782; Alox12b.  
DR InterPro; IPR000907; Lipoxygenase.  
DR InterPro; IPR001024; Lipoxygenase LH2.  
DR InterPro; IPR001885; Mam lipoxygenase.  
DR Pfam; PF00305; Lipoxygenase; 1.  
DR Pfam; PF01477; PLAT; 1.  
DR PRINTS; PR00087; LIPOXYGENASE.  
DR PRINTS; PR00467; MAMLOXGNASE.  
DR SMART; SM00308; LH2; 1.  
DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.





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Db 77 LGELVLYKE-----SPGSPESAFNCISIKVTCGSIYEFPFLWISGVGTPEIP 130
Qy 121 EGAKVSVQDHHPTLQDQKELSRQKQYKWKYIEGWPCRLDHTETVKDLDLNIKYSAM 180
Db 131 QGKGITLTSVPAIKQRESELNTRKQTHEWKTAKYAGAPHCISADAVTDLSPNDRFSYK 190
Qy 181 KNAKLFFKAHSAAYELKVGILLDRGLWSLRSEMRLENFRKTPAAEVVFAHWQEDAPFA 240
Db 191 KTIISGFFNLSGATLKGFLNCSWKDLNKKVFSIQWTKISDLVSELMNEDTFPG 250
Qy 241 SQFLNGINPLIRCHSLPNPNFVTDENVAPVLGPGTSLQAELEKSGSLFVDHGTLSGVH 300
Db 251 YQYLNGINPLMOKLRIPDNFPVDDVTVSATLKSITLQELQNGNIFLADYKILEGIP 310
Qy 301 TNLNGKPFQGAAPMTLLHQSSGSLPLPIAQLKQTPGPNPILPSPDDTMDLLAKTW 360
Db 311 TNVINGERQYIAAPMCLLWKP-NDLILPIALQLNQTGPEENPIFLPTDSKMDWTAKIW 369
Qy 361 VRNSEFYHEAVTHLLHAHLIPEVPALATLQLPCHPLPKLLPHIRYTHLHINTLAREL 420
Db 370 VRSEFQVHEIVSHLLYTHLAAEFNIAATRHLPMPGHPVYKLIIRPHLYTLEINTLARQT 429
Qy 421 LVAPGKLDKSTGTGTGSGFSLIKRMEQLNYSVLCLPEDIRARGVEDIPGVYVRDDGMQ 480
Db 430 LIGPKGLDQAVTVGNGVFPVLLARATESLYISALCLPDDIQAGVESIPNFRHDMGR 489
Qy 481 IWGAIKSVBSIVSYPSDTSVQDQLOQAVREIFSEGFLGREGSSGMPSLDITREALV 540
Db 490 IWEAMESPASIDVHYVYSDETSRDPQLQAVAEIFQEGFLSNKNSGIPSPATRVELT 549
Qy 541 QYITWVITCSAKHAASVSGQFSDCVMNPNLPPTMQLPPTSKGQARPESTIATLPVNS 600
Db 550 KYLTWVMTCTQHAASVSGQFDFYAMPNAPSTMRKDPPTAKGTTTYSILETILPAINT 609
Qy 601 SSVHIIALWLSABPGDORPLGHPYDEHFTEDAPRSVAAPQKLIQISKIRBNRGLA 660
Db 610 TATAMVTVSLSKGFLDQRLGRYKNKSFVEDVPKYYEQFKEKLSISESQIKORNTKK 669
Qy 661 LPYTVLDPDLIENSVI 677
Db 670 LTYHLDPEAVECSVSI 686

```

## RESULT 11

```

LOX5 MOUSE
ID _LOX5 MOUSE STANDARD; PRT; 673 AA.
AC P48999;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
GN Arachidonate 5-lipoxygenase (5-LO).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X 129/Sv; TISSUE=Peritoneal cavity;
RX MEDLINE=95355399; PubMed=7629107; DOI=10.1074/jbc.270.30.17993;
RA Chen X.-S., Naumann T.A., Kurte U., Jenkins N.A., Copeland N.G.,
RA Funk C.D.;
RT cDNA cloning, expression, mutagenesis, intracellular localization,
RT and gene chromosomal assignment of mouse 5-lipoxygenase.;
RL J. Biol. Chem. 270:17993-17999(1995).
CC -|- CATALYTIC ACTIVITY: Arachidonate + O(2) = (6E,8Z,11Z,14Z) - (5S) -5-
CC hydroperoxyicoso-6,8,11,14-tetraenoate.
CC -|- CATALYTIC ACTIVITY: (6E,8Z,11Z,14Z) - (5S) -5-hydroperoxyicoso-
CC 6,8,11,14-tetraenoate = (7E,9E,11Z,14Z) - (5S,6S) -5,6-epoxyicoso-
CC 7,9,11,14-tetraenoate + H(2)O.
CC -|- COFACTOR: Iron, also requires calcium and ATP for activity.
CC -|- PATHWAY: Leukotrienes biosynthesis; first step.

```

```

CC -|- PATHWAY: Leukotrienes biosynthesis; second step.
CC -|- SUBCELLULAR LOCATION: Cytoplasmic.
CC -|- SIMILARITY: Belongs to the lipoxygenase family.
CC -|- SIMILARITY: Contains 1 Pfam domain.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
CC EMBL: L42198; AAC37673.1; --
CC PIR: I49479; I49479.
CC HSSP: P12530; ILOX.
CC MGD: MGI:87999; Alox5.
CC GO: GO:0005737; C:cytoplasm; IDA.
CC GO: GO:0005634; C:nucleus; IDA.
CC GO: GO:0006954; P:inflammatory response; IMP.
CC GO: GO:0006931; P:leukotriene metabolism; IMP.
CC InterPro: IPR000907; Lipoxygenase.
CC InterPro: IPR001885; MamLipoxygenase.
CC Pfam: PF00305; Lipoxygenase; 1.
CC Pfam: PF01477; Pfam; 1.
CC PRINTS: PR00087; LIPOXYGENASE.
CC PRINTS: PR00467; MAMLIPOXYGENASE.
CC SMART: SM00308; LH2; 1.
CC PROSITE: PS00711; LIPOXYGENASE_1; 1.
CC PROSITE: PS00081; LIPOXYGENASE_2; 1.
CC PROSITE: PS00095; Pfam; 1.
CC Calcium; Dioxxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
KW INIT MET 0
FT DOMAIN 1 117 Pfam.
FT METAL 367 367 Iron (By similarity).
FT METAL 372 372 Iron (By similarity).
FT METAL 550 550 Iron (By similarity).
FT METAL 673 673 Iron (By similarity).
SQ SEQUENCE 673 AA; 77868 MW; 0B2910477A3B7085 CRC64;

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Query Match 40.2%; Score 1450.5; DB 1; Length 673;

Best Local Similarity 42.5%; Pred. No. 1.7e-107;

Matches 288; Conservative 133; Mismatches 242; Indels 15; Gaps 6;

Qy 6 VRVSTGEACAGTWDKVSIVTGHGSPVLPLDH-LGKEFSAGAEEDFEVTLPODVGV 64

Db 5 VTVATGQWFGATDDYIYLSIGSAGCEKLLDKAFYNDFERGAVDSYDVTVDLGEI 64

Qy 65 LMLRVHKAPPEVSLPLMSFRSDAWFCRWFELEWLPGAALHPCYOWLEGAGELVLRGAA 124

Db 65 YLVKIEKR-----KYWLHDDWLYKYLTKTPHGDYIEFPYCYRWITGEIIVLDGRA 116

Qy 125 KVSQDHHPTLQDORQKELSRQKQYKWKYIEGWPCRLDHTETVKDLDLNIKYSAMKNAK 184

Db 117 KLARDDQIHILKQHRKLEARQKQYRMWENPGLSLIDAKCHKDLPRDQFQSEKGV 176

Qy 185 LFFKAHSAYTELKVGKLLDR-TGLWRSLSREMRRLNFRKTPAAEVVFAHWQEDAPFA 243

Db 177 FVLNYSKAMENLFNRRFMHMFQSSWHDFADPEKIFVKISNTISERVKHWEDLMFGYQ 236

Qy 244 LINGINPVLIRCHSLPNPNFVTDENVAPVLGPGTSLQAELEKSGSLFVDHGTLSGVHTNI 303

Db 237 LNCNPNVLIRKCTALPKLPVTTMVECSLERQLSLQEQVQGNIFIVDYLDDGIDANK 296

Qy 304 LNC-KPQFSAAPMTLLHQSSGSLPLPIAQLKQTPGPNPILPSPDDTMDLLAKTW 362

Db 297 TDPCTHQFLAAPICLLYKNL-ANKIVPIAQLNQTGPEENPIFLPTDSKMDWTAKIW 355

Qy 363 NSEFYHEAVTHLLHAHLIPEVPALATLQLPCHPLPKLLPHIRYTHLHINTLARELV 422

Db 356 SSDPHVHTHTHLRTHLTVSEVFGIAMRYQLPFAVHPLFKLLVAHVRFRTIAINTKAREQLI 415

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QY 423 APGLKIDKSTGLTGTGSGFSLIKRNMQNLNYSVLCLPEDIARGV---EDIPGYVYRDDGM 479
Db 416 CEYGLFDKANATGGGHVQWQVQAVQDLTYVSSLCFPEAIKARGMDSTEDMPFFYRDDGL 475
QY 480 QIWGAIKTSFVSEIVSYIYPSDTSVQDDQLQAWREIFSEGFLGREGSSGMPSLDTRAL 539
Db 476 LWWEAIQSFTMEVSYIYPSDTSVQDDQLQAWREIFSEGFLGREGSSGMPSLDTRAL 535
QY 540 VOYITWVIFTSKAAHAUVSSGQFSCVWMPNLPPTWOLPPPTSKGQAPESFIATLPAVN 599
Db 536 SEYLTWVIFTASQAHAUVNFGQYDWCSPINAPPTWRAPPTAKGVVTTIEQVATLPDRG 595
QY 600 SSSYHIIALWLLSAPGQDQRLGHYPDEHFTEDAPRRSVAAPQKLIQISKIRENRGL 659
Db 596 RSCWHLGAVWALSQFQNEFLGMYPEEHFIEKPVKEAMIRFRKNLEAIVIAERNK 655
QY 660 ALPTYTLDPLPIENSIVI 677
Db 656 KLPYYLSPDRIPNSVAI 673

RESULT 12
LOX5_MESAU STANDARD; PRT; 672 AA.
AC PS1339;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).
GN Name=ALOX5;
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Syrian;
RX MEDLINE=97109716; PubMed=8951996; DOI=10.1016/S0952-3278(96)90008-3;
RA Kitzler J.W., Eling T.E.;
RT "Cloning, sequencing and expression of a 5-lipoxygenase from Syrian
RT hamster embryo fibroblasts.";
RL Prostaglandins Leukot. Essent. Fatty Acids 55:269-277(1996).
CC -1- CATALYTIC ACTIVITY: Arachidonate + O(2) = (6E,8Z,11Z,14Z) - (5S) -5-
CC hydroperoxyicosaa-6,8,11,14-tetraenoate.
CC -1- CATALYTIC ACTIVITY: (6E,8Z,11Z,14Z) - (5S) -5-hydroperoxyicosaa-
CC 6,8,11,14-tetraenoate = (7E,9E,11Z,14Z) - (5S,6S) -5,6-epoxyicosaa-
CC 7,9,11,14-tetraenoate + H(2)O.
CC -1- COFACTOR: Iron, also requires calcium and ATP for activity.
CC -1- PATHWAY: Leukotrienes biosynthesis; first step.
CC -1- PATHWAY: Leukotrienes biosynthesis; second step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the lipoxygenase family.
CC -1- SIMILARITY: Contains 1 PLAT domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43333; AAA85257.1; -.
DR HSSP; P12530; 1LOX.
DR InterPro; IPR000907; Lipoxygenase.
DR InterPro; IPR01024; Lipoxygenase LH2.
DR InterPro; IPR001885; Mam lipoxygenase.
DR Pfam; PF00305; Lipoxygenase; 1.
DR Pfam; PF01477; PLAT; 1.
DR PRINTS; PR00087; LIPQYGNASE.
DR PRINTS; PR00467; MAMLOXGNASE.
DR SMART; SM00308; LH2; 1.

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DR PROSITE; PS00711; LIPOXYGENASE 1; 1.
DR PROSITE; PS00081; LIPOXYGENASE_2; 1.
DR PROSITE; PS50095; PLAT; 1.
KW Calcium: dioxygenase; Iron; Leukotriene biosynthesis; Oxidoreductase.
FT INIT MET 0 By similarity.
FT DOMAIN 1 116 PLAT.
FT METAL 366 366 Iron (By similarity).
FT METAL 371 371 Iron (By similarity).
FT METAL 549 549 Iron (By similarity).
FT METAL 672 672 Iron (By similarity).
SQ SEQUENCE 672 AA; 77741 MW; 1F7234B5C297B30F CRC64;

Query Match 40.1%; Score 1447; DB 1; Length 672;
Best Local Similarity 42.9%; Pred. No. 3.3e-107;
Matches 291; Conservative 127; Mismatches 244; Indels 16; Gaps 7;

QY 6 VRVSTGEACGAGTWDKVSIVGTHGESPLVPLDH-LGKERSAGAEEDFEVTLPODVGV 64
Db 5 VTVATGSQWFAQTDDYIYLSLIGSAGCKHLLDKAFYNDFERGAVDSYDVTVDBELGEI 64
QY 65 LMLRVHKAPPEVSLPLMSFRSDAWFCRWFELEWLPGAALHPPCYQWLEGAGELVREGAA 124
Db 65 QLVRIEKR-----KYWLHDDWLYKYLTK-TFTDYIEPCYRWITGESEIVLRDGEA 115
QY 125 KVSQDHHPTLQDQROKESRQKMYSWKTYIEGWPCRLDHEVPCLDHETVKLDLNIKYSAWNAK 184
Db 116 KLARDQIHILKQHRKLEARQKQYRWENWNPGLSIDAKCHKDLPRDIQDSEKGYD 175
QY 185 LFFKAHSATBELKVGKLLDR-TGLWRSUREMRLNFRKTPAAEVYFAHWQDADFASQF 243
Db 176 FVLNYSKAVENLFINRFMHMFQSSWNPADFPEKIFVKISNTISERVYKXHWQEDLMFGYQF 235
QY 244 LINGINVLIRCHSLPNFPVTDEMVAFLVPGTSLQAELEKGSFLVDHGLSLGVHTNI 303
Db 236 LNCNPVLKRCRELPOKLPVTTEMWECSELRHLSLEQVEQENIFVDYELLDGIDANK 295
QY 304 LNG-KPQFSAAPMTLLHQSGLPLPIALQKQTPGPDNPIFLPSDDTWMLLAKTWVR 362
Db 296 TDPCTHQFLAAPICLLYKNL-ANKIVPIALQNAQGEKNPIFLPSDAKYDWLLAKIWR 354
QY 363 NSEFVIRHNAVTHLLHAHLIPEVPALATLROLPRCHPLKLLIPHRYTLHINTLARELIV 422
Db 355 SSDFVHVQITHTLLCTHLVSEVFGIYRQLPANVPIFKLLVAHVRFITAINTKAREQLI 414
QY 423 APGLKIDKSTGLTGTGSGFSLIKRNMQNLNYSVLCLPEDIARGV---EDIPGYVYRDDGM 479
Db 415 CEYGLFDKANATGGGHVQWQVQAVQDLTYVSSLCFPEAIKARGMDSTEDIPYFRRDGL 474
QY 480 QIWGAIKTSFVSEIVSYIYPSDTSVQDDQLQAWREIFSEGFLGREGSSGMPSLDTRAL 539
Db 475 LWWEAIQSFTSEVSYIYPSDTSVQDDQLQAWREIFSEGFLGREGSSGMPSLDTRAL 534
QY 540 VOYITWVIFTSKAAHAUVSSGQFSCVWMPNLPPTWOLPPPTSKGQAPESFIATLPAVN 599
Db 535 SEYLTWVIFTASQAHAUVNFGQYDWCSPINAPPTWRAPPTAKGVVTTIEQVATLPDRG 594
QY 600 SSSYHIIALWLLSAPGQDQRLGHYPDEHFTEDAPRRSVAAPQKLIQISKIRENRGL 659
Db 595 RSCWHLGAVWALSQFQNEFLGMYPEEHFIEKPVKEAMIRFRKNLEAIVIAERNK 654
QY 660 ALPTYTLDPLPIENSIVI 677
Db 655 KLPYYLSPDRIPNSVAI 672

RESULT 13
LOX5_RAT
ID LOX5 RAT STANDARD; PRT; 672 AA.
AC P12527;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Arachidonate 5-lipoxygenase (EC 1.13.11.34) (5-lipoxygenase) (5-LO).

```



RL Proc. Natl. Acad. Sci. U.S.A. 85:26-30(1988).  
 RN ERRATUM.  
 RP Matsumoto T., Funk C.D., Raadmark O., Hoeoeg J.-O., Joernvall H.,  
 RA Samuelsson B.; Proc. Natl. Acad. Sci. U.S.A. 85:3406-3406(1988).  
 RL [4]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=89320027; PubMed=2526519;  
 RA Matsumoto T., Funk C.D., Raadmark O., Hoeoeg J.-O., Joernvall H.,  
 RA Samuelsson B.;  
 RT "Molecular cloning and amino acid sequence of human 5-lipoxygenase.";  
 RL Adv. Prostaglandin Thromboxane Leukotriene Res. 19:466-469(1989).  
 RN [5]  
 RP SEQUENCE OF 1-49 FROM N.A.  
 RX MEDLINE=89202374; PubMed=2565035;  
 RA Funk C.D., Hoshiko S., Matsumoto T., Raadmark O., Samuelsson B.;  
 RT "Characterization of the human 5-lipoxygenase gene.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:2587-2591(1989).  
 RN [6]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RX MEDLINE=91067649; PubMed=2251250;  
 RA Hoshiko S., Raadmark O., Samuelsson B.;  
 RT "Characterization of the human 5-lipoxygenase gene promoter.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:9073-9077(1990).  
 RN [7]  
 RP MUTAGENESIS OF SOME HISTIDINE RESIDUES.  
 RX MEDLINE=92042124; PubMed=1939225;  
 RA Nguyen T., Faigueyret J.-P., Abramowitz M., Riendeau D.;  
 RT "Evaluation of the role of conserved His and Met residues among  
 RT lipoxygenases by site-directed mutagenesis of recombinant human 5-  
 RT lipoxygenase.";  
 RL J. Biol. Chem. 266:22057-22062(1991).  
 RN [8]  
 RP MUTAGENESIS OF SOME RESIDUES.  
 RX MEDLINE=92171971; PubMed=1540191;  
 RA Ishii S., Noguchi M., Miyano M., Matsumoto T., Noma M.;  
 RT "Mutagenesis studies on the amino acid residues involved in the iron-  
 RT binding and the activity of human 5-lipoxygenase.";  
 RL Biochem. Biophys. Res. Commun. 182:1482-1490(1992).  
 CC -!- CATALYTIC ACTIVITY: Arachidonate + O(2) = (6S,8Z,11Z,14Z)-(5S)-5-  
 CC hydroperoxyicoso-6,8,11,14-tetraenoate.  
 CC -!- CATALYTIC ACTIVITY: (6E,8Z,11Z,14Z)-(5S)-5-hydroperoxyicoso-  
 CC 6,8,11,14-tetraenoate = (7E,9E,11Z,14Z)-(5S,6S)-5,6-epoxyicoso-  
 CC 7,9,11,14-tetraenoate + H(2)O.  
 CC -!- COFACTOR: Iron, also requires calcium and ATP for activity.  
 CC -!- PATHWAY: Leukotrienes biosynthesis; first step.  
 CC -!- PATHWAY: Leukotrienes biosynthesis; second step.  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the lipoxygenase family.  
 CC -!- SIMILARITY: Contains 1 PLAT domain.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; J03600; AAA36183.1; -;  
 DR EMBL; J03571; AAA65450.1; -;  
 DR EMBL; J04520; AAA59522.1; -;  
 DR EMBL; M38191; AAA63212.1; -;  
 DR FIR; A28117; DAHUAL.  
 DR HSP; P12530; ILOX.  
 DR IntAct; P09917; -;  
 DR Genew; HGNC:435; ALOX5.  
 DR MIM; 152390; -;  
 DR GO; GO:0004051; F:arachidonate 5-lipoxygenase activity; TAS.  
 DR GO; GO:0006691; P:leukotriene metabolism; TAS.  
 DR InterPro; IPR000907; Lipoxygenase.  
 DR InterPro; IPR001024; Lipoxygenase\_LH2.

DR InterPro; IPR001885; Mam\_lipoxygenase.  
 DR Pfam; PF00305; Lipoxygenase; 1.  
 DR PRINTS; PF01477; PLAT; 1.  
 DR PRINTS; PR00087; LIPOXYGENASE.  
 DR PRINTS; PR00467; MAMLIPOXGNASE.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00711; LIPOXYGENASE\_1; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Calcium; Dioxigenase; Direct protein sequencing; Iron;  
 KW Leukotriene biosynthesis; Oxidoreductase.  
 FT INIT MET 0  
 FT DOMAIN 0  
 FT METAL 1 117 PLAT.  
 FT METAL 367 367 Iron (By similarity).  
 FT METAL 372 372 Iron (By similarity).  
 FT METAL 550 550 Iron (By similarity).  
 FT METAL 673 673 Iron (By similarity).  
 FT MUTAGEN 358 358 D->N: No loss of activity.  
 FT MUTAGEN 362 362 H->S,N: Still some substantial activity.  
 FT MUTAGEN 367 367 H->S,N,A: No activity.  
 FT MUTAGEN 372 372 H->S,N: No activity.  
 FT MUTAGEN 376 376 E->Q: No activity.  
 FT MUTAGEN 390 390 H->S,N: Still some substantial activity.  
 FT MUTAGEN 390 390 H->A: No activity.  
 FT MUTAGEN 399 399 H->S,N: Still some substantial activity.  
 FT MUTAGEN 399 399 H->A: No activity.  
 FT MUTAGEN 432 432 H->N,A: Almost no loss of activity.  
 FT MUTAGEN 550 550 H->N,A: No activity.  
 SQ SEQUENCE 673 AA; 77852 MW; 7DBB515D9A58F0EB CRC64;  
 Query Match 40.0%; Score 1441.5; DB 1; Length 673;  
 Best Local Similarity 42.8%; Pred. No. 9.2e-107;  
 Matches 291; Conservative 126; Mismatches 244; Indels 19; Gaps 7;  
 QY 6 VRVSTGEACGAGTWDKVSIVGTHGESPLVPLDH-LGKERSAGAEEDPEVTLPODVGV 64  
 DB 5 VTVATGQSWFAGTDYIYLSLVGSAGCSKHLDDPFYDFNFERGAUVDVTVDELGI 54  
 QY 65 LMLRVHKAPPEVSLPLMSFRSDAWFCRMFELEWLPFGAALHFFCYQWLEGAGELVLRGAA 124  
 DB 65 QLVRIEKR-----KYWLNDWDYLYKTYLTATPHGDIYEFPCYRWITGDVWVLDGRA 116  
 QY 125 KVSQDHPHTLQDQKQKESQKYSKTYIEGHPCLDHTVTVDLDLNKYSAKNAK 184  
 DB 117 KLARDQIHILKQHRKKELETRKQYRWMEWNPFGPLSIDAKCHKDLPREDIQFSEKVD 176  
 QY 185 LFFKAHSAVTELVKVGLLDR-TGLWRSLEMRRLNFRKTPAAEYVFAHQWQDAPFASQF 243  
 DB 177 FVLNYSKAWENLFNRFMHMFQSSWDFADFEKI FVKISNTISERVMMHWQDLMPGYQF 236  
 QY 244 LINGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKSGSLFLVDHGILSGVHTWI 303  
 DB 237 LNCNPNVLRCTELPEKLPVTTEVCSLERQLSLEQEVQGNIFIVDFELLGDIGAN- 295  
 QY 304 LMGKP---QFSAPMTLHQSSGSGPLPIALQLKQTGPDNPDPFLPSDDTWDWLLAKTW 360  
 DB 296 -KTDPCTLQFLAAPICLLYKXL-ANKIVPIATQLNQIPGDENPIFLPSDAKYDMLLAKTW 353  
 QY 361 VRNSEFYTHEAVTHLHAHLIPEVFALATLRQLPCHPLFKLLIPIHRYTLHINTLAREL 420  
 DB 354 VRSSDFHVTHTLRLTHLRLVSEVFGIAMYRQLPAVHPILKULVAHVARTIATNTKREQ 413  
 QY 421 LVAPGKLIDKSTGLGTGGFSDLIKENMEQLNYSVLCLPEDIRARGV---EDIPGYVRDD 477  
 DB 414 LICEGLFDKANATGGGGHVQVQAMKDLTYASLCFFPAIKARGMESKEDIPIYYFYRDD 473  
 QY 478 GNOIWAIKSFVSEIVSYPSDTSVQDDQELQAWVREIFSESGFLGREGSGMPSLLDTR 537  
 DB 474 GLLVWEAIRTFATAEVVDIYEGDQVVEDEPQLQDFVNDVYVGMGRKSGSPFKSKVRE 533  
 QY 538 ALVQVITWVIFTCSAKHAHVSSGQSDSCVMMNLPPTMQLPPTPSKGOARPSFIATLPA 597  
 DB 534 QLSEYLTWVIFTASAQHAHVNFQYDMCSWIPNAPPTMRAPPTAKGVVTIEQIVDTLPD 593

QY 598 VNSSYHIALWLLSAERDQPLGHYPDEHTEFDAPRRSVAAPFORKLIQISKGIRERNR 657  
 Db 594 RGRSCHWLGAWALSQFQENELFLGMPYEEHFIEKPVKEARFRKNLEAIVSVIAERNK 653  
 QY 658 GLALPYTLDPELIENSYSI 677  
 Db 654 KKQLPYTLDPELIENSVAI 673

RESULT 15  
 Q7T2A9 PRELIMINARY; PRT; 670 AA.  
 AC Q7T2A9;  
 DT 01-OCT-2003 (TREMELrel. 25, Created)  
 DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)  
 DT 01-MAR-2004 (TREMELrel. 26, Last annotation update)  
 DE Hypothetical protein zgc:64120.  
 GN ORFNames=zgc:64120;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxID=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,  
 RA Leschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Jones S.J., Marra M.A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Straubeberg R.;  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 CC -1- COFACTOR: Iron (By similarity).  
 CC -1- SIMILARITY: Belongs to the lipoxigenase family.  
 CC -1- SIMILARITY: Contains 1 PLAT domain.  
 DR EMBL; BC054621; AAH54621.1; -;  
 DR ZFIN; ZDB-GENE-030131-1452; zgc:64120.  
 DR GO; GO:0005508; F:iron ion binding; IEA.  
 DR GO; GO:0016165; F:lipoxigenase activity; IEA.  
 DR GO; GO:006118; P:electron transport; IEA.  
 DR InterPro; IPR000907; Lipoxigenase.  
 DR InterPro; IPR001024; Lipoxigenase\_LH2.  
 DR Pfam; PF00305; Lipoxigenase; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR SMART; SM00308; LH2; 1.  
 DR PROSITE; PS00081; LIPOXYGENASE\_2; 1.  
 DR PROSITE; PS00095; PLAT; 1.  
 KW Dioxigenase; Hypothetical protein; Oxidoreductase.  
 SQ SEQUENCE 670 AA; 77006 MW; E68DD2A2B7472D1B CRC64;

Query Match 37.6%; Score 1355; DB 2; Length 670;  
 Best Local Similarity 41.4%; Pred. No. 8.2e-100;

Matches 280; Conservative 119; Mismatches 264; Indels 14; Gaps 6;  
 QY 5 RRVYSTGEACAGTWDKVSIVGTHGESPLVDHLGKFSAGAEDEFEVTLPODVGV 64  
 Db 4 KVTATGTSYSESTNNYVVTLLIGKSGKSTLLDNPGLDFCRGAVDDYIVKSDTDLGL 63  
 QY 65 LMLRVHKAPPEVSLPLMSFRSDAFCWFLEWLP--AALHFPCYQWLEGAGELV-LRE 121  
 Db 64 ILVRLEKH-----KYFIEDNMFRCYRVKVS-VPERCCVTFPCYRWLVGQGVFVLE 114  
 QY 122 GAAKVSQDHHPTLQDORQKESRQKMSYKWTIEGWPRCLDHETVTKDLNLINIKYSAMK 181  
 Db 115 GTAKLSEDSLPLEMAHQSELOERQKTYRWAVAPGPKCIDAKSEADLPQDAFEDNEK 174  
 QY 182 NAKLFFKAHSAYTELKVKGLDRTG-LWRSUREMRLFNFRKTPAAEVVFAHQWQDAFPA 240  
 Db 175 RSDPEGSLHYALLELSLKLAIREFGKSWSDLEDFRRIFWKLRSPIAETMEHWKEDWFFA 234  
 QY 241 SDFLNGINPVLRCHSLPNNFPVTDENVAPVLGGTSLQAELEKGSFLVDHGLTSGVH 300  
 Db 235 YQFLNGSNPRNITLKKVPSNFLTGMVQSSLIPTTTLNBELEKGNIFLVDHAILDGLP 294  
 QY 301 TNLNGKPPQFSAAPMTLLHQSSGGPILLPIAIQLKQTPGPNPILPSPDDTWDMLLAKTW 360  
 Db 295 ANVTENSEPQYIAAPCLLYEHEPKG-LIPIAIQLEQKDKDTPVLPSPDPLAWLLAKMW 353  
 QY 361 VRNSEFYIHEAVTHLHAHLPIEVFALATLRLQRPCHPLFKLLIPHYTLHINTLAREL 420  
 Db 354 VRHAEFQVQLLSHLRLTHLMVEVICVATLRLPAVHPYIKLLTPLRAYTLEINCRGTQ 413  
 QY 421 LVAPGKLIDKSTGLGTGGFSLIKRNEQLNYSVLCLPEDIRARGVEDIPGYYYEDDGMQ 480  
 Db 414 LLSPEGIFKRVVSTGGEGLLILAQREYKVLTYRSLOPKFDFLDRGVTKVGYVYDYSLM 473  
 QY 481 IWGAIKSFVSIIVSYPSDTSVDDOELQAWREIPSEGLGREGSGMPSLLDTREALV 540  
 Db 474 LWDIQNFVSGIVSYLQCDSDVQSDSELOQWIDHVAEGVDVPEFGLASDKTKEELI 533  
 QY 541 QYITWIFTCSAKHAASVSSGQFSCVMMNPPTMQLPPTPSKGOARPESTIATLPVNS 600  
 Db 534 TLLSVAIFTSTAQAHAATNNGQFNCWVPNTCTMRHPPRDKDAVTMEMIMDTLPDISQ 593  
 QY 601 SSYHIALWLLSAEPGDRPLGHYPDEHTEFDAPRRSVAAPFORKLIQISKGIRERNRGLA 660  
 Db 594 SCVQMAITWHLGRAQPDAPIMGQYVEQYFTEPAALKVIDKPRKELKELEDKIMAQNEGLE 653  
 QY 661 LPYTYLDPPLIENSYSI 677  
 Db 654 LOYLYLCPSRMENSITI 670

Search completed: July 18, 2005, 22:01:13  
 Job time : 116.351 secs

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PT New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed  
PT additives for livestock, or as antigens for producing antibodies.  
XX  
PS Example 2; Fig 6; 51pp; English.  
XX  
CC The present sequence is mouse 8S-lipoxygenase (8-Lox) protein.  
CC lipoxygenases are a structurally related family of non-haeme iron  
CC dioxygenases that function in the production of fatty acid  
CC hydroperoxides. 8-Lox acts in the metabolism of arachidonic acid to 8S-  
CC hydro(pero)xyeicosatetraenoic acid. Lipoxygenase DNA can be used as  
CC diagnostic tools to detect normal and abnormal DNA sequences derived from  
CC patient cells, for detecting and isolating other members of the  
CC polypeptide family and related polypeptides from a DNA library  
CC potentially containing the sequences, as primers for hybridising to  
CC related sequences for amplifying those sequences or for altering native  
CC lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives  
CC for livestock and as antigens for producing antibodies  
XX  
SQ Sequence 677 AA;

Query Match 100.0%; Score 3604; DB 4; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSSPLVPLDLHLGKFSAGAEEDFEVTLPOD 60  
Db 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSSPLVPLDLHLGKFSAGAEEDFEVTLPOD 60

QY 61 VGTVLMLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPALHFPFCYQWLEGAGELVLR 120  
Db 61 VGTVLMLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPALHFPFCYQWLEGAGELVLR 120

QY 121 EGAAKVSWQDHHTLQDQKQKESRQKMSWKTYIEGWPRCLDHTETVKDLDLNIKYSAM 180  
Db 121 EGAAKVSWQDHHTLQDQKQKESRQKMSWKTYIEGWPRCLDHTETVKDLDLNIKYSAM 180

QY 181 KNAKLPFFKAHSAYTELKVKGLLDRTPGLMRSLEMRNLFNFRKTPAAEYVFAHWQEDAFPA 240  
Db 181 KNAKLPFFKAHSAYTELKVKGLLDRTPGLMRSLEMRNLFNFRKTPAAEYVFAHWQEDAFPA 240

QY 241 SOFLANGINVLIRCHSLNNPVPVTDENVAPVLGCTSLQAELEKSLPLVDHGLSGVH 300  
Db 241 SOFLANGINVLIRCHSLNNPVPVTDENVAPVLGCTSLQAELEKSLPLVDHGLSGVH 300

QY 301 TWILNGKPOFSAAPMTLLHQSSGSLPLPIALQKOTPGDPNPFLPSDDTWDMLLAKTW 360  
Db 301 TWILNGKPOFSAAPMTLLHQSSGSLPLPIALQKOTPGDPNPFLPSDDTWDMLLAKTW 360

QY 361 VRNSEFYIHEAVTHLHAHLIPEVFALATLRLPRCHPLFKLLIPIHRYTLHINTLAREL 420  
Db 361 VRNSEFYIHEAVTHLHAHLIPEVFALATLRLPRCHPLFKLLIPIHRYTLHINTLAREL 420

QY 421 LVAPGKLIDKSLCTGCGSDLIKRMEQLNYSVLCLPEDIRARGVEDIPGVYRDDGNQ 480  
Db 421 LVAPGKLIDKSLCTGCGSDLIKRMEQLNYSVLCLPEDIRARGVEDIPGVYRDDGNQ 480

QY 481 IWGAIKSFVSEIYSIYPDSVTQDDQELQAWREIFSEGFLGRSSGMPSLDTRREALV 540  
Db 481 IWGAIKSFVSEIYSIYPDSVTQDDQELQAWREIFSEGFLGRSSGMPSLDTRREALV 540

QY 541 QYITWVIFCSAKHAASVSGQFSDSCVMPNLPPTMQLPPTSKGQARPSFATIPAVNS 600  
Db 541 QYITWVIFCSAKHAASVSGQFSDSCVMPNLPPTMQLPPTSKGQARPSFATIPAVNS 600

QY 601 SSVHIITALLNSPCDQRLGHPYDEHETEDAPRPSVAAFORKLIOISKGRIRNRGLA 660  
Db 601 SSVHIITALLNSPCDQRLGHPYDEHETEDAPRPSVAAFORKLIOISKGRIRNRGLA 660

QY 661 LPPTYLDPPLEIENSVS 677  
Db 661 LPPTYLDPPLEIENSVS 677

RESULT 2  
ADQ91765  
ID ADQ91765 standard; protein; 677 AA.  
XX  
AC ADQ91765;  
XX  
DT 07-OCT-2004 (first entry)  
XX  
DE Mouse 8S-lipoxygenase.  
XX  
KW lipoxygenase; iron ligand; arachidonic acid metabolism; mouse;  
KW 8S-lipoxygenase; 8-Lox.  
XX  
OS Mus sp.  
XX  
PN US2004137483-A1.  
XX  
PD 15-JUL-2004.  
XX  
PF 18-NOV-2003; 2003US-00716204.  
XX  
PR 16-APR-1998; 98US-00061768.  
PR 17-JAN-2001; 2001US-00764246.  
XX  
PA (BRAS/) BRASH A R.  
PA (BOEG/) BOEGLIN W E.  
PA (JISA/) JISAKA M.  
XX  
PI Brash AR, Boeglin WE, Jisaka M;  
XX  
XX WPI; 2004-533356/51.  
DR N-PSDB; ADQ91764.  
XX  
XX New lipoxygenase nucleic acid segment comprises an isolated gene encoding  
XX a lipoxygenase containing an iron ligand comprising a serine, useful for  
XX arachidonic acid metabolism.  
XX  
XX Claim 11; SEQ ID NO 4; 39pp; English.  
XX  
XX The invention describes a nucleic acid segment (I) comprising an isolated  
XX gene encoding a lipoxygenase containing an iron ligand comprising a  
XX serine, or comprises at least a 10 nucleotides long contiguous stretch of  
XX the nucleic acid sequence not given in the specification (SEQ ID NO. 1)  
XX or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a  
XX nucleic acid segment comprising at least 10 nucleotides long contiguous  
XX stretch of the nucleic acid sequence not given in the specification (SEQ  
XX ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is  
XX a polypeptide having the amino acid sequence Trp-Leu-leu-Ala-Lys (SEQ ID  
XX NO. 5) and Gly-Gin-Tyr-Asp-Trp (SEQ ID NO. 35). The lipoxygenase nucleic  
XX acids and proteins are useful in arachidonic acid metabolism. This is the  
XX amino acid sequence of mouse 8S-lipoxygenase (8-Lox).  
XX  
SQ Sequence 677 AA;

Query Match 100.0%; Score 3604; DB 8; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSSPLVPLDLHLGKFSAGAEEDFEVTLPOD 60  
Db 1 MAKCRVRVSTGEACGAGTWDKVSIVTGHGSSPLVPLDLHLGKFSAGAEEDFEVTLPOD 60

QY 61 VGTVLMLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPALHFPFCYQWLEGAGELVLR 120  
Db 61 VGTVLMLRVHKAPPEVSLPLMSFRSDAFCRWFELEWLPALHFPFCYQWLEGAGELVLR 120

QY 121 EGAAKVSWQDHHTLQDQKQKESRQKMSWKTYIEGWPRCLDHTETVKDLDLNIKYSAM 180  
Db 121 EGAAKVSWQDHHTLQDQKQKESRQKMSWKTYIEGWPRCLDHTETVKDLDLNIKYSAM 180

QY 181 KNAKLPFFKAHSAYTELKVKGLLDRTPGLMRSLEMRNLFNFRKTPAAEYVFAHWQEDAFPA 240  
Db 181 KNAKLPFFKAHSAYTELKVKGLLDRTPGLMRSLEMRNLFNFRKTPAAEYVFAHWQEDAFPA 240

QY 241 SQFLNGINPVLIRCHSLPNNPVTDEMVAFLVGRGTSLOALEKSGSLFVDHGILSGVH 300  
DB 241 SQFLNGINPVLIRCHSLPNNPVTDEMVAFLVGRGTSLOALEKSGSLFVDHGILSGVH 300  
QY 301 TNLNGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPIFLPSSDDTWDLAKTW 360  
DB 301 TNLNGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPIFLPSSDDTWDLAKTW 360  
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLAREL 420  
DB 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLAREL 420  
QY 421 LVAPGKLDKSTGLTGSGFSDLIKRMEQLNYSVLCLEDIRARGVEDIPGYYYRDDGMQ 480  
DB 421 LVAPGKLDKSTGLTGSGFSDLIKRMEQLNYSVLCLEDIRARGVEDIPGYYYRDDGMQ 480  
QY 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWREIFSEGFLGREGSSGMPSLDTRALV 540  
DB 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWREIFSEGFLGREGSSGMPSLDTRALV 540  
QY 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMPNLPPTMQLPPTTSKGOARPESTIATLPVNS 600  
DB 541 QYITWVIFTCSAKHAASVSGQFSDSCVMMPNLPPTMQLPPTTSKGOARPESTIATLPVNS 600  
QY 601 SSYHIIALLWSAEPGQDQPLGHYPDEHFTEDAPRRSVAAPFORKLIOISKGIERNRGLA 660  
DB 601 SSYHIIALLWSAEPGQDQPLGHYPDEHFTEDAPRRSVAAPFORKLIOISKGIERNRGLA 660  
QY 661 LPYTYLDPLPIENSYSI 677  
DB 661 LPYTYLDPLPIENSYSI 677

## RESULT 3

AAW93832  
ID AAW93832 standard; protein; 676 AA.

AC AAW93832;  
XX

DT 25-JUN-1999 (first entry)  
XX

DE Human 15S lipoxigenase PS213 protein.  
XX

KW Lipoxigenase; PS213; human; diagnosis; prostate disease; cancer;  
KW metastases; benign prostatic hypertrophy; prostatitis; immunoassay;  
KW prostatic intraepithelial neoplasia; cytotoxic agent; drug screening;  
KW therapy.  
XX

OS Homo sapiens.  
XX

PN WO9913111-A1.  
XX

PD 18-MAR-1999.  
XX

PF 11-SEP-1998; 98WO-US018983.  
XX

PR 11-SEP-1997; 97US-00927978.  
XX

PA (ABBO ) ABBOTT LAB.  
XX

PI Billing-Medel PA, Cohen M, Colpitts TL, Friedman PN, Gordon J;  
PI Granados EN, Hodges SC, Klass MR, Kratochvil JD, Ruseell JC;  
PI Stroupe SD;  
XX

DR WPI; 1999-229254/19.  
DR N-PSDB; AAX23827.  
XX

PT Diagnosis of prostatic disease using lipoxigenase PS213 as marker.  
PS Claim 26; Page 94-96; 101pp; English.  
XX  
CC This invention describes methods for diagnosing prostate disease using

CC the human 15S-lipoxigenase PS213, or its nucleic acid or specific  
CC antibodies, as markers. Detecting the presence of PS213, a derived  
CC amplicon, the encoded polypeptide or specific antibody, basically in  
CC standard hybridization, amplification or immuno assays, indicates  
CC prostatic disease. These methods are used for diagnosis, staging,  
CC monitoring, prognosticating, in vivo imaging and determining  
CC predisposition to prostatic cancer (and metastases), benign prostatic  
CC hypertrophy, prostatitis, and prostatic intraepithelial neoplasia. Host  
CC cells transfected with PS213 are used to produce recombinant polypeptides  
CC which are used to generate antibodies or as immunoassay reagents. The  
CC antibodies, and their fragments, are also immunoassay reagents and can be  
CC used therapeutically, either directly or as carriers for cytotoxic  
CC agents. The recombinant polypeptides are also used for drug screening and  
CC as targets for therapy  
XX

SQ Sequence 676 AA;

Query Match 79.9%; Score 2880.5; DB 2; Length 676;

Best Local Similarity 78.0%; Pred. No. 2.8e-266;

Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGVTHGESPLVPLDHLGKFSAGAEEDFVTLPOD 60

DB 1 MAEPRVRVSTGEACGAGTWDKVSIVGVTHGESPLVPLDHLGKFSAGAEEDFVTLPOD 60

QY 61 VGTVMILRVHKAPPEVSLPLMS -FRSDAWFCRWELEWLPGAALHPFCYQWLEGAGELVL 119

DB 61 VGRVLLLRVHKAPP -VLPGLGLAPDAWFCRWFQLTTPRGHLLFPYQWLEGAGTLVL 118

QY 120 REGAAKVSQWDDHPTDOROKELSRQKYSWKTYTEGWPCRLDHTVKDLNLKYSY 179

DB 119 QEGTAKSVADHHPVLOQOQOELOARQEMQWKAYNPGWPHCLDEKVEDLELNKYST 178

QY 180 MNAKLFFKAHSAYTELKVKGLLDRGTGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFF 239

DB 179 AKNANFYLQAGSAFAEMKIKGLLDKGLWRSLEMRRLFNFRKTPAAEYVFAHWQEDAFF 238

QY 240 ASQFLNGINPVLIRCHSLPNNPVTDEMVAFLVGRGTSLOALEKSGSLFVDHGILSGV 299

DB 239 ASQFLNGINPVLIRCHSLPNNPVTDEMVAFLVGRGTSLOALEKSGSLFVDHGILSGI 298

QY 300 HTNLTNGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPIFLPSSDDTWDLAKT 359

DB 299 QTNVINGKQFSAAPMTLLHQSSGSGPLPIATOLKQTPGDPNPIFLPSSDDTWDLAKT 358

QY 360 WVRNSEFYIHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLARE 419

DB 359 WVRNSEFYIHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLARE 418

QY 420 LLVAPGKLDKSTGLTGSGFSDLIKRMEQLNYSVLCLEDIRARGVEDIPGYYYRDDGM 479

DB 419 LLVAPGQVDRSTGIGIEGFSGLIQRNMKQLNYSLLCLPEDIIRTRGVEDIPIGYYYRDDGM 478

QY 480 QIWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWREIFSEGFLGREGSSGMPSLDTRAL 539

DB 479 QIWGAIRFVSEIIGIYYPDESVDQDRELQAWREIFSGFLNQESGSISSLETRAL 538

QY 540 VQYITWVIFTCSAKHAASVSGQFSDSCVMMPNLPPTMQLPPTTSKGOARPESTIATLPVN 599

DB 539 VQYITWVIFTCSAKHAASVSGQFSDSCVMMPNLPPTMQLPPTTSKGLATCEGFIATLPVN 598

QY 600 SSSYHIIALLWSAEPGQDQPLGHYPDEHFTEDAPRRSVAAPFORKLIOISKGIERNRGL 659

DB 599 ATCDVILALWLLSXEPGQDQPLGHYPDEHFTEDAPRRSVAAPFORKLIOISKGIERNRGL 658

QY 660 ALPYTYLDPLPIENSYSI 677

DB 659 VLPYTYLDPLPIENSYSI 676

## RESULT 4

AAE00935

ID AAE00935 standard; protein; 676 AA.

XX	AAE00935;	
XX	04-JUL-2001 (first entry)	
XX	Human 15S-lipoxygenase (15-Lox-2) protein.	
XX	Human; 15S-lipoxygenase; 15-Lox-2; non-haeme iron dioxygenase;	
KW	arachidonic acid; feed additive; livestock; antigen.	
XX	Homo sapiens.	
OS		
XX	Key	Location/Qualifiers
FH	Region	353..357
FT	Binding-site	/note= "Consensus sequence"
FT	Binding-site	374
FT	Binding-site	/note= "Iron ligand"
FT	Region	379
FT	Region	507..511
FT	Binding-site	/note= "Consensus sequence"
FT	Binding-site	553
FT	Binding-site	/note= "Iron ligand"
FT	Region	557
FT	Region	559..563
FT	Binding-site	/note= "Consensus sequence"
FT	Binding-site	676
FT	Binding-site	/note= "Iron ligand"
XX	US6204037-B1.	
XX	20-MAR-2001.	
XX	16-APR-1998;	98US-00061768.
XX	16-APR-1998;	98US-00061768.
XX	(UYVA-) UNIV VANDERBILT.	
XX	Brash AR, Boeglin WE, Jisaka M;	
XX	WPI; 2001-289517/30.	
DR	N-PSDB; AAD04501.	
XX	New 15S-lipoxygenase nucleic acids and polypeptides, useful as feed	
PT	additives for livestock, or as antigens for producing antibodies.	
XX	Claim 2; Fig 1; Sipp; English.	
XX	The present sequence is human 15S-lipoxygenase (15-Lox-2) protein.	
CC	Lipoxygenases are a structurally related family of non-haeme iron	
CC	dioxygenases that function in the production of fatty acid	
CC	hydroperoxides. 15-Lox-2 acts in the metabolism of arachidonic acid to	
CC	15S-hydro(pero)xyoctatetraenoic acid. Lipoxygenase DNA can be used as	
CC	diagnostic tools to detect normal and abnormal DNA sequences derived from	
CC	patient cells, for detecting and isolating other members of the	
CC	polypeptide family and related polypeptides from a DNA library	
CC	potentially containing the sequences, as primers for hybridizing to	
CC	related sequences for amplifying those sequences or for altering native	
CC	lipoxygenase DNA sequences. The lipoxygenase is useful as feed additives	
CC	for livestock and as antigens for producing antibodies	
XX	Sequence 676 AA;	
SQ		
Query Match		
Best Local Similarity 79.9%; Score 2880.5; DB 4; Length 676;		
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;		
Qy	1	MAKCRVSTGECAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60
DB	1	MAEFRVSTGEAFGAGTWDKVSIVGTHGESPLVPLDNLGKFTAGAEEDFQVTLPED 60

Qy	61	VGTVLMLRVHKAPPEVSLPLMS-FRSDAWFCRWELEWLPGAALHPCPCVOWLEGAGELVL 119
Db	61	VGRVLLLRVHKAPP--VLPLLGLPLADAWFCRWFOITPPRGHLLFPCCYQWLEGAGTLVL 118
Qy	120	REGAAKSVQDHHPTLODQROKELESROKMTSWKTYIEGWPRCLDHEVTVKOLDLNIKYSA 179
Db	119	QEGTRAKSWADHHPVLQOORQEELQARQEMQWKAYNFGWPHCLDEKTVEDLELNIKYST 178
Qy	180	MKNAKLFFKAHSAYTELKVKGLLDRDTGLWRSLSREMRRLFNFRKTPAAEYVFAHWQEDAFP 239
Db	179	AKNANFYLAQSAPAEEMKIKGLLDRKGLWRSLSNEMKRIFNFRRTPAEHAPEHWQEDAFP 238
Qy	240	ASQFLNGINPVLIRCHSLPNNFPVYDDEWAPVLCGPTSLQAELEKGSFLVDHGILSOV 299
Db	239	ASQFLNGINPVLIRCHYLKPNFPVYDAMVASLLGPGTSLQAELEKGSFLVDHGILSGI 298
Qy	300	HTNILINGKQPSAAPMTLLHOSGSGPLLPALAIQLKQTPGDPNPFLPSSDDTDWMLLAKT 359
Db	299	QTNVINGKQPSAAPMTLLYQSGCGPLPLAIQLSQTPGNSPFLPTDDKDWMLLAKT 358
Qy	360	WYRNSEFYIHEAVTHLLHAHLIPEVPFALATLRLQPRCHPLFKLLIPHIRYTHINTLARE 419
Db	359	WYRNAEFSFHEALTHLLHSHLLPEVFTLATLRLQPHCHPLFKLLIPHTRYTHINTLARE 418
Qy	420	LLVAPGKLIKSTGLTGGFSDLIKRNWEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 479
Db	419	LLIVPGQVDRSTGIGIEGSELIQRNMKQLNYSLLCLPEDIRTRGVEDIPGYVYRDDGM 478
Qy	480	QIWGAIKSFVSEIVSIYYPSDTSVODDQLOAWVREIFSEGFLGRESGMPSLDRTREAL 539
Db	479	QIWGAVERFVSEIIGIYYPSDESVDQDRELQAWVREIFSKGFLNQESSGIPSSLETREAL 538
Qy	540	VOYITWVIFTSAKHAAYSSGQFDSVVMNPLPPTMQLPPTPSKQARPESFIATLPAYN 599
Db	539	VOYVTWVIFTSAKHAAYSAQOFDSCAMWNLPPSQMLPPPTPSKGLATCEGFIATLPVYN 598
Qy	600	SSSYHIIALWLLSAPGQORPLGHYPDEHFTEDAPRSVAAFQKLIQISKGIRERNRGL 659
Db	599	ATCDVILALWLLSKFQORPLGTYPDBHFTTEAPRPSIATFQSRLAQISRGIQERNRGL 658
Qy	660	ALPTYLDPLPLIENSVSI 677
Db	659	VLPYTYLDPLPLIENSVSI 676
RESULT 5		
ABG61866		
ID	ABG61866	standard; protein; 676 AA.
XX	AC	ABG61866;
XX	DT	15-AUG-2002 (first entry)
XX	DE	Prostate cancer-associated protein #67.
XX	KW	Prostate cancer; prostate tumour tissue; human; mammal; cytostatic.
XX	OS	Mammalia.
XX	PN	WO200230268-A2.
XX	PD	18-APR-2002.
XX	PF	12-OCT-2001; 2001WO-US032045.
XX	PR	13-OCT-2000; 2000US-00687576.
XX	PR	08-DEC-2000; 2000US-00733286.
XX	PR	08-DEC-2000; 2000US-00733742.
XX	PR	24-JAN-2001; 2001US-0263957P.
XX	PR	16-MAR-2001; 2001US-0276791P.
XX	PR	16-MAR-2001; 2001US-0276888P.
XX	PR	06-APR-2001; 2001US-0281922P.
XX	PR	24-APR-2001; 2001US-0286214P.

PR 30-APR-2001; 2001US-00847046.  
PR 04-MAY-2001; 2001US-0288589P.  
XX  
XX PA (EOSB-) EOS BIOTECHNOLOGY INC.  
XX  
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;  
XX WPI; 2002-471335/50.  
DR N-PSDB; ABK92181.  
XX  
PT Detecting a prostate cancer-associated transcript in a cell in a patient,  
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,  
PT by determining if prostate cancer-associated genes are expressed in a  
PT prostate tissue.  
XX  
XX  
PS Claim 27; Page 351-352; 436pp; English.  
XX  
XX The present invention relates to methods of detecting a prostate cancer-  
CC associated transcript in a cell from a patient. The method comprises  
CC contacting a biological sample from the patient with prostate cancer-  
CC associated polynucleotides (designated PC genes) that selectively  
CC hybridize to a sequence that is at least 80% identical to them. The  
CC prostate cancer-associated polynucleotide sequences are differentially  
CC expressed in prostate tumour tissue or in prostate cancer and are derived  
CC from the tissues of various organisms such as humans or other mammals  
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for  
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-  
CC associated genes are useful for diagnosing or treating prostate cancer,  
CC as well as for identifying modulators of prostate cancer or agents that  
CC inhibit prostate cancer. The nucleic acid sequences are particularly  
CC useful in gene therapy, as a vaccine or in antisense applications.  
CC ABG61800-ABG61944 represent prostate cancer-associated proteins  
XX  
SQ Sequence 676 AA;  
  
Query Match 79.9%; Score 2880.5; DB 5; Length 676;  
Best Local Similarity 78.0%; Pred. No. 2.8e-266;  
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;  
  
QY 1 MAKCRVRYSTGEACGAGTWDKVSIVGTGTHGESPLVPLDLHLGKFSAGAEDFEVTLPOD 60  
DB 1 MAEFVRVSTGEAFAGTWDKVSIVGTGTHGESPLVPLDLNLGKFTAGAEEDFVTLFED 60  
  
QY 61 VGTVLMRLVHKAPPEVSLPLMS -FRSDAWFCWFLEWLPGLAALHFPYQWLEGAGELVL 119  
DB 61 VGRVLLLRVHRAPP--VLPGLGPLADAWFCWFQFTPPRGHLLFPYQWLEGAGTLLV 118  
  
QY 120 REGAKVSWQHHPTLQDORQKELSRQKYSWKTYIEGWPRCLDHTETVKDLNLIKYS 179  
DB 119 QEGTAKVSWADHHPVLQOQOQEEQARQEMQKAYNFGWPHCLDEKTVDELNLKYST 178  
  
QY 180 MKNAKLFPKANSAYTELKVKGLLDRDTGLWRSIREMRRLFNFRKTPAAEYVFAHMOEDAFF 239  
DB 179 AKNANFYLAQSAPAEKIKGLDRKGLWRSLENEMKRFNFRTPAAEHAHEHMOEDAFF 238  
  
QY 240 ASQFLNGINVLIRCHSLPNFPVTDENAVPZLGFTSLQAELEKSGSLFLVDHGILSGV 299  
DB 239 ASQFLNGINVLIRCHSLPNFPVTDENAVPZLGFTSLQAELEKSGSLFLVDHGILSGI 298  
  
QY 300 HTNILINGPQPSAAPTLLHQSOGSGLIPTAIQLKOTPGDNPFLPSDDTWDWLLAKT 359  
DB 299 QTNVINGPQPSAAPTLLYQSPGCGLLPLAQLSQTGPNSPFLPTDDKWDWLLAKT 358  
  
QY 360 WYRNSEFIHVAHTLLHAHLIPEVFALATLRLPRCHPLFKLLIPHYTLHINTLARE 419  
DB 359 WYRNSEFIHVAHTLLHSHLLPEVFTLATLRLPRCHPLFKLLIPHYTLHINTLARE 418  
  
QY 420 LLVAPGKIDKSTGLTGCGFSDLIKRNMQLNYSVLCPLPDIRARGVEDIPGYVYRDDGM 479  
DB 419 LLVPGQVVDKSTGIGEGFSELIQRNMQLNYSVLCPLPDIRTRGVEDIPGYVYRDDGM 478  
  
QY 480 QIWGAIKFVSEIYIPSDTSVDDDELQAWREIFSEGPLGREGSGMPSLLDTRAL 539  
DB 479 QIWGAVERFVSEIIGIYPPDESVDDELQAWREIFSGFLNQESSGIPSSLETRAL 538  
540 VQYITWIFTCSAKHAASVSCQFSCVWMPNLPPTMQLPPTTSKQAPESPFIATLPVN 599  
539 VQYVTVIFTCSAKHAASVSCQFSCVWMPNLPPTSMQLPPTTSKGLATCEGFIATLPVN 598  
600 SSSYHIIATLLSAPGDPORPLGHYPDEHFTEDAPRRSVAAPQKLIQISKIGIRENRGL 659  
599 ATCDVILALWLLSKPGDQRPGLGYPDEHFTEDAPRRSVAAPQKLIQISKIGIRENRGL 658  
660 ALPTYLDPPPLIENSIVI 677  
659 VLPYTYLDPPPLIENSIVI 676

Db 479 QIWGAVERFVSEIIGIYPPDESVDDELQAWREIFSGFLNQESSGIPSSLETRAL 538  
QY 540 VQYITWIFTCSAKHAASVSCQFSCVWMPNLPPTMQLPPTTSKQAPESPFIATLPVN 599  
Db 539 VQYVTVIFTCSAKHAASVSCQFSCVWMPNLPPTSMQLPPTTSKGLATCEGFIATLPVN 598  
QY 600 SSSYHIIATLLSAPGDPORPLGHYPDEHFTEDAPRRSVAAPQKLIQISKIGIRENRGL 659  
Db 599 ATCDVILALWLLSKPGDQRPGLGYPDEHFTEDAPRRSVAAPQKLIQISKIGIRENRGL 658  
QY 660 ALPTYLDPPPLIENSIVI 677  
Db 659 VLPYTYLDPPPLIENSIVI 676  
  
RESULT 6  
ABU89734  
ID ABU89734 standard; protein; 676 AA.  
XX  
AC ABU89734;  
XX  
DT 10-JUL-2003 (first entry)  
XX  
DE Protein differentially expressed in cardiovascular disease #28.  
XX  
KW Cardiovascular disease; arteriosclerosis; ischaemia; angina pectoris;  
KW myocardial infarction; cardiant; antiarteriosclerotic; antianginal;  
KW gene therapy; differential gene expression.  
XX  
OS Homo sapiens.  
XX  
FN WO2003031850-A2.  
XX  
PD 17-APR-2003.  
XX  
PF 02-OCT-2002; 2002WO-EP011034.  
XX  
PR 08-OCT-2001; 2001GB-00024145.  
XX  
PA (FARB ) BAYER AG.  
PI Munnes M, Gehrman M, Wick M, Schmitz G;  
XX  
DR WPI; 2003-403108/38.  
DR N-PSDB; ACA89907.  
XX  
PT Predicting, diagnosing or prognosing a cardiovascular disease, e.g.  
PT angina, ischemia, myocardial infarction or arteriosclerosis by detection  
PT of a polynucleotide in a biological sample comprises detecting a  
PT hybridization complex.  
XX  
PS Claim 3; Page 330-333; 454pp; English.  
XX  
CC The invention describes a method of predicting, diagnosing or prognosing  
CC a cardiovascular disease by detection of a polynucleotide in a biological  
CC sample comprises hybridising at least one of the polynucleotide to a  
CC nucleic acid material of a biological sample, thus forming a  
CC hybridisation complex, and detecting the hybridisation complex. The  
CC polynucleotides, polypeptides, antisense molecule, antibody and reagent  
CC are useful for preparing compositions for preventing, predicting or  
CC diagnosing, or a medicament for treating a cardiovascular disease, e.g.  
CC arteriosclerosis, ischaemia, angina pectoris, or myocardial infarction.  
CC This sequence represents a protein identified in the invention a being  
CC differentially expressed in individuals with cardiovascular disease  
XX  
SQ Sequence 676 AA;  
  
Query Match 79.9%; Score 2880.5; DB 6; Length 676;  
Best Local Similarity 78.0%; Pred. No. 2.8e-266;  
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;  
  
QY 1 MAKCRVRYSTGEACGAGTWDKVSIVGTGTHGESPLVPLDLHLGKFSAGAEDFEVTLPOD 60  
DB 1 MAEFVRVSTGEAFAGTWDKVSIVGTGTHGESPLVPLDLNLGKFTAGAEEDFVTLFED 60

Db	1	MAEFRVRVSTGEAFGAGTWDKVSIVGTRGSPPLPLDNLGKEFTAGABEDFQVTLPED	60
Qy	61	VGTVMLRVHKAAPPEVSPLMS - FRSDAWFCWFLEWLPGLAALHPFCYQWLEGAGELYL	119
Db	61	VGRVLLRVHKAAP - VLPLGLPLADAWFCWFQLTTPRGGHLLFPCCYQWLEGAGTLVL	118
Qy	120	REGAAKVSQDHHPTLQDQORQKELSRQKQYKWKYIEGWPCLDHETVKDLDLNIKYS	179
Db	119	QEGTAKVSWADHHPVLQOQOQBELQARQEMQKAYNPGWPHCLDEKTVEDLELNIKYST	178
Qy	180	MKNAKLFFKAHSAYTELVKGLDRTGLWRSREMRLENFRKTPAAEVVFAHMQEDAF	239
Db	179	AKNANFYLQAGSAFAEMKIKGLDRLKGLWRSLENMKRIENFRTPAAEHAFHMQEDAF	238
Qy	240	ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGV	299
Db	239	ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGI	298
Qy	300	HTNILNGKPFQSAAPMTLLHQSSGSGPLPIAIQLKQTPGPNPFLPDDTDWMLLAKT	359
Db	299	QTNVINGKPFQSAAPMTLLYQSGCGPLPLAIQLSQTGPNSPFLPTDDKDWMLLAKT	358
Qy	360	WYRNSEFYTHEAVTHLLHAHLIPEVFALATLQLPCHPLFKLLIPHRYTHINTLARE	419
Db	359	WYRNAEFSFHEALTHLLHSHLLPEVFTLATLQLPCHPLFKLLIPHRYTHINTLARE	418
Qy	420	LLVAPGKLIDKSTGLTGTFSDLIKRNMEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM	479
Db	419	LLVFPQVVDVRSSTGIEGFSLEIQRNMKQLNYSVLCLPEDIRTRGVEDIPGYVYRDDGM	478
Qy	480	QIWAIAKSFVSEIVSYIYPSDTSVQDDQELQAWREIFSEGLGRSSGMPSLDTRREAL	539
Db	479	QIWAVERFVSEIIGIYPSDESVDQDRELQAWREIFSKGFLNQESSIPSSLETREAL	538
Qy	540	VQYITWVITCSAKHAASVSGQFDCVMMNPPLPTMQLPPTSKGOARPESTIATLPVNV	599
Db	539	VQYVTVVITCSAKHAASVAGQFDCVMMNPPLPSSMQLPPTSKGLATCEGFIATLPVNV	598
Pa	(BRAS/)	BRASH A R.	
Pa	(BOEG/)	BOEGLIN W E.	

RESULT 7

ID	ADQ91763
XX	ADQ91763 standard; protein; 676 AA.
AC	ADQ91763;
XX	
DT	07-OCT-2004 (first entry)
XX	
DE	Human lipoxigenase 15-Lox-2.
XX	
KW	lipoxigenase; iron ligand; arachidonic acid metabolism; human;
KW	lipoxigenase 15-Lox-2.
XX	
OS	Homo sapiens.
XX	
PN	US2004137483-A1.
XX	
PD	15-JUL-2004.
XX	
PF	18-NOV-2003; 2003US-00716204.
XX	
PR	16-APR-1998; 98US-00061768.
PR	17-JAN-2001; 2001US-00764246.
XX	
PA	(BRAS/)
Pa	(BOEG/)

PA	(JISA/) JISAKA M.
XX	
PI	Brash AR, Boeglin WE, Jisaka M;
XX	
DR	WPI; 2004-533356/51.
DR	N-PSDB; ADQ91798.
XX	
XX	New lipoxigenase nucleic acid segment comprises an isolated gene encoding a lipoxigenase containing an iron ligand comprising a serine, useful for arachidonic acid metabolism.
PT	
PT	
XX	
PS	Claim 36; SEQ ID NO 2; 39pp; English.
XX	
CC	The invention describes a nucleic acid segment (I) comprising an isolated gene encoding a lipoxigenase containing an iron ligand comprising a serine, or comprises at least 10 nucleotides long contiguous stretch of the nucleic acid sequence not given in the specification (SEQ ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Specifically claimed is a nucleic acid segment comprising at least 10 nucleotides long contiguous stretch of the nucleic acid sequence not given in the specification (SEQ ID NO. 1) or a sequence comprising 900 bp (SEQ ID NO. 3). Also claimed is a polypeptide having the amino acid sequence Trp-Leu-Ala-Lys (SEQ ID NO. 5) and Gly-Gln-Tyr-Asp-Trp (SEQ ID NO. 35). The lipoxigenase nucleic acids and proteins are useful in arachidonic acid metabolism. This is the amino acid sequence of human lipoxigenase 15-Lox-2.
XX	
SQ	Sequence 676 AA;
Qy	Query Match 79.9%; Score 2880.5; DB 8; Length 676;
Db	Best Local Similarity 78.0%; Pred. No. 2.8e-266;
XX	Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;
Qy	1 MAKCRVRVSTGEACAGTWDKVSIVGTHGSPVLPLDHLGKFSAGAEEDFEVTLPOD 60
Db	1 MAEFRVRVSTGEAFGAGTWDKVSIVGTRGSPPLPLDNLGKEFTAGAEEDFQVTLPED 60
Qy	61 VGTVMRLRVHKAAPPEVSPLMS - FRSDAWFCWFLEWLPGLAALHPFCYQWLEGAGELYL 119
Db	61 VGRVLLRVHKAAP - VLPLGLPLADAWFCWFQLTTPRGGHLLFPCCYQWLEGAGTLVL 118
Qy	120 REGAAKVSQDHHPTLQDQORQKELSRQKQYKWKYIEGWPCLDHETVKDLDLNIKYS 179
Db	119 QEGTAKVSWADHHPVLQOQOQBELQARQEMQKAYNPGWPHCLDEKTVEDLELNIKYST 178
Qy	180 MKNAKLFFKAHSAYTELVKGLDRTGLWRSREMRLENFRKTPAAEVVFAHMQEDAF 239
Db	179 AKNANFYLQAGSAFAEMKIKGLDRLKGLWRSLENMKRIENFRTPAAEHAFHMQEDAF 238
Qy	240 ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGV 299
Db	239 ASQFLNGINPVLIRCHSLPNNFPVTDENVAPVLGPGTSLQAELEKGSFLVDHGLTSGI 298
Qy	300 HTNILNGKPFQSAAPMTLLHQSSGSGPLPIAIQLKQTPGPNPFLPDDTDWMLLAKT 359
Db	299 QTNVINGKPFQSAAPMTLLYQSGCGPLPLAIQLSQTGPNSPFLPTDDKDWMLLAKT 358
Qy	360 WYRNSEFYTHEAVTHLLHAHLIPEVFALATLROLPRCHPLFKLLIPHRYTHINTLARE 419
Db	359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLROLPHCHPLFKLLIPHRYTHINTLARE 418
Qy	420 LLVAPGKLIDKSTGLTGTFSDLIKRNMEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 479
Db	419 LLVFPQVVDVRSSTGIEGFSLEIQRNMKQLNYSVLCLPEDIRTRGVEDIPGYVYRDDGM 478
Qy	480 QIWAIAKSFVSEIVSYIYPSDTSVQDDQELQAWREIFSEGLGRSSGMPSLLDTRREAL 539
Db	479 QIWAVERFVSEIIGIYPSDESVDQDRELQAWREIFSKGFLNQESSGIPSSLETREAL 538
Qy	540 VQYITWVITCSAKHAASVSGQFDCVMMNPPLPTMQLPPTSKGOARPESTIATLPVNV 599
Db	539 VQYVTVVITCSAKHAASVAGQFDCVMMNPPLPSSMQLPPTSKGLATCEGFIATLPVNV 598
Qy	600 SSSYHIALWLLSAEPGDORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNRGL 659



Db	599	ATCDVIALWLKSPGQDRPLGTYPDEHFTTEAPRRSIATPQSRLAQISRGIQERNRGL	658
Qy	660	ALPYTYLDPPLIENSVSII	677
Db	659	VLPYTYLDPPLIENSVSII	676
RESULT 8			
ADQ37896	ID	ADQ37896 standard; protein; 676 AA.	
XX	AC	ADQ37896;	
XX	XX	07-OCT-2004 (first entry)	
XX	XX	Human 15-lipoxygenase 2 protein.	
XX	KW	Dry eye; 15-lipoxygenase; 15-LO; ophthalmological; gene therapy;	
KW	KW	postmenopausal.	
XX	XX	Homo sapiens.	
XX	XX	W02004060274-A2.	
XX	PN	22-JUL-2004.	
XX	PD	17-OCT-2003; 2003WO-US033139.	
XX	PF	20-DEC-2002; 2002US-0435988P.	
XX	PR	(ALCO-) ALCON INC.	
XX	PA	Yanni JM, Gamache DA, Miller ST;	
XX	PI	WFI; 2004-543776/52.	
DR	DR	N-PSDB; ADQ37895.	
XX	XX	Treating dry eyes in postmenopausal women comprises administering a	
PT	PT	composition comprising the 15-lipoxygenase (15-LO)-1 or 15-LO-2 gene to	
PT	PT	the ocular surface cells of the post-menopausal women with dry eyes.	
PS	PS	Claim 14; SEQ ID NO 4; 20pp; English.	
XX	XX	The invention relates to a novel method for treating dry eyes. The method	
CC	CC	comprises obtaining a composition containing the nucleotide sequence of	
CC	CC	15-lipoxygenase (15-LO)-1 or 15-LO-2, and administering the composition	
CC	CC	to a patient suffering from dry eye under conditions such that the	
CC	CC	nucleotide sequence of 15-LO-1 or 15-LO-2 is expressed. The invention	
CC	CC	further comprises a composition for the treatment of dry eye, comprising	
CC	CC	a vector having the above nucleotide sequence and an excipient. The 15-LO	
CC	CC	compositions have ophthalmological activity and may be used in gene	
CC	CC	therapy to treat disorders. The method is useful for treating dry eyes in	
CC	CC	postmenopausal women. This sequence represents the 15-lipoxygenase 2	
XX	XX	protein of the invention.	
XX	XX	Sequence 676 AA;	
Query Match		79.9%; Score 2880.5; DB 8; Length 676;	
Best Local Similarity		78.0%; Pred. No. 2.8e-266;	
Matches 529; Conservative		69; Mismatches -77; Indels 3; Gaps 2	
Qy	1	MAKCRVRVSTGEACGAGTWDKVSIVSIVCTHGESPLAVLDHLGKFPESAGAEEDFVTLPOD	60
Db	1	MAEFPRVRVSTGEAFGAGTWDKVSIVSIVGTRESPPPLDNLNGKFTAGAEEDFQVTLPE	60
Qy	61	VGTVLMRLVRHKAPPEVSLPLMS-FRSDAWFCRWFELEWLPGAALHPCYQWLEGAGELVL	119
Db	61	VGRVLLRLVRHKAPP--VLPLGLAPLADAWFCRWFLQTPPRGGHLLFPCYQWLEGAGT	118
Qy	120	REGAAKVSQDHHPTLQDQOKELRESRKQYSWKTYIEGNPRCLDTHETVKOLDLNIKYSA	179
Db	119	QEGTAKYSWADHHPVLQOQOEELQARQEMTQWKAYNPGWPHCLDEKTVDELDLELNKIST	178

Qy	180	MONAKLFFKAHSAYTELKVGGLDRDTGLWRSLSREMRLEFNPRKTPAAEYVFAHWQEDAFF	238
Db	179	AKVANFYLOAGSFAENKIKGLGLDRKGLWRSLSNEMKRIFNFRRTTPAAASHAPEHWQEDAFF	238
Qy	240	ASQFLNGINPVLIRRCHSLPNRPVTDWMAVPLGPGTSLQAELEKGSILFLVDHGILSGV	299
Db	239	ASQFLNGINPVLIRRCHYLPPKNFPVTDAMVASLGGPGTSLQAELEKGSILFLVDHGILSGI	298
Qy	300	HTNILKPKQFSAAPMTLLHQSSGSGPLLPITAIQLKOTPGPDNPILFSPDDTDWMLLAKT	359
Db	299	QTNVINGKPKQFSAAPMTLLYQSGPCGPLLPITAIQLSQTGPGNSPIFLPTDDKWDMLLAKT	358
Qy	360	WVRNSEFYIHEAVTHLLHAHLIPRVFALATLROLPQRCHLPKLLIPHTRYTLHIINTLARE	419
Db	359	WVRNAEFSFHEALTHLLHSHLLPEVFTLATLROLPCHCHLPKLLIPHTRYTLHIINTLARE	418
Qy	420	LLVAPGKLIIDKSTGLGTGFGPSDLIKRNEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGM	479
Db	419	LLIVFGQVDRSGVIGIEGFSSELLIORMKNQNLNYSLLCLPEDIRKGVEDIPGYVYRDDGM	478
Qy	480	QINGAIKSFVSSEIYSIYPSDTSYDDOELQAWVREIPSEGLRGHRESSGMPSLDPTREAL	539
Db	479	QINGAVERFVSSEIIGIYPSDESYYDDRELQAWVREIPSKGFLNQESSGIPSSLETREAL	538
Qy	540	VQYITWVITFCSAKHAAYSSGQPDSCVWMPNLPPTMQLPPDTSKQARPESFIATLPAYN	599
Db	539	VQYVTVWVITFCSAKHAAYSGQFDSCAWMPNLPPESMQLPPDTSKGLATCEGFIATLPVYN	598
Qy	600	SSSVHIIALLSAGPDQDRPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNRGL	659
Db	599	ATCDVIALWLLSKPGQDRPLGTYPPDEHFTEEAPRRSIATFQSLAQISRGIOERNRGL	658
Qy	660	ALPYTYLDPLIENSYSI	677
Db	659	VLPYTYLDPLIENSYSI	676
RESULT	9		
ABM84236	ID	ABM84236 standard; protein; 671 AA.	
XX	AC	ABM84236;	
XX	XX		
DT	18-NOV-2004	(first entry)	
XX		Human diagnostic and therapeutic pprotein seq ID NO:4485.	
DE		gene therapy; human diagnostic and therapeutic polynucleotide; dithp.	
KW			
XX			
OS		Homo sapiens.	
XX			
PN		WO2004023973-A2.	
XX			
PD		25-MAR-2004.	
XX			
PF		12-SEP-2003; 2003WO-US028227.	
XX			
PR		12-SEP-2002; 2002US-0410259P.	
XX		12-SEP-2002; 2002US-0410260P.	
XX			
PA		(INCY-) INCYTE CORP.	
XX			
PI		Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;	
PI		Harthshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;	
PI		Mooney EW, Delegeane AM, Panesar IS, Banville SC, Reddy TP;	
PI		Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstein EH;	
PI		Peralta CH, Anderson SB, Rioux P, Shen BJ, Wu MC, Stuve LL;	
PI		Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirtton ES;	
PI		Xu Y, Kwong M, Pollicky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;	
PI		Patory S, Shi X, Suarez CJ;	
XX			
DR		WPI; 2004-329368/30.	

DR N-PSDB; ACM42888.  
XX New diagnostic and therapeutic polynucleotides and polypeptides, useful  
PT in diagnosing a condition, disease or disorder associated with human  
PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or  
PT in gene mapping.  
XX  
PS Claim 27; Page; 190pp; English.  
XX  
XX The invention relates to novel diagnostic and therapeutic polynucleotides  
CC selected from one of the 2722 sequences defined in the specification. A  
CC polynucleotide of the invention may have a use in gene therapy. The human  
CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be  
CC used to diagnose a particular condition, disease or disorder associated  
CC with human molecules, e.g. cell proliferative disorders,  
CC autoimmune/inflammatory disorder, developmental disorder, endocrine  
CC disorder, neurological disorders, gastrointestinal disorders, or  
CC infections caused by virus, bacteria, fungi or parasite. The dithp  
CC molecules may also be used in genetic mapping, in identifying individuals  
CC from minute biological samples, in detecting single nucleotide  
CC polymorphisms, as molecular weight markers, and for somatic or germline  
CC gene therapy. The present sequence represents a dithp protein or germline  
CC invention. Note: The sequence data for this patent is not represented in  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at [www.wipo.int/pct/en/sequences/listing.htm](http://www.wipo.int/pct/en/sequences/listing.htm)  
XX  
SQ Sequence 671 AA;

Query Match 51.8%; Score 1868; DB 8; Length 671;  
Best Local Similarity 52.9%; Pred. No. 3.1e-169;  
Matches 359; Conservative 112; Mismatches 199; Indels 8; Gaps 3;  
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGTGSPVLPLDLHGKFGAGAEDEFVTLPOD 60  
DB 1 MAVYRLCVTGPYLRAGTLDNISVTLVGCGSPKQRLDRMGDRDPAGSVQKYKVRCTAE 60  
QY 61 VGTVMRLVRHKAPEVSLPLMSFRSDAMFCRWFELWLPALHFPYQWLGAGSLVLR 120  
DB 61 LGELLRLVRHKE-----RYAFFRKDSWYCSRICVTEPDGVSVSHFPYQWIEGYCTVELR 114  
QY 121 EGAAKVSWODHHTLQDQKESLRQKMY-SKTYIEGWPRCLDHTVKDLDLAIKYSA 179  
DB 115 PGTARTICODSLPLLLDHRTRELRAQECYRSGNRYLPGFPMKIDIPSLMYEPNRYSA 174  
QY 180 MKNAKFFFAHSAYTELKVKGLDRLTGLWRSLEMRRLFNFRKTPAAEYVFAHWQDAFP 239  
DB 175 TKTISLLFNALPASLGMKGLGLDRGSKWKLDDMQNIWCHTKTPTKIVTEHWCEDEF 234  
QY 240 ASQFLNGINPVLIRCHSLPNFPVTDEMVAIVLPGTSLQAELEKSLFLVDHGLSGV 299  
DB 235 GYQLNGVNPVMLHCISLPSKLPVNDMVAPLLGQDTCLQTELRGNIFLADYWIIEA 294  
QY 300 HTNILINGKQFSAAPMTLLHQSSGSLPLPIALQKQTGPONPIPLPSDDTDWMLLAKT 359  
DB 295 PTHCLNGRQOYVAAPLCLLWLSL-P-QGALVPLAQLSQTFGPDSPIFLPTDSEWDMLAKT 353  
QY 360 WVNSEFYIHEATVLLHAAHLEVEPALATRLQPRCHPLFKLLIPIHYTHINTLARE 419  
DB 354 WVNSEFLVHNTNTHFLCTHLLCEAFAMATRLQPLCHFIYKLLLPHYTYLQVNTIARA 413  
QY 420 LLVAPGLKDKSTGLGTGGSFSLIKRMBQLANYSVLCLPEDIRARVEDIPGYRRDDGM 479  
DB 414 TLLNPEGLVDQVTSIGRQGLIYLMSTGLAHFTYTNFCLPDSLARGVLAIPNYHYRDDGL 473  
QY 480 QIWGALKSFVSEIVSYIYSDTSVQDDQELQAWREIFSEGFLGRSSGMPSLLDREAL 539  
DB 474 KIWAATESFVSETVGYIYPSDASVQDDSELAQTGIFPAQFLGREGSGFPRLCTPGEM 533  
QY 540 VOYITWVIFTCSAKHAASVSGQFSDCVWMPNLPPTWQLPPTSKQARPESTIATPAVN 599  
DB 534 VKFETAILFNCSAQHAASVSGQHDFGAWPNAPSSMRQPPPTGTGTTTLKTYLDTLPEVN 593  
QY 600 SSSYHIALWLLSAEFDQORPLGHYPDEHFTEDAPRRSVAAFQKLIQISKGIRERNRGL 659

DB 594 TSCNNLLFWLVSQKQDRPLGTVPDEHFTTEAPRRSIAAFQSLRAQLSDIQRNQL 653  
QY 660 ALPTYLDPPLIENSVSI 677  
DB 654 ALPTYLDPPLIENSVSI 671  
RESULT 10  
AAB19379  
ID AAB19379 standard; protein; 711 AA.  
AC AAB19379;  
DT 06-MAR-2001 (first entry)  
DE Amino acid sequence of a human lipoxigenase protein.  
XX Human; lipoxigenase; leukotriene; lipid; chemotactic agent; inflammation;  
KW smooth muscle contraction; asthma; eye disease; arthritis; lung disease;  
KW cancer; acne; psoriasis.  
XX Homo sapiens.  
OS  
XX WO2000061765-A2.  
PN  
XX  
PD 19-OCT-2000.  
PF 12-APR-2000; 2000WO-US009657.  
XX  
PR 12-APR-1999; 99US-0128817P.  
PR 24-AUG-1999; 99US-0150454P.  
XX  
PA (LEXI-) LEXICON GENETICS INC.  
XX  
PI Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;  
DR WPI; 2000-665134/64.  
DR N-PSDB; AAC61747.  
XX  
PT Novel polynucleotides encoding human lipoxigenase proteins useful for  
XX producing transgenic animals preferably mouse.  
PS Claim 3; Page 58-60; 83pp; English.  
XX  
CC AAB19379-92 represent novel human lipoxigenase proteins. Lipoxigenases  
CC oxidise lipids to produce leukotrienes. Leukotrienes bind cognate  
CC receptors and trigger biological effects. Leukotrienes influence a  
CC variety of biological processes, and can serve as, inter alia, potent  
CC chemotactic agents and mediators of inflammation, smooth muscle  
CC contractions, etc. Lipoxigenases and leukotrienes are implicated in a  
CC variety of diseases and disorders, such as asthma, eye diseases,  
CC arthritis, lung disease, cancer, acne, psoriasis, etc  
XX  
SQ Sequence 711 AA;  
Query Match 51.7%; Score 1864; DB 3; Length 711;  
Best Local Similarity 50.1%; Pred. No. 8.1e-169;  
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;  
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVTGTGSPVLPLDLHGKFGAGAEDEFVTLPOD 60  
DB 1 MAVYRLCVTGPYLRAGTLDNISVTLVGCGSPKQRLDRMGDRDPAGSVQKYKVRCTAE 60  
QY 61 VGTVMRLVRHKAPEVSLPLMSFRSDAMFCRWFELWLPALHFPYQWLGAGSLVLR 120  
DB 61 LGELLRLVRHKE-----RYAFFRKDSWYCSRICVTEPDGVSVSHFPYQWIEGYCTVELR 114  
QY 121 EGAAKVSWODHHTLQDQKESLRQKMY-SKTYIEGWPRCLDHTVKDLDL----- 173  
DB 115 PGTARTICODSLPLLLDHRTRELRAQECYRSGNRYLPGFPMKIDIPSLMYEPNRYSA 174  
QY 174 -----NIKYSAMKNVAKLFFKAHSAYTELKVK 199



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Db 594 GQHDFGAMNPAPSSMRQPPQTKGTTTLTKYTLDTLPEVNI SCNNLLLFWLVSQBPQDQR 653
QY 620 PLGHPYDEHFTEDAPRRSVAAPQKLIQISKGIRNRGLALPYTYLDPPLIENS VSI 677
Db 654 PLGTYPDEHFTTEAPRRSIAAFQSLAQISRDIOERNQGLALPYTYLDPPLIENS VSI 711

RESULT 12
ID ABB04578 standard; protein; 711 AA.
XX ABB04578;
XX 21-MAR-2002 (first entry)
XX Human lipoxigenase 46638.
XX Human; lipoxigenase; 46638; cytostatic; antiarrhythmic; hypotensive;
XX antiatherosclerotic; cardiant; vasotropic; hypertensive;
XX antiinflammatory; neuroprotective; nootropic; antiparkinsonian;
XX anticonvulsant; hepatotropic; dermatological; antipsoriatic; fungicide;
XX antidiarrheic; antiulcer; antidiabetic; antiasthmatic; antiarthritic;
XX antirheumatic; osteopathic; antithyroid; antiallergic; gene therapy;
XX ophthalmological; antianaemic; analgesic; virucide; anorectic; vulnery;
XX immunomodulator.
XX Homo sapiens.
XX OS
XX PN WO200190323-A2.
XX PD 29-NOV-2001.
XX 21-MAY-2001; 2001WO-US016380.
XX 19-MAY-2000; 2000US-0205675P.
XX (MILL-) MILLENNIUM PHARM INC.
XX PA Meyers RA;
XX PI
XX DR WPI; 2002-083104/11.
XX DR N-PSDB; ABA05868.
XX PT Novel human lipoxigenase family member polypeptide and polynucleotide for
XX diagnosing, treating immune, blood vessel, cardiovascular, inflammatory,
XX ovarian, lung, colon, skin disorders and disorders involving placenta.
XX PS Claim 9; Page 102; 118pp; English.
XX CC The present invention provides the protein and coding sequences of a
XX human protein, which is a member of lipoxigenase family, and is referred
XX to as 46638. The sequences can be used in the treatment of immune, blood
XX vessels, cardiovascular, inflammatory, cell differentiation,
XX neurodegenerative, liver, ovarian, lung, colon, breast, skin disorders,
XX disorders associated with bone metabolism, pain or metabolic disorders,
XX disorders involving the placenta and viral diseases. The present sequence
XX is the protein of the invention
XX Sequence 711 AA;

Query Match 51.7%; Score 1864; DB 5; Length 711;
Best Local Similarity 50.1%; Pred. No. 8.1e-169;
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;

QY 1 MAKCRVRSVTGACGAGTWDKVSIVTGHSGSPVLPDLHLGKERSAGAEDEFVTLPOD 60
Db 1 MAVYRLCVTTGPLYRAGTLDNISVTLVGTCGSPKQRLDRMGDRDFAPGVSQYKVRCTAE 60
QY 61 VGTVLMRLRVHKAPPEVSLPLMGFSRDAWCFRWFELWLPAAALHPPCYOWLEGAGELVLR 120
Db 61 LGELLRLRVHKE-----RYAFRKDSVCSRICVTEPDGVSVSHPPCYQWIEGYCTVELR 114
QY 121 EGAAKVSWQDHHPTLQDQRQKLESQRKMYSMKTYIEGWPRCLDHETVKDLDL----- 173
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Db 115 PGTARTICQDSLPLLLDHRTRARQECYRWKIYAPGPFPCWVDVNSFOEMESDKKFAIT 174
QY 174 -----NIKYSAMNAKLFFKAHSAYTELKVK 199
Db 175 KTTYCVDOGDSGNRYLPGFPKMDIPSLMYMEPNVRSATKTI SLLFNAPASLGMKLR 234
QY 200 GLLDRGTGLWRSRLREMRRLNFRKTPAAEYVFAHQOEDAFFASQFNGINPVLIIRCHSLP 259
Db 235 GLLDRKGSWKLLDDMONIFWCHKTFTTKYVTEHWCEDHFFGYQLNGVNPVLMHLCISLIP 294
QY 260 NNFPVTDEMVAIVLPGTSLQAELEKGSFLVDHGILSGVHTNIILNGPQPSAAAPKTLH 319
Db 295 SKLPVTNDWVAPLLGQDTCLQTELEGRGNIFLADYWIABEAPTHCLNGRQYVAAFLCLLW 354
QY 320 QSSGSGPLLPALIAOLKQTPGPNPIFLPSDDTDWMLLAKTWVRNSEFYTHEAVTHLLHAH 379
Db 355 LSP-QGALVPAIAIQSQTPGPDSPFLFTDSEWMLLAKTWVRNSEFLVHNNTHFLCTH 413
QY 380 LIPEVFPALATLRLQPRCHPLFKLIPHIYRITLHINTLARELIVAPGKIDKSTGLGTGTF 439
Db 414 LLCEAFAMATLRLQPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVDQVTSIGRQGL 473
QY 440 SDLIKRMEQLNYSVLCPEDIRARGVEDIPGYYYRDDGMQIWGAIKSFVSIVGIYPS 499
Db 474 IYLMSTGLAHFTYTNFCLPDSLARGVLAIPNYHYRDDGLKTIWAAIESFVSIVGIYPS 533
QY 500 DTSVQDDQELQAWVREIFSEGFLGREGSSMPSLLDTREALVOYITWVITFCSAKHAAVSS 559
Db 534 DASVOQDSELQAWTGEIFAQFLGREGSGFRLCTPGEMVKFLTAIFNCSAQHAAVNS 593
QY 560 GQFDSVVMVNPMLPPTMQLPPTSKQARPESFIATLPVNSSSYHIIALWLASAPGQDR 619
Db 594 GQHDFGAMNPAPSSMRQPPQTKGTTTLTKYTLDTLPEVNI SCNNLLLFWLVSQBPQDQR 653
QY 620 PLGHPYDEHFTEDAPRRSVAAPQKLIQISKGIRNRGLALPYTYLDPPLIENS VSI 677
Db 654 PLGTYPDEHFTTEAPRRSIAAFQSLAQISRDIOERNQGLALPYTYLDPPLIENS VSI 711

RESULT 13
AAE39890
ID AAE39890 standard; protein; 711 AA.
XX AAE39890;
XX 18-DEC-2003 (first entry)
XX Human lipoxigenase, 46638.
XX Human; cytochrome p450; dehydrogenase/reductase; osteomalacia; psoriasis;
XX lipoxigenase; hydrtase; proliferative disorder; haematopoietic disorder;
XX differentiative disorder; carcinoma; sarcoma; leukaemia; immune disorder;
XX anorexia nervosa; neural degeneration; muscular disorder; lipid disorder;
XX multiple sclerosis; encephalomyelitis; metabolic disorder; osteoporosis;
XX myasthenia gravis; bone metabolism; immunomodulator; obesity; anorectic;
XX eating disorder; osteodystrophy; arthritis; diabetes; anabolic; rickets;
XX milk fever; diabetes mellitus.
XX Homo sapiens.
XX Key Location/Qualifiers
XX Domain 267..703
XX /note= "Lipoxigenase domain"
XX US2003092658-A1.
XX 15-MAY-2003.
XX 20-JUN-2002; 2002US-00175696.
XX 02-FEB-2001; 2001US-0266140P.
XX 04-FEB-2002; 2002US-00067668.
PR
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CC	reductases 21509 (ADQ48409-ADQ48411) and 33770 (ADQ48412-ADQ48414);	XX	06-MAR-2001 (first entry)
CC	lipoxigenase 46638 (ADQ48418-ADQ48420) and hydratase 50090 (ADQ48424-ADQ48426). The sequences are useful for diagnosing and treating	DT	Amino acid sequence of a human lipoxigenase protein.
CC	disorders, such as genetic disorders of the membrane transport	DE	
CC	(aminoacidurias, cystinosis), CNS disorders (Alzheimer's disease,	KW	Human lipoxigenase; leukotriene; lipid; chemotactic agent; inflammation;
CC	epilepsy, Parkinson's disease), liver disorders, skeletal muscle	KW	smooth muscle contraction; asthma; eye disease; arthritis; lung disease;
CC	disorders, cellular proliferative and/or differentiative disorders	KW	cancer; acne; psoriasis.
CC	(cancer), hormonal disorders (diabetes, thyroid disorders), immune and	OS	Homo sapiens.
CC	inflammatory disorders (rheumatoid arthritis, osteoarthritis, ulcer),	XX	
CC	cardiovascular disorders, blood vessel disorders, neutrophil disorders	XX	WO2000061765-A2.
CC	(neutropenia, lupus), testicular disorder (mumps) and platelet disorders.	XX	
CC	The present sequence is a lipoxigenase of the invention.	XX	
XX		XX	19-OCT-2000.
SQ	Sequence 711 AA;	XX	12-APR-2000; 2000WO-US009657.
	Query Match 51.7%; Score 1864; DB 8; Length 711;	XX	12-APR-1999; 99US-0128817P.
	Best Local Similarity 50.1%; Pred. No. 8.1e-169;	PR	24-AUG-1999; 99US-0150454P.
	Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;	FR	(LEXI-) LEXICON GENETICS INC.
QY	1 MAKCRVRVSTGEACGATWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60	XX	
Db	1 MAVYRLCVTTGPLYRAGTLDNISVTLVGTGCGSPKQRLDRMGDRDFAPGSVQKYKVRCTAE 60	PA	
QY	61 VGTVLMLRVHKAPPEVSLPLMSFRSDAMFCRWFELWLPGAALHFPICYOWLGADELVL 120	XX	
Db	61 LGELLRLRVHKE-----RYAFRKDSWYCSRICVTEPDGVSHPFCYQWIEGYCTVELR 114	PI	Turner CA, Zambrowicz B, Nehls M, Friedrich G, Sands AT;
QY	121 EGAAKVSQDHHPTLQDQKLESRQKWSWKTYIEGWPRCLDHTETVKDLDL----- 173	XX	WPI; 2000-665134/64.
Db	115 PGTARTICQDSILPLLDHRTRELRAQECYRWKIYAPGFPFCWVDVNSFQEMESDKKFALT 174	DR	N-PSDB; AAC61758.
QY	174 -----NIKYSAMKNNAKLFKFAHSAYTELKVK 199	XX	Novel polynucleotides encoding human lipoxigenase proteins useful for
Db	175 KTTTCVDQGDSSGNRYLPFPFKIDIPSLMWEPNVRYSATKTISSLFNAIPASLGMKLR 234	XX	producing transgenic animals preferably mouse.
QY	200 GLLDRTGLRSLREMRLLNFRKTPAAEVFAHWQEDAFSAQFLNGINPVLIRCHSLP 259	PT	Claim 3; Page 74-76; 83pp; English.
Db	235 GLLDKRGSKKLDMDQNIWFCHKTFTTYKVTHEWCEDHFFGYQYLNGVNPVLMHCISL 294	XX	
QY	260 NNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVHTNINLNGKPKQFSAAPMTLLH 319	CC	AAB19379-92 represent novel human lipoxigenase proteins. Lipoxigenases
Db	295 SKLPVTNDMVAFLPGQDTCLQTELEKGNIFLADYWLAEAPTHCLNGRQYVAAPLCLLW 354	CC	oxidise lipids to produce leukotrienes. Leukotrienes bind cognate
QY	320 QSSGSGPLLPALAIQLKOTPGDNPIFLPSDDTDWMLLAKTWVRNSFEYTHEAVTHLLHAH 379	CC	receptors and trigger biological effects. Leukotrienes influence a
Db	355 LSP-QGALVFLAIQLSQTGPDSPILFPTDSEWDLAKTWVRNSEFLVHENTHFLCTH 413	CC	variety of biological processes, and can serve as, inter alia, potent
QY	380 LIPEVEFALATLQPLPCHPLFKLLIPIHRYTLHINTLARELLVAPCKLIDKSGTGTGCF 439	CC	chemotactic agents and mediators of inflammation, smooth muscle
Db	414 LLCEAFAMATLRLQLPCHPIYKLLLPHTRYTLQVNTIARATLNPBGLVDQVTSIGRQGL 473	CC	contractions, etc. . Lipoxigenases and leukotrienes are implicated in a
QY	440 SDLIKRMELQNVSLCLPEDIRARGVEDIPGYRRDGMQIOWGATKSFVSEIVSYIYPS 499	CC	variety of diseases and disorders, such as asthma, eye diseases,
Db	474 IYLMSTGLAHFYTNELCLPSLRARGLAIPNHYRDDGLKJWAALESFVSEIVGYIYPS 533	CC	arthritis, lung disease, cancer, acne, psoriasis, etc
QY	500 DTSVQDDQELQAWREIFSEGLFRESSGMPSLDTRREALVOYITWVITCSAKHAAVSS 559	XX	Sequence 867 AA;
Db	534 DASVQDSELAQTGFIQAQFLGESSGFPSRLCTPGEMVFLTAIIFNCSAQHAAVNS 593	Query Match 51.7%; Score 1864; DB 3; Length 867;	
QY	560 QPDSQVWNPVLPPTQLPPTSKQARPESFIATLPVNSSSYHIIALWLLSAPGDOR 619	Best Local Similarity 50.1%; Pred. No. 1.1e-168;	
Db	594 GQHDFGAMFNAPSSMRQPPQTKGTTTLKTLDTLPEVNISSNNLLFLWLSQBPDKOR 653	Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;	
QY	620 PLGHHYPDEHFTEDAPRRSVAAFORKLIQISKGRERNRGLAPYTYLDPPLIENSVSI 677	QY	1 MAKCRVRVSTGEACGATWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD 60
Db	654 PLGTYPDEHFTEDAPRRSVAAFQSRUAQISRDIQERNQGLALPYTYLDPPLIENSVSI 711	Db	157 MAVYRLCVTTGPLYRAGTLDNISVTLVGTGCGSPKQRLDRMGDRDFAPGSVQKYKVRCTAB 216
RESULT 15		QY	61 VGTVLMLRVHKAPPEVSLPLMSFRSDAMFCRWFELWLPGAALHFPICYOWLGADELVL 120
AAB19390		Db	217 LGELLRLRVHKE-----RYAFRKDSWYCSRICVTEPDGVSHPFCYQWIEGYCTVELR 270
ID AAB19390		QY	121 EGAAKVSQDHHPTLQDQKLESRQKWSWKTYIEGWPRCLDHTETVKDLDL----- 173
XX	standard; protein; 867 AA.	Db	271 PGTARTICQDSILPLLDHRTRELRAQECYRWKIYAPGFPFCWVDVNSFQEMESDKKFALT 330
AC AAB19390;		QY	174 -----NIKYSAMKNNAKLFKFAHSAYTELKVK 199
		Db	331 KTTTCVDQGDSSGNRYLPFPFKIDIPSLMWEPNVRYSATKTISSLFNAIPASLGMKLR 390
		QY	200 GLLDRTGLRSLREMRLLNFRKTPAAEVFAHWQEDAFSAQFLNGINPVLIRCHSLP 259
		Db	391 GLLDKRGSKKLDMDQNIWFCHKTFTTYKVTHEWCEDHFFGYQYLNGVNPVLMHCISL 450
		QY	260 NNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVHTNINLNGKPKQFSAAPMTLLH 319
		Db	451 SKLPVTNDMVAFLPGQDTCLQTELEKGNIFLADYWLAEAPTHCLNGRQYVAAPLCLLW 510
		QY	320 QSSGSGPLLPALAIQLKOTPGDNPIFLPSDDTDWMLLAKTWVRNSEFIHEAVTHLLHAH 379



Db 511 LSP-QGALVPLAIQISQTPGDPSPIFLPTDSEWDMLLAKTWVRNSEFLVHNNTHFLCTH 569  
Qy 380 LIPEVPALATLQLPCHPLFKLLIPHRYTLHINTLARELLVAPKLDKSTGLTGGP 439  
Db 570 LLCEAFAMATLQLPCHPLFYKLLPHRYTLQVNTIARATLLNPEGLVDQVTSIGROGL 629  
Qy 440 SDLIKRNNEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGMOIWGAIKSFVSEIYSIYVPS 499  
Db 630 IYLMSTGLAHFTYTNFCLPDSIRARGVLAIPNYHYRDDGLKIWAIESFVSEIVGYIYVPS 689  
Qy 500 DTSVQDDOELQAWVREIFSEGLGREGSSCMPSLDREALVQYITMWIFTCSAKHAAVSS 559  
Db 690 DASVQODSELQAWTGEIIFAQAFLGREGSGFPFSLCTPGEMVKFLTAIIFNCSAQHAAVNS 749  
Qy 560 GQFDSQVWMPNLPTMQLPPTTSKQARPESFIATLPVNSSSYHIIALWLLSABPGDQR 619  
Db 750 GQHDFGAWNPANPSSMRQPPQTKGTTTKTYLDTLPEVNTSCNNLLFLWLVSQEPKQOR 809  
Qy 620 PLGHYPDEHFTEDAPRRSVAAPORKLIQISKGIRERNEGLALPYTYLDPPLIENSVSI 677  
Db 810 PLGTYPDEHFTEEAPRRSIAAPQSRLAQISRDIOERNQGLALPYTYLDPPLIENSVSI 867

Search completed: July 18, 2005, 21:57:22  
Job time : 118.375 secs

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GenCore version 5.1.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 18, 2005, 21:50:48 ; Search time 30.8647 Seconds  
(without alignments)  
1637.384 Million cell updates/sec

Title: US-10-688-676A-4

Perfect score: 3604

Sequence: 1 MAKCRVRVSTGEACGAGTWD.....GLALPYTYLDPLIENSVSI 677

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pap:\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pap:\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pap:\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pap:\*  
5: /cgn2\_6/ptodata/1/iaa/ECTUS\_COMB.pap:\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3604	100.0	677	3	US-09-061-768A-4
2	3604	100.0	677	4	US-09-764-246-4
3	2883.5	80.0	679	4	US-09-949-016-8912
4	2880.5	79.9	676	3	US-09-061-768A-2
5	2880.5	79.9	676	4	US-09-764-246-2
6	2880.5	79.9	676	4	US-09-949-016-6027
7	1864	51.7	711	4	US-09-547-435-2
8	1864	51.7	867	4	US-09-547-435-24
9	1795	49.8	701	3	US-09-087-727-2
10	1795	49.8	701	4	US-09-853-053-2
11	1795	49.8	701	4	US-09-949-016-6026
12	1588	44.1	556	4	US-09-547-435-6
13	1464	40.6	615	4	US-09-547-435-10
14	1464	40.6	771	4	US-09-547-435-28
15	1442.5	40.0	674	4	US-09-949-016-5980
16	1442.5	40.0	689	4	US-09-949-016-11692
17	1212	33.6	663	4	US-09-641-638-653
18	1212	33.6	663	4	US-10-170-097-653
19	1188	33.0	460	4	US-09-547-435-12
20	1186.5	32.9	662	3	US-09-061-768A-25
21	1186.5	32.9	662	4	US-09-764-246-25
22	1077.5	29.9	489	4	US-09-547-435-4
23	1077.5	29.9	645	4	US-09-547-435-26
24	953	26.4	291	4	US-09-547-435-14
25	801.5	22.2	334	4	US-09-547-435-8
26	799.5	22.2	675	4	US-09-902-540-12713
27	710	19.7	360	4	US-09-949-016-8911
					Sequence 4, Appli
					Sequence 4, Appli
					Sequence 8912, Ap
					Sequence 2, Appli
					Sequence 2, Appli
					Sequence 6027, Ap
					Sequence 2, Appli
					Sequence 24, Appl
					Sequence 2, Appli
					Sequence 6026, Ap
					Sequence 6, Appli
					Sequence 10, Appl
					Sequence 28, Appl
					Sequence 5980, Ap
					Sequence 11692, A
					Sequence 653, App
					Sequence 653, App
					Sequence 12, Appl
					Sequence 25, Appl
					Sequence 4, Appli
					Sequence 26, Appl
					Sequence 14, Appl
					Sequence 8, Appli
					Sequence 12713, A
					Sequence 8911, Ap

28 524 17.3 592 3 US-09-413-814-83 Sequence 83, Appli  
29 598 16.6 692 4 US-09-252-991A-19668 Sequence 19668, A  
30 553 15.3 195 4 US-09-547-435-20 Sequence 20, Appli  
31 544.5 15.1 862 4 US-09-978-522-1 Sequence 1, Appli  
32 534 14.8 859 4 US-09-978-522-3 Sequence 3, Appli  
33 520 14.4 864 4 US-09-810-268-3 Sequence 3, Appli  
34 518.5 14.4 857 4 US-09-751-687-17 Sequence 17, Appli  
35 516.5 14.3 864 4 US-09-751-687-18 Sequence 18, Appli  
36 495 13.7 865 4 US-09-751-687-9 Sequence 9, Appli  
37 493 13.7 862 4 US-09-751-687-12 Sequence 12, Appli  
38 486 13.5 862 4 US-09-751-687-12 Sequence 12, Appli  
39 483 13.4 139 4 US-09-547-435-18 Sequence 18, Appli  
40 460.5 12.8 901 4 US-09-714-767A-4 Sequence 4, Appli  
41 457 12.7 839 4 US-09-751-687-15 Sequence 15, Appli  
42 389 10.8 110 4 US-09-547-435-22 Sequence 22, Appli  
43 166.5 4.6 69 4 US-09-547-435-16 Sequence 16, Appli  
44 158.5 4.4 131 4 US-09-641-638-654 Sequence 654, App  
45 158.5 4.4 131 4 US-10-170-097-654 Sequence 654, App

#### ALIGNMENTS

RESULT 1  
US-09-061-768A-4  
; Sequence 4, Application US/09061768A  
; Patent No. 6204037  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; APPLICANT: BOEGLIN, WILLIAM E.  
; APPLICANT: JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/061,768A  
; FILING DATE: APRIL 16, 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: NONE  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 677 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
US-09-061-768A-4

Query Match 100.0%; Score 3604; DB 3; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAKCRVRVSTGEACGAGTWDKVSIVSGTHGESPLVDHLGKFSAGAEEDFEVTLFQD 60

Db 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60  
QY 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPFGAALHPPCYQWLEGAGELVLR 120  
Db 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPFGAALHPPCYQWLEGAGELVLR 120  
QY 121 EGAAKVSWQDHHPTLQDQKELSRQKMSWKTYIEGWPRCLDHTETVKDLNLKYSAM 180  
Db 121 EGAAKVSWQDHHPTLQDQKELSRQKMSWKTYIEGWPRCLDHTETVKDLNLKYSAM 180  
QY 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240  
Db 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240  
QY 241 SQFLNGINPVLIIRCHSLPNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVH 300  
Db 241 SQFLNGINPVLIIRCHSLPNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVH 300  
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSDDTWDMLLAKTW 360  
Db 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSDDTWDMLLAKTW 360  
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420  
Db 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420  
QY 421 LVAPGKLDKSTGLGTGGSFSLIKRMEQLNYSVLCPLPEDIRARGVEDIPGYYYRDDGMQ 480  
Db 421 LVAPGKLDKSTGLGTGGSFSLIKRMEQLNYSVLCPLPEDIRARGVEDIPGYYYRDDGMQ 480  
QY 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFLEGGSGMPSLLDTREALV 540  
Db 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFLEGGSGMPSLLDTREALV 540  
QY 541 QYITWVIFTCSAKHAASVSGQFSDSCVMPNLPPTMQLPPPTSGKQARPESTIATLPVNS 600  
Db 541 QYITWVIFTCSAKHAASVSGQFSDSCVMPNLPPTMQLPPPTSGKQARPESTIATLPVNS 600  
QY 601 SSVHIIALWLSAEPGDQRLGHPYDEHFTEDAPRRSVAAFORKLIQISKGRIRNRGLA 660  
Db 601 SSVHIIALWLSAEPGDQRLGHPYDEHFTEDAPRRSVAAFORKLIQISKGRIRNRGLA 660  
QY 661 LPYTYLDPPLIENSVS I 677  
Db 661 LPYTYLDPPLIENSVS I 677

RESULT 2

US-09-764-246-4  
; Sequence 4, Application US/09764246  
; Patent No. 6649355  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; BOEGLIN, WILLIAM E.  
; JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/764,246  
; FILING DATE: 17-Jan-2001

CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 677 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-764-246-4  
Query Match 100.0%; Score 3604; DB 4; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60  
Db 1 MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60  
QY 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPFGAALHPPCYQWLEGAGELVLR 120  
Db 61 VGTVLMLRVHKAPEVSLPLMSFRSDAWFCRWFLEWLPFGAALHPPCYQWLEGAGELVLR 120  
QY 121 EGAAKVSWQDHHPTLQDQKELSRQKMSWKTYIEGWPRCLDHTETVKDLNLKYSAM 180  
Db 121 EGAAKVSWQDHHPTLQDQKELSRQKMSWKTYIEGWPRCLDHTETVKDLNLKYSAM 180  
QY 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240  
Db 181 KNAKLFFKAHSAYTELKVKGLDRTGLWLSREMRRLFNFRKTPAAEYVFAHWQEDAFPA 240  
QY 241 SQFLNGINPVLIIRCHSLPNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVH 300  
Db 241 SQFLNGINPVLIIRCHSLPNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVH 300  
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSDDTWDMLLAKTW 360  
Db 301 TNILNGKQFSAAPMTLLHQSSGSGPLPIAQLKQTPGDPNPIFLPSDDTWDMLLAKTW 360  
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420  
Db 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLRLQPRCHPLFKLLIPIRHYTLHINTLAREL 420  
QY 421 LVAPGKLDKSTGLGTGGSFSLIKRMEQLNYSVLCPLPEDIRARGVEDIPGYYYRDDGMQ 480  
Db 421 LVAPGKLDKSTGLGTGGSFSLIKRMEQLNYSVLCPLPEDIRARGVEDIPGYYYRDDGMQ 480  
QY 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFLEGGSGMPSLLDTREALV 540  
Db 481 IWGAIKSFVSEIYIYPSDTSVQDDQELQAWVREIFSEGFLEGGSGMPSLLDTREALV 540  
QY 541 QYITWVIFTCSAKHAASVSGQFSDSCVMPNLPPTMQLPPPTSGKQARPESTIATLPVNS 600  
Db 541 QYITWVIFTCSAKHAASVSGQFSDSCVMPNLPPTMQLPPPTSGKQARPESTIATLPVNS 600  
QY 601 SSVHIIALWLSAEPGDQRLGHPYDEHFTEDAPRRSVAAFORKLIQISKGRIRNRGLA 660  
Db 601 SSVHIIALWLSAEPGDQRLGHPYDEHFTEDAPRRSVAAFORKLIQISKGRIRNRGLA 660  
QY 661 LPYTYLDPPLIENSVS I 677  
Db 661 LPYTYLDPPLIENSVS I 677

## RESULT 3

US-09-949-016-8912  
; Sequence 8912, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 8912  
; LENGTH: 679  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-8912

Query Match 80.0%; Score 2883.5; DB 4; Length 679;  
Best Local Similarity 78.2%; Pred. No. 1e-316;  
Matches 530; Conservative 68; Mismatches 77; Indels 3; Gaps 2;

Qy	1	MAKCRVSTGEACAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFVTLPOD	60
Db	4	MAEPRVSTGEAFGAGTWDKVSIVGTRGESPLDNLGKFTAGAEEDFQVTLPE	63
Qy	61	VGTVMLRVHKAPEVSVPLMS - FRSDAFCRWFPELWPGAAHFPVQWLEGAGELVL	119
Db	64	VGRVLLRVHKAPEVSVPLMS - VLPGLGLAPDAWFCRWFQTPRGHLLFPVQWLEGAGTLVL	121
Qy	120	REGAAKVSQDHHPTLPDQROKESRQKYSWKTYIEGWPRCLDHTVTKDLNLIKYS	179
Db	122	QEGTAKVSQDHHPTLPDQROKESRQKYSWKTYIEGWPRCLDHTVTKDLNLIKYS	181
Qy	180	MKNAKLFFKAHSATYELKVGLLDRGTGLWSLRMRRLFNFRKTPAAEYVFAHQEDAFF	239
Db	182	AKNANFYLQAGSAFAEMKIKGLDRKGLWSLRMRRLFNFRKTPAAEYVFAHQEDAFF	241
Qy	240	ASQFLNGINPVLIRCHSLPNNFVPTDMSVAPVLGPGTSLQAELEKSGSLFLVDHGILSGV	299
Db	242	ASQFLNGINPVLIRCHSLPNNFVPTDMSVAPVLGPGTSLQAELEKSGSLFLVDHGILSGI	301
Qy	300	HTNLNGKPFSAAPMTLLHSGSGPLLPALAIQLKQTPGPDNPIFLPSSDDTWDWLLAKT	359
Db	302	QTNVINGKPFSAAPMTLLHSGSGPLLPALAIQLKQTPGPDNPIFLPSSDDTWDWLLAKT	361
Qy	360	WRNSEFVHIAVTHLLHAHLIPEVFALATLQRPCHPLPKLLIPHYRYLHINTLARE	419
Db	362	WRNRAEFSFEALHLLSHLLPEVFTLRLQPLCHPLPKLLIPHYRYLHINTLARE	421
Qy	420	LLVAPGLIKDSTGLGTGFSGLIKRNEQLNYSVLCLPEDIRARGVEDIPGYYYRDDGM	479
Db	422	LLVPGQVVDSTGIGIEGFSGLIKRNEQLNYSVLCLPEDIRARGVEDIPGYYYRDDGM	481
Qy	480	QIWGAIKSFVSEIYSYPSDTSVQDQELQAWREIFSEGFLGREGSSGMPSSLDLTREAL	539
Db	482	QIWGAVERFVSEIIGIYPSDESQDDELQAWREIFSKGFLNQESSGIPSSLETREAL	541
Qy	540	VOYITWVITCSAKHAAVSSGQFDSVVMNLPPTMQLPPTPSKQQAPEPSFIATLPVAV	599
Db	542	VOYITWVITCSAKHAAVSSGQFDSVVMNLPPTMQLPPTPSKQQAPEPSFIATLPVAV	601
Qy	600	SSSVHIIALWLLSAPGQDPLGHVDEHFTEDAPRRSVAAFQKLIQISKGIERNRGL	659
Db	602	ATCDVILALWLLSAPGQDPLGHVDEHFTEDAPRRSVAAFQKLIQISKGIERNRGL	661

Qy 660 ALPYTYLDPPLIENSIVI 677  
Db 662 VLPYTYLDPPLIENSIVI 679

## RESULT 4

US-09-061-768A-2  
; Sequence 2, Application US/09061768A  
; Patent No. 6204037  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; APPLICANT: BOEGLIN, WILLIAM E.  
; APPLICANT: JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER-READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/061,768A  
; FILING DATE: APRIL 16, 1998  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA: NONE  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 676 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
US-09-061-768A-2

Query Match 79.9%; Score 2880.5; DB 3; Length 676;  
Best Local Similarity 78.0%; Pred. No. 2.2e-316;  
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

Qy	1	MAKCRVSTGEACAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFVTLPOD	60
Db	1	MAEPRVSTGEAFGAGTWDKVSIVGTRGESPLDNLGKFTAGAEEDFQVTLPE	60
Qy	61	VGTVMLRVHKAPEVSVPLMS - FRSDAFCRWFPELWPGAAHFPVQWLEGAGELVL	119
Db	61	VGRVLLRVHKAPEVSVPLMS - VLPGLGLAPDAWFCRWFQTPRGHLLFPVQWLEGAGTLVL	118
Qy	120	REGAAKVSQDHHPTLPDQROKESRQKYSWKTYIEGWPRCLDHTVTKDLNLIKYS	179
Db	119	QEGTAKVSQDHHPTLPDQROKESRQKYSWKTYIEGWPRCLDHTVTKDLNLIKYS	178
Qy	180	MKNAKLFFKAHSATYELKVGLLDRGTGLWSLRMRRLFNFRKTPAAEYVFAHQEDAFF	239
Db	179	AKNANFYLQAGSAFAEMKIKGLDRKGLWSLRMRRLFNFRKTPAAEYVFAHQEDAFF	238
Qy	240	ASQFLNGINPVLIRCHSLPNNFVPTDMSVAPVLGPGTSLQAELEKSGSLFLVDHGILSGV	299

Db 239 ASQFLNGLNPVLIIRCHYLPKNFPVTDAMVASLLGGTSLQAELEKGSFLVDHGILSGI 298  
QY 300 HTNILNGKQFSAAPMTLLHQSSGGSLPLPIAIQKQTEGPDNPFLPSSDDTWDMLLAKT 359  
Db 299 QTNVINGKQFSAAPMTLLYQSPGCGPLPLAIQLSQTGPNSPFLPTDDKDWMLLAKT 358  
QY 360 WYRNSEFYTHEAVTHLLHAHLIPEVPALATLQRLPCHPLFKLLIPHRYTLHINTLARE 419  
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLQRLPCHPLFKLLIPHRYTLHINTLARE 418  
QY 420 LLAAPKLDKSTGLTGCGFSDLIKENMEOLANYSLCLPEDIRANGVEDIPGYVYRDDGM 479  
Db 419 LLIIPGQVDRSTGIGIEGSELIQRMKQLNYSLLCLPEDIRANGVEDIPGYVYRDDGM 478  
QY 480 QIWAIGKSFVSEIVSYIYPSDTSVQDDQELQAWVREIFSEGFLGRESSQMPSLLOTREAL 539  
Db 479 QIWAVERFVSEIIGIYPSDESVDQDRELQAWVREIFSKGFLNQESSGIPSSLETREAL 538  
QY 540 VOYITWVITCSAKHAASVSGQFDSVWMPNLPPTWQLPPTSKGQARPESTIATLPVN 599  
Db 539 VOYVTVMTVITCSAKHAASVAGQFDSVWMPNLPPTSKGLATCEGFIATLPVN 598  
QY 600 SSSYHIIALWLSAEPGQORPLGHPYDEHFTEDAPRSVAARQKLIQISKGIERNRGL 659  
Db 599 ATCDVILALWLSKEPGQORPLGTYPDEHFTEDAPRSVAARQKLIQISKGIERNRGL 658  
QY 660 ALPTYTLDPLIENSYSI 677  
Db 659 VLPYTYLDPPLIENSYSI 676

RESULT 5  
US-09-764-246-2  
; Sequence 2, Application US/09764246  
; Patent No. 6649355  
; GENERAL INFORMATION:  
; APPLICANT: BRASH, ALAN R.  
; BOEGLIN, WILLIAM E.  
; JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: AKLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; COMPUTER: IBM PC/XT/AT compatible  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/764,246  
; FILING DATE: 17-Jan-2001  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELETYPE: <Unknown>  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 676 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single

; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-764-246-2  
Query Match 79.9%; Score 2880.5; DB 4; Length 676;  
Best Local Similarity 78.0%; Pred. No. 2.2e-316;  
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;  
QY 1 MAKCRVRVSTGEACAGTWDKVSIVSTHGESPLVPLDLHLGKEFSAGAEEDFEVTLPOD 60  
Db 1 MAEFVRVSTGEAFGAGTWDKVSIVSTGRGESPLPLDLNLGKEFTAGAEEDFQVTLPED 60  
QY 61 VGTVLMVLRVHKAPPEVSLPLMS-FRSDAWFCWFELEWLPGLAALHFPYCOWLEGAGELVL 119  
Db 61 VGRVLLLRVHKAPP--VLPLGLPLADAWFCWFOQTTPRGHLLFPYCOWLEGAGTLLV 118  
QY 120 REGAAKVSQDHPHTLOQROKELEROKYSWKTYIEGWPRCLDHEVTVDLDLNIKYS 179  
Db 119 QEGTAKVSWADHPVLOQROQELQARQEMTQWKAYNFGWPHCLDEKTVEDLELNKYST 178  
QY 180 MKNAKLPFKAHSAVTELKVGGLDRTGLWRSILREMRRLFNFRKTPAAEYVFAHWQEDAFF 239  
Db 179 AKNANFYLAQSAPAEKMKGLLDRKGLWRSILNEMKRIFNFRTPAAEHAFAHEWQEDAFF 238  
QY 240 ASQFLNGINPVLIIRCHSLPNNFPVTDENAPVLGPGTSLQAELEKGSFLVDHGILSOV 299  
Db 239 ASQFLNGLNPVLIIRCHYLPKNFPVTDAMVASLLGGTSLQAELEKGSFLVDHGILSGI 298  
QY 300 HTNILNGKQFSAAPMTLLHOSGGSLPLPIAIQKQTPGPDNPFLPSSDDTWDMLLAKT 359  
Db 299 QTNVINGKQFSAAPMTLLYQSPGCGPLPLAIQLSQTGPNSPFLPTDDKDWMLLAKT 358  
QY 360 WYRNSEFYTHEAVTHLLHAHLIPEVPALATLQRLPCHPLFKLLIPHRYTLHINTLARE 419  
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLQRLPCHPLFKLLIPHRYTLHINTLARE 418  
QY 420 LLAAPKLDKSTGLTGCGFSDLIKENMEOLNYSVLCLPEDIRANGVEDIPGYVYRDDGM 479  
Db 419 LLIIPGQVDRSTGIGIEGSELIQRMKQLNYSLLCLPEDIRANGVEDIPGYVYRDDGM 478  
QY 480 QIWAIGKSFVSEIVSYIYPSDTSVQDDQELQAWVREIFSEGFLGRESSQMPSLLOTREAL 539  
Db 479 QIWAVERFVSEIIGIYPSDESVDQDRELQAWVREIFSKGFLNQESSGIPSSLETREAL 538  
QY 540 VOYITWVITCSAKHAASVSGQFDSVWMPNLPPTWQLPPTSKGQARPESTIATLPVN 599  
Db 539 VOYVTVMTVITCSAKHAASVAGQFDSVWMPNLPPTSKGLATCEGFIATLPVN 598  
QY 600 SSSYHIIALWLSAEPGQORPLGHPYDEHFTEDAPRSVAARQKLIQISKGIERNRGL 659  
Db 599 ATCDVILALWLSKEPGQORPLGTYPDEHFTEDAPRSVAARQKLIQISKGIERNRGL 658  
QY 660 ALPTYTLDPLIENSYSI 677  
Db 659 VLPYTYLDPPLIENSYSI 676

RESULT 6  
US-09-949-016-6027  
; Sequence 6027, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498



;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 6027  
;; LENGTH: 676  
;; TYPE: PRT  
;; ORGANISM: Human  
US-09-949-016-6027

Query Match 79.9%; Score 2880.5; DB 4; Length 676;  
Best Local Similarity 78.0%; Pred. No. 2.2e-316;  
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;  
QY 1 MAKCRVRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPDQ 60  
DB 1 MAFPRVRVSTGEAGAGTWDKVSIVGTHGESPLVPLDLNLGKFTAGAEEDFQVTLPE 60  
QY 61 VGTVLMRLVHKAPPEVSLPLMS-PRSDAWFCRWFELEWLPAAALHPPCYQWLEGAGELVL 119  
DB 61 VGRVLLLRVHKAPP--VLPLGLPADDAWFCWFOQTTPRGHLLFPYQWLEGAGTULV 118  
QY 120 REGAAKVSQDHHPTLPQORQKESRQKYSWKTYIEGWPRCLDHEVTKDLMIKYSA 179  
DB 119 QEGTAKVSMADHHPVLQQORQELQARQEMQKAYNPGWPHCLDEKTVEDLELNKYST 178  
QY 180 MNAKLPFAKHSAYTELKVGLLDRTGLWRSLEWRRLFNFRKTPAAEYVFAHWQEDAFF 239  
DB 179 AKNANFYLAQSAFAEMKIKGLDRKGLWRSLEWRRLFNFRKTPAAEYVFAHWQEDAFF 238  
QY 240 ASQFLNGINPVLRIRCHSLPNNFPVTDMAVAPLVPGTSLQAELEKSGSLFLVDHGILSGV 299  
DB 239 ASQFLNGINPVLRIRCHSLPNNFPVTDMAVAPLVPGTSLQAELEKSGSLFLVDHGILSGI 298  
QY 300 HTNILINGKQPSAAPTLLHOSGSGPLPIAIQKOTPGDNPFIPLPSDDTWDWLLAKT 359  
DB 299 QTNVINGKQPSAAPTLLYQSPGCGPLPIAIQKOTPGDNPFIPLPSDDTWDWLLAKT 358  
QY 360 WVRNSEFYHRAVTHLLHAHLIPEVVALATLQRLPRCHPLFKLLPHRYTLHINTLARE 419  
DB 359 WVRNAEFSFHEALTHLLSHLLPEVFTLATLRLPHCHPLFKLLPHRYTLHINTLARE 418  
QY 420 LLVAPGLIKDSTGLTGCGFSDLIKRNEQLNYSVLCIPEDIRARGVEDIPGYRRDDGM 479  
DB 419 LLVPGQVQVDRSTGIGISGSELIRNNKQLNYSLLCLPEDIRARGVEDIPGYRRDDGM 478  
QY 480 QIWGAIKSFVSEIYIPSDTSVQDDQELQAWVREIFSEGFLGREGSGMPSLLDREAL 539  
DB 479 QIWGAVERFVSEIIGIYIPSDTSVQDDQELQAWVREIFSEGFLGREGSGMPSLLDREAL 538  
QY 540 VOYITWVFTCSAKHAASVSGQFDSVCMWPNLPPTMQLPPTPSKQARPEFSFIATLPVN 599  
DB 539 VOYVTVWVFTCSAKHAASVSGQFDSVCMWPNLPPTMQLPPTPSKQARPEFSFIATLPVN 598  
QY 600 SSSVHIIALWLLSAPGQDPLGHYPDEHFTEDAPRRSVAAPFQKLIQISGIERNEGL 659  
DB 599 ATCDVILWLLSKSPGQDPLGHYPDEHFTEDAPRRSVAAPFQKLIQISGIERNEGL 658  
QY 660 ALPTYLDPPPIIENSVS 677  
DB 659 VLPYLDPPPIIENSVS 676

## RESULT 7

US-09-547-435-2  
; Sequence 2, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides

;; TITLE OF INVENTION: Encoding the Same  
;; FILE REFERENCE: 7705.0009-00000  
;; CURRENT APPLICATION NUMBER: US/09/547,435  
;; CURRENT FILING DATE: 2000-04-12  
;; NUMBER OF SEQ ID NOS: 29  
;; SOFTWARE: FastSeq for Windows Version 3.0  
;; SEQ ID NO 2  
;; LENGTH: 711  
;; TYPE: PRT  
;; ORGANISM: Homo sapiens  
US-09-547-435-2

Query Match 51.7%; Score 1864; DB 4; Length 711;  
Best Local Similarity 50.1%; Pred. No. 3.3e-201;  
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;  
QY 1 MAKCRVRVSTGEACAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPDQ 60  
DB 1 MAVYRLCVTTGTPYLRAGTLDNISVTLVGTGSPKQRLDRMRDPAFGSVQKYKVRCTAE 60  
QY 61 VGTVLMRLVHKAPPEVSLPLMS-PRSDAWFCRWFELEWLPAAALHPPCYQWLEGAGELVL 120  
DB 61 LGELLRLVRHKE-----RVAFPRKDSWYCSRICVTEPDGVSHPPCYQWIEGYCTVELR 114  
QY 121 EGAAKVSQDHHPTLPQORQKESRQKYSWKTYIEGWPRCLDHEVTKDLDL----- 173  
DB 115 PGTARTICQDLSPLLLDHRTRELRARGCYRWKIYAPGFCMVVDVNSFQEMESDKKFAIT 174  
QY 174 -----NIKYSAMNAKLPFAKHSAYTELKVK 199  
DB 175 KTTTCVQDSSGNRYLPGGFPMKIDIPSLMYMENVRYSATKTSLLFNATPASLGMLK 234  
QY 200 GLLDRTGLWRSLEWRRLFNFRKTPAAEYVFAHWQEDAFFASQFLNGINPVLRIRCHSLP 259  
DB 235 GLLDRKSGWKLLDQWQIFWCHKTFTTKYVTEHWCEDHFFGQYLVNGVNVMLHICISL 294  
QY 260 NNPVTVDEMVAIVLPGTSLQAELEKSGSLFLVDHGILSGVHTNILINGKQPSAAPTLLH 319  
DB 295 SKLPVTNDMAVAPLVPGTSLQAELEKSGSLFLVDHGILSGVHTNILINGKQPSAAPTLLH 354  
QY 320 QSSGSGPLPIAIQKOTPGDNPFIPLPSDDTWDWLLAKTWRNSEFYHRAVTHLLHAH 379  
DB 355 LSP--QGAIVPLAIQISQTPGDSPIFLPTDSEWDLAKTWRNSEFYHRAVTHLLHAH 413  
QY 380 LIPEVVALATLQRLPRCHPLFKLLPHRYTLHINTLARELLVAPGLIKDSTGLTGCGF 439  
DB 414 LLCEAFAMATLQRLPLCHPIYKLLPHRYTLQVNTIARATLLNPEGLVDQVTSIGRQGL 473  
QY 440 SLLIKRNEQLNYSVLCIPEDIRARGVEDIPGYRRDDGMQIWGAIKSFVSEIYIPYS 499  
DB 474 IYLMSTGLAHFTYTNFCLPSLRARGVLAIPNHYRDDGLKIAWAIESFVSEIYIPYS 533  
QY 500 DTSVQDDQELQAWVREIFSEGFLGREGSGMPSLLDREALVOYITWVFTCSAKHAASV 559  
DB 534 DASVQDSELOQWTEIGEIPAQFLGREGSGFSPRLCTGEMVKFLTAIIPNCSAQHAASV 593  
QY 560 GQFDSVCMWPNLPPTMQLPPTPSKQARPEFSFIATLPVNSSSVHIIALWLLSAPGQD 619  
DB 594 GQHDFGAWPNAPSSMRQPPQTGTTTLTKYTLDTLPVNI SCNNLLFLWVSQEPKQD 653  
QY 620 PLGHYPDEHFTEDAPRRSVAAPFQKLIQISGIERNEGLALPTYLDPPPIIENSVS 677  
DB 654 PLGTYPDEHFTEDAPRRSVAAPFQKLIQISGIERNEGLALPTYLDPPPIIENSVS 711

## RESULT 8

US-09-547-435-24  
; Sequence 24, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael



```

; GENERAL INFORMATION:
; APPLICANT: Brash, Alan
; APPLICANT: Boeglin, William
; APPLICANT: Kim, Richard
; TITLE OF INVENTION: ISOLATED AND PURIFIED 12R-LIPOXYGENASE PROTEIN AND NUCLEIC ACIDS
; FILE REFERENCE: Attorney Docket No. 6569644 1242/7/2
; CURRENT APPLICATION NUMBER: US/09/853,053
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-853-053-2

```

Query Match	49.8%	Score 1795;	DB 4;	Length 701;
Best Local Similarity	47.9%	Pred. No. 2.1e-193;		
Matches 339;	Conservative 121;	Mismatches 210;	Indels 38;	Gaps 31;
Qy	1	MAKCRVSVTGEACGAGTMDKVSIVSVGTHGESPLVPLDLHLGKFSAGAESEDFEVLTPOD	60	
Db	1	MATYKRVATGDTLLSGTRDSISITVGTQESHKQLLNHFRGFATGAVGOYTVQCCPD	60	
Qy	61	VGTVLMRLVRHKAPPEVSLPMSFRSDAWFCRWFLEMLPGAALHFFPCYQWLEGAGELVLR	120	
Db	61	LGELIIRLHKE-----RYAFFPKDPWCYCNVQICAPNGRIYHFPAYQWMDGVETLALR	114	
Qy	121	EGAAKVSQDHPHTLPQDOROKELSRQKMSWKT-----	155	
Db	115	EATGKTTADDLSPLVLEHREKEIRAKQDFYHWRVFLPGLPSYVHIPSVRPPVRHRPNR	174	
Qy	155	-----YIEGPRCLDHETVKDLDNIKYSAMQNAKLFPKAHSATELKVKGILLDRGLWR	209	
Db	175	PEWNGYTPGPFILINFKATPLNLNRYSFUKTASFVRLGPMALAFKVRGLLCKHSWK	234	
Qy	210	SLREMRLLNFRKTPAAEYFAHWQEODAFFASQFLNGINPVLIRRHSLPNPNFPVTDMMV	269	
Db	235	RLKDRIKIPCKSVSVSEYAEHWAEDTFPGQYLVNGVNPGLIRRCTIIPKFPVTDMMV	294	
Qy	270	APVLGPTSLQAELEKSLFLVDDHGLISGVHNTILNGKPSAAPMTLLHSGSGPLLP	329	
Db	295	APFLGEGTCLQAELEKGVNIADYRIMEGIPTELSGRKQHCAPLCLLH-FGPEGKMP	353	
Qy	330	IAIQLKOTPGDNDPIFLPSDDTDMWLAKTWRNSEFVIHEAVTHLLHAHLIPEVFALAT	389	
Db	354	IAIQLSOTPGDCDPIFLPSDSEWDLAKTWRVYAEFYSHAEIAHLLETHLIAFAFCLAL	413	
Qy	390	LRQLPRCHPLFKLLIPIHRYTHINTLARELLVAPGKLDKSTGLGTGFSDFLKRNEQ	449	
Db	414	LRNLPMCHPLYKLLIPIHRYTVQINSIGRAVLNNEGSLSAKGMISGVEGFAGVNRVASE	473	
Qy	450	LNTSVLCIPEDIRARGVEDIPGYYYRDGQMIQWAIKSFVSEIVSVIYYPSTSVDDOQEL	509	
Db	474	LTYDLSLVPNDFVERGVQDLPGYYRDDSLAVMNALEKYVTEIITYYYPSDAAVEGDPEL	533	
Qy	510	QAWVREYFSGFGLRESSGWSLLDTREALVOYITWVITFTCSAKHAAVSSQFDSVCWMP	569	
Db	534	QSWVQEIFKBCGLRESSGPPRCURTVPSELIRYVITVITCSAKHAAVNTQMEFTAMP	593	
Qy	570	NLPPTMQLPPTSKQARPESFIATLPVANSSSYHIIALMILLSAEPGQDRPLGHYPDEHF	629	
Db	594	NFPASMRNPQTQKGLTLETFTMDTLPDVKTTCTLLVLWTLSEPDRLPLGHFFDIHF	653	
Qy	630	TEDAPRSVAAPQKLQIQISGIRERNRGLALPYTYLDPPLIENSIVI	677	
Db	654	VEGAPRSISAEFRQLNQISHDIRQNKCLPIPYTYLDPPLIENSISI	701	

## RESULT 11

US-09-949-016-6026  
; Sequence 6026, Application US/09949016  
; Patent No. 6812339

```

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 6026
; LENGTH: 701
; TYPE: PRT
; ORGANISM: Human
; US-09-949-016-6026

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Query Match	49.8%	Score 1795;	DB 4;
Best Local Similarity	47.9%	Pred. No. 2.1e-193;	
Matches 339;	Conservative	121;	Mismatches 210;
		Indels	38;
		Gaps	3

Qy	1	MAKRVVSTGEACGAGTWDKVSIVSVIGTHGESPLVLPHDHLGKBFSAGAEDEFVTLPOD	60
Db	1	MATYKVRVATGTDLLSSTRDSISLTVGTQGESHKQLLNHFGRDPATGAVGQYTVQCPOD	60
Qy	61	VGTVLMLRVHKAPEVSVSLPLMSFRSDAWFCWFLEWLPGAALHPCVQWLEGAGELVLR	120
Db	61	LGELIILIRLHK-----RYAFFPKDPWCYNVQICAPNGRIYHFPAYQWMDGYETLALR	114
Qy	121	EGAAKVSWDBHPTLODOROKELSRGKMYSWKT-----	154
Db	115	EATGKTTADDLSPLVLEHRRKEERAKQDFYHVRVFLPCLPSYVHI PSVRPPVRRHNPNR	174
Qy	155	-----YIEGPRCLDHTVDOLDINIKYSAMKNAKLFFKAHSATYELTKYGLLDRGLWR	209
Db	175	PEWNGYIPGPILINFKATKFLNLNRLAYSFLKTASFVRLGPMALAFKVRGLLDCKHSWK	234
Qy	210	SLREMRLLNFRKTPAAEYVFAKWOEDAPASQFLNGINPVLIRCHSLPNNFPVTDENV	269
Db	235	RLKDIRKIFPKGKSVSEYVAEHWAEOTFFGYQYGLNGVNPGLIRRCTRIPDKFPVTDNV	294
Qy	270	APVLGPTCSQAEEKGSLFLVDHGLSGVHTNLTNGKPOFSAAPMTLLHQSSGSGPLLP	329
Db	295	APFGEBTCQAEEUKENIYLADYIRMEGPTVELSRKQHKHCAPLCULH-FGPGKKMP	353
Qy	330	IAIQLAKTQPGDNPIFLPSSDDTWDMLAKTWRNSEFYIHEAVTHLLHAHLIPEVFALAT	389
Db	354	IAIQLSQTGPDCEPIFLPSSDEMDLLAKTWRYAEFYSEHIAHLLETHLIAEAFCLAL	413
Qy	390	LROLPRCHPLFKLLIPIHRYTLHINTLARELLVAPGKLI DKSTGLGTGFGFSDLIKRNMEQ	449
Db	414	LRNLPMPCHPLYKLLIPHTRYTVQINSIGRAVLLNEGGLSAKMSGLGVEGFAGVMVRALSE	473
Qy	450	LNYSVLCLPEDIARGVEDIPGYYYRDDGQWICAIKSFVSEIYSIYYPSDTSVQDDQEL	509
Db	474	LTYDSLYLPNDFVERGVQDHPGYYYRDDSLAVMNALEKYVTEIITYYYPSDAAVEGDP	533
Qy	510	QAWREIFSGFGRESSGMPSLDTRREALVOYITWFTCSAKHAAVSSGQFDCVWMP	569
Db	534	QSWQELFKCLLGRSSGFPRLCTRVPELIRYVTIYITCSAKHAAVNTQOMETAWMP	593
Qy	570	NLPPTWQLPPTSKGQARPESFIATPAVNSSSYHIIALMLLSAEPGQRPGLHYDPDEHF	629
Db	594	NPEASMRNPPIQTKGLTTLTTFDNTLPDVKTTCTILLVLMTLSREPDRRRLPGHFPHIF	653
Qy	630	TEDAPRRSVAAPORKLIQISKGIRERNRGLAPTYTLDPPLIENSVISI	677
Db	654	VEBAPRRSEAPQRNLQIASHDIRQNKCLPIPYTYLDPVLIENSISI	701

630 TEDAPRRSVAAFORKLIOISKGIRERNRGLALPYTYLDPPLIENSVSI 677

[illegible]

RESULT 12  
US-09-547-435-6  
; Sequence 6, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705.0009-00000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 556  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-547-435-6

Query Match 44.1%; Score 1588; DB 4; Length 556;  
Best Local Similarity 54.9%; Pred. No. 3.9e-170;  
Matches 302; Conservative 88; Mismatches 146; Indels 14; Gaps 2;

QY 141 KELESQKMYSWKT-----YIEGPRCLDHTETKDLNINIKYSAMKNAKLPF 187  
Db 8 QEMESDKKALTKTTTCVDQSSGNRYLPFGPMKIDIPSLMYMPEPNVRYSAKTIISLFF 67

QY 188 KAHSAYTELVKGLLDRTGLWRSRLRMRLNFRKTPAAEYVFAHQEDAFASQFLNGI 247  
Db 68 NAIPASLGMKRLGLDRKSKWKLLDMQNIWFCHKTFTTKYVTEHWCEDEHFFGYQLNGV 127

QY 248 NPVLIRRHSLNNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVHTNLNGK 307  
Db 128 NPVMLHCISLPSKLPVTNDMVAFLPGTSLQAELEKSLFLVDHGILSGVHTNLNGK 187

QY 308 PQFSAAPMTLLHQSSGSLPPLTAIQKOTPGDNPIFLPSDDTWDMLLAKTWVRNSEFY 367  
Db 188 QQYVAAPLCLLWSP-QGALVPLAIQLSQTTPGDSPIFLPTDSEMDWLLAKTWVRNSEFL 246

QY 368 IHEAVTHLHAHLPVFAFALRQLPRCHPLFKLLIPHRYTLHINTLARELLVAPGKL 427  
Db 247 VHENTHFLCTHLLCEAFAMATLRLPLCHPIYKLLPHRYTLQVNTIARATLNPGL 306

QY 428 IDKSTGLGTGGSFSLIKRMEQLNYSVLCPLPDIRARGVEDIPGYYYRDGMOIWAIGS 487  
Db 307 VQVTSIGRQLIYLMSTGLAHFTYTNFCLPDSLRARGVLAIPNYHYRDDGLKIAAIES 366

QY 488 FVSEIYSIYPSDTSVQDDQELQAWREIFSGFLGREGSGMPSLLDTREALVOYITWVI 547  
Db 367 FVSEIYGYIYPSDASVQDSELQAWTGEIFAQFLGREGSGFPSPRLCTPGEMVKFETAI 426

QY 548 FTCSAKHAIVSSQFQSCVWPNLPPTMOLPPPTSKGOARPSFTATLPAVNSSVHIIA 607  
Db 427 FNCSAQAAVNSGQHDFFGAWNPAPSMRQPPPTQTKGTTLYLDTLPEVNISCNLL 486

QY 608 LMLLSAEPDQRLPHYPDEHFTEDAPRRSVAAPQKLIQISKGINRNRGLALPYTLD 667  
Db 487 FVLVSQEPKQRLPYTPDEHFTEDAPRRSVAAPQKLIQISKGINRNRGLALPYTLD 546

QY 668 PPLIENSVS 677  
Db 547 PPLIENSVS 556

RESULT 13  
US-09-547-435-10  
; Sequence 10, Application US/09547435  
; Patent No. 6582957

; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705.0009-00000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-547-435-10

Query Match 40.6%; Score 1464; DB 4; Length 615;  
Best Local Similarity 47.5%; Pred. No. 5.1e-156;  
Matches 286; Conservative 95; Mismatches 173; Indels 48; Gaps 3;

QY 1 MAKCEVRVSTGEACGAGTMDKVSIVGTHGESPLVPLDHLGKESAGAEEDFEVTLPOD 60  
Db 1 NAVYELCVTTGPEYLRAGTLDNISVTLVGTGSGPQRLDRMGDRFAGPSVQYIKVRCYAE 60

QY 61 VGTVLMLRVHAKAPPEVSLPLMSFRSDAWFCRWFLEWLFGAALHFPFCYQWLLEGAGELVLR 120  
Db 61 LGELLLLVHKE-----RYAFFRDKSWCSRICVTEPDGVSVSHFPYQWIEGYCTVELR 114

QY 121 EGAAKVSQDHHPTIQQORQKELESQRQMYSWKTYIEGWPRCLDHTETKDLN----- 173  
Db 115 PGTARTICQDSLPLLLDHRTELRLARQECYRWKIYAPGPPCMVDVNSFOEMESDKKFALT 174

QY 174 -----NIKYSAMKNAKLFKAHSAYTELKVK 199

Db 175 KTTTCVDQDSSGNRYLPFGPMKIDIPSLMYMPEPNVRYSAKTIISLFLNAPSLGMMKR 234

QY 200 GLLDRTGLWRSRLRMRLNFRKTPAAEYVFAHQEDAFASQFLNGINPVLIRRHCHSLP 259  
Db 235 GLLDRTGSKWKLLDMQNIWFCHKTFTTKYVTEHWCEDEHFFGYQLNGVNPVMLHCISL 294

QY 260 NNFPVTDEMVAFLPGTSLQAELEKSLFLVDHGILSGVHTNLNGKQFSAAPMTLLH 319  
Db 295 SKLPVTNDMVAFLPGTSLQAELEKSLFLVDHGILSGVHTNLNGKQFSAAPMTLLH 354

QY 320 QSSGSLPPLTAIQKOTPGDNPIFLPSDDTWDMLLAKTWVRNSEFYIHEAVTHLHAH 379  
Db 355 LSP-QGALVPLAIQLSQTTPGDSPIFLPTDSEMDWLLAKTWVRNSEFLVHENTHFLCTH 413

QY 380 LIPEVPFALATRLQPRCHPLFKLLIPHRYTLHINTLARELLVAPGKLIDKSTGLGTGSP 439  
Db 414 LCEAFAMATLRLPLCHPIYKLLPHRYTLQVNTIARATLNPGLVDQVTSIGRQL 473

QY 440 SDLIKRNMEQLNYSVLCPLPDIRARGVEDIPGYYYRDGMOIWAIGKSPVSEIYSIYPS 499  
Db 474 IYLMSTGLAHFTYTNFCLPDSLRARGVLAIPNYHYRDDGLKIAAIESFPVSEIYGYIYS 533

QY 500 DTSVQDDQELQAWREIFSGFLGREGSGMPSLLDTREALVOYITWVIITCSAKHAIVSS 559  
Db 534 DASVQDDQELQAWTGEIFAQFLGREGSGFPSPRLCTPGEMVKFETAIIFNCQAQAHAIVS 593

QY 560 GQ 561  
Db 594 GQ 595

RESULT 14  
US-09-547-435-28  
; Sequence 28, Application US/09547435  
; Patent No. 6582957  
; GENERAL INFORMATION:

; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6582957el Lipoxigenase Proteins and Polynucleotides  
; FILE REFERENCE: 7705.0009-00000  
; CURRENT APPLICATION NUMBER: US/09/547,435  
; CURRENT FILING DATE: 2000-04-12  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 28  
; LENGTH: 771  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-547-435-28

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Query Match      40.6%; Score 1464; DB 4; Length 771;
Best Local Similarity 47.5%; Pred. No. 7.6e-156;
Matches 286; Conservative 95; Mismatches 173; Indels 48; Gaps 3;

Qy 1 MAKCRVRVSTGACAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60
Db 157 MAVYRLCVTTGPLYLAGTLDNISVLVGTGCGSPKQRLDRGRDPAGSVQKYKRCRTAR 216

Qy 61 VGTVLMLRVHKAPPEVSLPMSFRSDAWFCRWFELWLPGAALHPPCYQWLLEGAGELVLR 120
Db 217 LGELLLLRVHKE-----RYAFPRKDSWYCSRICVTEPDGSGVSHPPCYQWIEGYCTVELR 270

Qy 121 EGAAKVSWQDHHTPLQDOROKELSRQKMYSKTYIEGWPRCLDHTETVKDLDL----- 173
Db 271 PGTARTICODSLFLDLHRTRELRAQBCYRWKIYAPGPPCMVDVNSFOEMESDKKFALT 330

Qy 174 -----NIKYSAMNNAKLPFAKHSAYTELKVK 199
Db 331 KTTTCVDOGSSGNRYLPGFPKIDIPSLMYMEPNVRYSATKTSILLFNAIPASLGMLR 390

Qy 200 GLLDRGTGLWRSLRMRRLFNFRKTPAAEYVFAHWQEDAFFASQFLNGINPVLIRCHSLP 259
Db 391 GLLDRKGSWKLLDDMQNIFWCHKTFTTKYVTEHWCEDEHFFGYQLNGVNPVMLHCISLP 450

Qy 260 NNPVTDWAVPVLGPGTSLQAELEKGLSLFLVDHGLSGVHTNILINGKPOPSAAPTLLH 319
Db 451 SKLPVTNDWAVPVLGPGTSLQAELEKGLSLFLVDHGLSGVHTNILINGKPOPSAAPTLLH 510

Qy 320 QSSGSGPLLPALQALQKTPGPNPFLPSDDTMDLLAKTWNRSSEFYTHEAVTHLHAH 379
Db 511 LSP-QGALVPLAIQSQTGPDSPFLPDTSEWDLAKTWNRSSEFYTHEAVTHLHAH 569

Qy 380 LIPEVFALATLQRLPRCHPLFKLLIPIHRYTLIHTLARELIVAPGKLIDKSTGLGTGF 439
Db 570 LLCEAFAMATLRLPLCHPIYKLLPHRYTLIHTLARELIVAPGKLIDKSTGLGTGF 629

Qy 440 SDLIKRNMEQLNYSVLCPEDIRARGVEDIPGYRRDDGMQIWAIGKFSVSEIVSIYPS 499
Db 630 IYLMSTGLAHFTYTNFLCPDLSLRARGVLAIPNYHYRDDGLKTIWAIESFVSEIVSIYPS 689

Qy 500 DTSVDDDELOQAWVREIFSEGLFGRESSGMPSLDREALVOYITWVLTCSAKHAAYSS 559
Db 690 DASVQDDSELQAWTGEIIFAQALFGRESSGMPSLDREALVOYITWVLTCSAKHAAYSS 749

Qy 560 GQ 561
Db 750 GQ 751
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RESULT 15  
US-09-949-016-5980  
; Sequence 5980, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5980  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Human  
US-09-949-016-5980

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Query Match      40.0%; Score 1442.5; DB 4; Length 674;
Best Local Similarity 42.6%; Pred. No. 1.6e-153;
Matches 292; Conservative 126; Mismatches 248; Indels 19; Gaps 7;

Qy 1 MAKCRVRVSTGACAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPO 59
Db 1 MPSYTVTVATGVSQWAGTDDYIYLSVGSAGCSEKHLDDKPFYNDFERGAVDSYDVTVDE 60

Qy 60 DVGTVLMLRVHKAPPEVSLPMSFRSDAWFCRWFELWLPGAALHPPCYQWLLEGAGELVLR 119
Db 61 ELGEIQLVRIEKR-----KWLNDNDWLYKLTILTKPHGDYIEFFPCYRMITGDVEVL 112

Qy 120 REGAAKVSQDHHTPLQDOROKELSRQKMYSKTYIEGWPRCLDHTETVKDLDLIKISA 179
Db 113 RDRAKLARDQIHLKQHRKELETRQKQWRWEMWNPFPPLSIDAKCHKDLPDIQEDS 172

Qy 180 MNAKLPPKAHSAYTELKVKGLDRL-TGLWRSLSRMRLEFNFRKTPAAEYVFAHWQEDAF 238
Db 173 EKVDFVLNYSKAMENLFINRPMFQSSWDFADFEKIFVKISNTISERVVNHQEDLM 232

Qy 239 FASQFLNGINPVLIRRHCHSLPNNFPVTDWAVPVLGPGTSLQAELEKGLSLFLVDHGLSL 298
Db 233 FGYQLGNCNPLVIRRHCHSLPNNFPVTDWAVPVLGPGTSLQAELEKGLSLFLVDHGLSL 292

Qy 299 VHTNILINGK-----QFSAPMTLLHQSOGSGLPLTAIQLKOTPGDNPIFLPSDDTWDWL 355
Db 293 IDAN--KTDPCTQLQFLAAPICLLYKNL-ANKIVPIAIQLNQIPGDNPIFLPSDAKYDNL 349

Qy 356 LAKTWNRSSEFYTHEAVTHLHAHLIPEVPALATLQRLPRCHPLFKLLIPIHRYTLIHTN 415
Db 350 LAKTWNRSSEFYTHEAVTHLHAHLIPEVPALATLQRLPRCHPLFKLLIPIHRYTLIHTN 409

Qy 416 LARELLVAPGKLIDKSTGLGTGFSDLIKRNMEQLNYSVLCPEDIRARGV---EDIPGY 472
Db 410 KARQLICECGLFDKANATGGGHVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQVQV 469

Qy 473 YRRDGMQIWAIGKFSVSEIVSIYPSDTSVDDDELOQAWVREIFSEGLFGRESSGMPSL 532
Db 470 FYRDDGLLWMEARITFTAEVVDIYVEGQVVEEDPELQDFVNDVYVYVYVYVYVYVYVYV 529

Qy 533 LDTREALVOYITWVLTCSAKHAAYSSQDPSCVWMPNLPTMQLPPPTSGQARPEPSI 592
Db 530 VKSEQLSEYITWVLTCSAKHAAYSSQDPSCVWMPNLPTMQLPPPTSGQARPEPSI 589

Qy 593 ATLPAVNSSSYHIIATLMLLSAEPDQRLPHGYPDEHFTEDAPRRSVAAFQKLIQISKI 652
Db 590 DTLPRGSCWHLGAVWALSQFQENELFLGNYPEHFIKPKVKEAMARFRKNLEAIVSVI 649

Qy 653 RERNRGLALPTYLDPPPLIENSIVI 677
Db 650 AERNKKQLPYLYLSPDRIPINSVAI 674
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: July 18, 2005, 21:53:28 ; Search time 105.244 Seconds  
(without alignments)  
2497.095 Million cell updates/sec

Title: US-10-688-676A-4  
Perfect score: 3604  
Sequence: 1 MAKCRVRSVGEACGCTWD.....GLALPYTLDPLIENSYSI 677

Scoring table: BLOSUM62

Gapop 10.0 ; Gapext 0.5

Searched: 1736639 seqs, 368188149 residues

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

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2:	/cgn2_6/ptodata/2/pubaa/FCT_NEW_PUB.pep:*
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20:	/cgn2_6/ptodata/2/pubaa/US11_NEW_PUB.pep:*
21:	/cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep:*
22:	/cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3604	100.0	677	9	US-09-764-246-4
2	3604	100.0	677	16	US-10-716-204-4
3	3604	100.0	677	15	US-10-688-676A-4
4	2880.5	79.9	676	9	US-09-764-246-2
5	2880.5	79.9	676	16	US-10-716-204-2
6	1864	51.7	711	9	US-09-862-658-2
7	1864	51.7	711	14	US-10-175-696-23
8	1864	51.7	711	14	US-10-422-264-2
9	1864	51.7	711	16	US-10-776-871-23
10	1864	51.7	867	14	US-10-422-264-24
11	1858	51.6	711	15	US-10-275-998-3

12	1795	49.8	701	9	US-09-853-053-2
13	1795	49.8	701	15	US-10-445-484-2
14	1588	44.1	556	14	US-10-422-264-6
15	1464	40.6	615	14	US-10-422-264-10
16	1464	40.6	771	14	US-10-422-264-28
17	1442.5	40.0	674	14	US-10-240-305-14
18	1442.5	40.0	674	16	US-10-485-310-22
19	1422.5	39.5	663	14	US-10-240-305-16
20	1227	34.0	663	16	US-10-741-601-516
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22	1227	34.0	663	17	US-10-741-600-1499
23	1227	34.0	663	17	US-10-741-600-1500
24	1212	33.6	663	15	US-10-170-097-653
25	1212	33.6	663	17	US-10-926-684-653
26	1188	33.0	460	14	US-10-422-264-12
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28	1186.5	32.9	662	16	US-10-716-204-25
29	1184	32.8	661	16	US-10-688-676A-2
30	1182.5	32.8	684	15	US-10-398-663-5
31	1077.5	29.9	489	14	US-10-422-264-4
32	1077.5	29.9	645	14	US-10-422-264-26
33	953	26.4	291	14	US-10-422-264-14
34	801.5	22.2	334	14	US-10-422-264-8
35	799.5	22.2	671	15	US-10-369-493-19529
36	733	20.3	389	16	US-10-485-310-3
37	706	19.6	472	15	US-10-369-493-19890
38	628.5	17.4	487	15	US-10-369-493-19963
39	610.5	16.9	491	9	US-09-862-658-4
40	610.5	16.9	491	14	US-10-175-696-25
41	610.5	16.9	491	16	US-10-776-871-25
42	605.5	16.8	399	17	US-10-498-788-27
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44	568.5	15.8	807	14	US-10-132-350-42
45	568.5	15.8	807	14	US-10-132-350-44

#### ALIGNMENTS

#### RESULT 1

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US-09-764-246-4
; Sequence 4, Application US/09764246
; Patent No. US20010046672A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/764,246
; FILING DATE: 17-Jan-2001
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: <Unknown>
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/5
; TELECOMMUNICATION INFORMATION:

```

TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 677 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-09-764-246-4

Query Match 100.0%; Score 3604; DB 9; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MAKCRVSTGEACGAGTWDKVSIVTGHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60
DB |||||
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAFCRWFELWLPGAALHPCYQWLKGAGELVLR 120
DB |||||
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAFCRWFELWLPGAALHPCYQWLKGAGELVLR 120
DB |||||
QY 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLDLNKYSAM 180
DB |||||
QY 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLDLNKYSAM 180
DB |||||
QY 181 KNAKLFKKAHSAYTELKVGGLDRTGLWLSREMRLEFNFRKTPAAEYVFAHQEDAFPA 240
DB |||||
QY 181 KNAKLFKKAHSAYTELKVGGLDRTGLWLSREMRLEFNFRKTPAAEYVFAHQEDAFPA 240
DB |||||
QY 241 SQFLNGINPVLLRCHSLPNPVTDEMVAFLGPTSLQAELEKSLFLVDHGILSGVH 300
DB |||||
QY 241 SQFLNGINPVLLRCHSLPNPVTDEMVAFLGPTSLQAELEKSLFLVDHGILSGVH 300
DB |||||
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLLPALQKQTPGPNPIPLPSDDTWDWLLAKTW 360
DB |||||
QY 361 VRNSEFYTHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLAREL 420
DB |||||
QY 361 VRNSEFYTHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLAREL 420
DB |||||
QY 421 LVAPGKLDKSTGLGTGGFSDLIKRNMEOQNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
DB |||||
QY 421 LVAPGKLDKSTGLGTGGFSDLIKRNMEOQNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
DB |||||
QY 481 IMAKISFVSEIYSIYPSDTSVQDDQELQAWVREIFSEGFLGREGSGMPSLLDTREALV 540
DB |||||
QY 481 IMAKISFVSEIYSIYPSDTSVQDDQELQAWVREIFSEGFLGREGSGMPSLLDTREALV 540
DB |||||
QY 541 QYITWVIFCSAKHAIVSSGQFSDSCVMNLPPTMQLPPTSGKQARPESFIATLPVNS 600
DB |||||
QY 541 QYITWVIFCSAKHAIVSSGQFSDSCVMNLPPTMQLPPTSGKQARPESFIATLPVNS 600
DB |||||
QY 601 SSVHITALLSAEPGDQPLGHYPDEHTEADAPRSVAAFQKLIQISKGIRERNRGLA 660
DB |||||
QY 601 SSVHITALLSAEPGDQPLGHYPDEHTEADAPRSVAAFQKLIQISKGIRERNRGLA 660
DB |||||
QY 661 LPPTYLDPPLIENSVS I 677
DB |||||
QY 661 LPPTYLDPPLIENSVS I 677
DB |||||
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## RESULT 2

US-10-716-204-4  
Sequence 4, Application US/10716204  
Publication No. US20040137483A1  
GENERAL INFORMATION:  
APPLICANT: BRASH, ALAN R.  
BOEGLIN, WILLIAM E.  
JISAKA, MITSUO

TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
NUMBER OF SEQUENCES: 36  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ARLES A. TAYLOR, JR.  
STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
CITY: DURHAM  
STATE: NORTH CAROLINA  
COUNTRY: USA  
ZIP: 27707  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
COMPUTER: IBM PC/XT/AT compatible  
OPERATING SYSTEM: Windows 3.1  
SOFTWARE: WORD PERFECT 6.1 and ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/716,204.  
FILING DATE: 18-Nov-2003  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: ARLES A. TAYLOR, JR.  
REGISTRATION NUMBER: 39,395  
REFERENCE/DOCKET NUMBER: 1242/5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (919) 493-8000  
TELEFAX: (919) 419-0383  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 677 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:  
US-10-716-204-4

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Query Match 100.0%; Score 3604; DB 16; Length 677;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVSTGEACGAGTWDKVSIVTGHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60
DB |||||
QY 1 MAKCRVSTGEACGAGTWDKVSIVTGHGSPVPLDHLGKFSAGAEEDFEVTLPOD 60
DB |||||
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAFCRWFELWLPGAALHPCYQWLKGAGELVLR 120
DB |||||
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAFCRWFELWLPGAALHPCYQWLKGAGELVLR 120
DB |||||
QY 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLDLNKYSAM 180
DB |||||
QY 121 EGAAKVSWQDHHPTLQDQKQKESRQKMSWKTYIEGWPCRLDHTVTKDLDLNKYSAM 180
DB |||||
QY 181 KNAKLFKKAHSAYTELKVGGLDRTGLWLSREMRLEFNFRKTPAAEYVFAHQEDAFPA 240
DB |||||
QY 181 KNAKLFKKAHSAYTELKVGGLDRTGLWLSREMRLEFNFRKTPAAEYVFAHQEDAFPA 240
DB |||||
QY 241 SQFLNGINPVLLRCHSLPNPVTDEMVAFLGPTSLQAELEKSLFLVDHGILSGVH 300
DB |||||
QY 241 SQFLNGINPVLLRCHSLPNPVTDEMVAFLGPTSLQAELEKSLFLVDHGILSGVH 300
DB |||||
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLLPALQKQTPGPNPIPLPSDDTWDWLLAKTW 360
DB |||||
QY 301 TNILNGKQFSAAPMTLLHQSSGSGPLLPALQKQTPGPNPIPLPSDDTWDWLLAKTW 360
DB |||||
QY 361 VRNSEFYTHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLAREL 420
DB |||||
QY 361 VRNSEFYTHEAVTHLLHAHLIPEVFALATLRLPCHPLFKLLIPIHRYTLHINTLAREL 420
DB |||||
QY 421 LVAPGKLDKSTGLGTGGFSDLIKRNMEOQNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
DB |||||
QY 421 LVAPGKLDKSTGLGTGGFSDLIKRNMEOQNSVLCPLPEDIARGVEDIPGYYYRDDGMQ 480
DB |||||
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QY 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 540  
DB 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 540  
QY 541 QYITWVIFTSKAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 600  
DB 541 QYITWVIFTSKAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 600  
QY 601 SSYHIIALWLLSAEPGQORPLGHYPDEHFTEDAPRRSVAARQKLIQISKGIRNRGLA 660  
DB 601 SSYHIIALWLLSAEPGQORPLGHYPDEHFTEDAPRRSVAARQKLIQISKGIRNRGLA 660  
QY 661 LPYTYLDPPLIENSUSI 677  
DB 661 LPYTYLDPPLIENSUSI 677

## RESULT 3

US-10-688-676A-4  
; Sequence 4, Application US/10688676A  
; Publication No. US20040248794A1  
; GENERAL INFORMATION:  
; APPLICANT: Alcon, Inc.  
; APPLICANT: Yamni, John M.  
; APPLICANT: Gamache, Daniel A.  
; APPLICANT: Miller, Steven T.  
; TITLE OF INVENTION: Treatment of Dry Eye in Postmenopausal Women by Restoring 15-lipo  
; FILE REFERENCE: 2394 US  
; CURRENT APPLICATION NUMBER: US/10/688,676A  
; PRIOR FILING DATE: 2003-10-17  
; PRIOR APPLICATION NUMBER: US 60/435,988  
; PRIOR FILING DATE: 2002-12-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4  
; LENGTH: 677  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-10-688-676A-4

Query Match 100.0%; Score 3604; DB 16; Length 677;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAKCRVSTGACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60  
DB 1 MAKCRVSTGACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60  
QY 61 VGTVLMLRVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGLAALHPPCYQWLEGAGELVLR 120  
DB 61 VGTVLMLRVHKAPPEVSLPLMSFRSDAMFCRWFELEWLPGLAALHPPCYQWLEGAGELVLR 120  
QY 121 EGAAKVSWODHHTPLDQORQKESRQKXWKTVEGWPCLDHETVKDLDLNIKYSAM 180  
DB 121 EGAAKVSWODHHTPLDQORQKESRQKXWKTVEGWPCLDHETVKDLDLNIKYSAM 180  
QY 181 KNAKLFKAHSAYTELKYGILLDRGLRSLEWRLENFRKTPAAEYVFAHWQEDAFPA 240  
DB 181 KNAKLFKAHSAYTELKYGILLDRGLRSLEWRLENFRKTPAAEYVFAHWQEDAFPA 240  
QY 241 SOFLNGINPVLIRRSCHSLPNNPPVTDVMAVPLGPGTSLQAELEKGSFLVDHGLISGVH 300  
DB 241 SOFLNGINPVLIRRSCHSLPNNPPVTDVMAVPLGPGTSLQAELEKGSFLVDHGLISGVH 300  
QY 301 TNLNGKQFSAAPMTLLHQSSGSGFLPIAQLKQTPGPNPIFLPSDDTMDWLAKTW 360  
DB 301 TNLNGKQFSAAPMTLLHQSSGSGFLPIAQLKQTPGPNPIFLPSDDTMDWLAKTW 360  
QY 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLQPRCHPLFKLLIPIHRYTLHINTLREL 420  
DB 361 VRNSEFYIHEAVTHLLHAHLIPEVFALATLQPRCHPLFKLLIPIHRYTLHINTLREL 420

QY 421 LVAPGKLIKSTGLTGCTGFSDLIKRNMEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGMQ 480  
DB 421 LVAPGKLIKSTGLTGCTGFSDLIKRNMEQLNYSVLCLPEDIRARGVEDIPGYVYRDDGMQ 480  
QY 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 540  
DB 481 IWGAIKSFVSEIVSYIYPSDTSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 540  
QY 541 QYITWVIFTSKAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 600  
DB 541 QYITWVIFTSKAKHAASVSSGQFDSVQDDQELQAWVRIFSEGFGRSSGMPSLDTRALV 600  
QY 601 SSYHIIALWLLSAEPGQORPLGHYPDEHFTEDAPRRSVAARQKLIQISKGIRNRGLA 660  
DB 601 SSYHIIALWLLSAEPGQORPLGHYPDEHFTEDAPRRSVAARQKLIQISKGIRNRGLA 660  
QY 661 LPYTYLDPPLIENSUSI 677  
DB 661 LPYTYLDPPLIENSUSI 677

## RESULT 4

US-09-764-246-2  
; Sequence 2, Application US/09764246  
; Patent No. US20010046672A1  
; GENERAL INFORMATION:  
; APPLICANT: BOEGLIN, WILLIAM E.  
; APPLICANT: JISAKA, MITSUO  
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS  
; NUMBER OF SEQUENCES: 36  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: ARLES A. TAYLOR, JR.  
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD  
; CITY: DURHAM  
; STATE: NORTH CAROLINA  
; COUNTRY: USA  
; ZIP: 27707  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage  
; OPERATING SYSTEM: Windows 3.1  
; SOFTWARE: WORD PERFECT 6.1 and ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/764,246  
; FILING DATE: 17-Jan-2001  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: <Unknown>  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: ARLES A. TAYLOR, JR.  
; REGISTRATION NUMBER: 39,395  
; REFERENCE/DOCKET NUMBER: 1242/5  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (919) 493-8000  
; TELEFAX: (919) 419-0383  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 676 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: unknown  
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
US-09-764-246-2

Query Match 79.9%; Score 2880.5; DB 9; Length 676;  
Best Local Similarity 78.0%; Pred. No. 5.1e-268;  
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

QY 1 MAKCRVSTGACGAGTWDKVSIVGTHGESPLVPLDHLGKFSAGAEEDFEVTLPOD 60

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Db 1 MAEFRVSTGEAFAGTWDKVSIVGTRGSPPLDNLNKEFTAGAEEDFQVTLPED 60
QY 61 VGTVMMLRVHKAPPEVSLPLMS - FRSDAWFCWFLEWLPGAALHPFPCQWLEGAGELVL 119
Db 61 VGRVLLLRVHKAPP--VLPLGLPLADAWFCWFQLTTPRGHLLFPFPCQWLEGAGTLVL 118
QY 120 REGAAKVSQDHHPTLDQORQKESRQVYVSWKTYIEGWPRCLDHTVTKDLDLNIKYSA 179
Db 119 QEGTAKVSWADHHPVLVQOQRELOARQEMQWKAYNPGWPHCLDEKTVEDLELNIKYST 178
QY 180 MNAKLFFKAHSAYTELKVGLLDRGLWRSIREMRRLNFRKTPAAEYVFAHWQEDAFF 239
Db 179 AKNANFYLQAGSAFAEMKIKGLLDKGLWRSINEMKRIENFRRTPAAEHAFEHQEDAFF 238
QY 240 ASOFLNGINPLVLRCHSLPNNPVTDEMVAFLVPGTSLQAELEKGSFLVDHGILSGV 299
Db 239 ASOFLNGLNPLVLRCHYLPKNFPVTDMVAVSLGPGTSLQAELEKGSFLVDHGILSGI 298
QY 300 HTNILNGKPFQSAAPMTLLHOSGSGPLPIAQLKQTEGPNPIFLPSSDDTMDWLLAKT 359
Db 299 QTNVINGKPFQSAAPMTLLYQSPGCGPLPLAQLSQTGPNSPFLPTDDKMDWLLAKT 358
QY 360 WYRNSEFYTHEAVTHLLHAHLIPEVPALATLRQLPRCHPLFKLLIPHRYTLHINTLARE 419
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLRQLPHCHPLFKLLIPHRYTLHINTLARE 418
QY 420 LLVAPKGLDKSTGLTGCGFSDLIKNMEOLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 479
Db 419 LLIVPGQVDRSTGIGIEGSELIQRNMKQLNYSLLCLPEDIRTRGVEDIPGYVYRDDGM 478
QY 480 QIWGAIKSVSEIVSIYYPSTVSQDDOELQAWREIFSEGFLGRESGMPSLDRTREAL 539
Db 479 QIWGAVERFVSEIIGIYYPDESQDDRELQAWREIFSKGFLNQGESSGIPSSLETREAL 538
QY 540 VOYITWVITCSAKHAASVSSGQFDSQVWMPNLPPTWQLPPPTS KGOARPESTIATLPAYN 599
Db 539 VOYVTWVITCSAKHAASVAGQFDSQVWMPNLPSPMQLPPTS KGLATCEGFIATLPAYN 598
QY 600 SSSYHIIALWLLSAEPGDORPLGHPDHEFTEDAPRSVAARFKLIQISKIGIRNRNGL 659
Db 599 ATCDVILALWLLSKPEQDORPLGTYPDEHFTTEAPRSIATQSRLAQISRGIQERNRGL 658
QY 660 ALPTYTLDPPPLIENSYSI 677
Db 659 VLPTYTLDPPPLIENSYSI 676
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RESULT 5

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US-10-716-204-2
; Sequence 2, Application US/10716204
; Publication No. US20040137483A1
; GENERAL INFORMATION:
; APPLICANT: BRASH, ALAN R.
; BOEGLIN, WILLIAM E.
; JISAKA, MITSUO
; TITLE OF INVENTION: LIPOXYGENASE PROTEINS AND NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1400, UNIVERSITY TOWER, 3100 TOWER BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4 MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/716, 204
; FILING DATE: 18-Nov-2003
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 676 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-716-204-2
```

Query Match 79.9%; Score 2880.5; DB 16; Length 676;  
Best Local Similarity 78.0%; Pred. No. 5.1e-268;  
Matches 529; Conservative 69; Mismatches 77; Indels 3; Gaps 2;

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QY 1 MAKCRVRVSTGEAGAGTWDKVSIVGTHGESPLVLDHLGKESFAGAEEDFVTLPOD 60
Db 1 MAEFRVSTGEAFAGTWDKVSIVGTRGESPPPLDNLNKEFTAGAEEDFQVTLPED 60
QY 61 VGTVMMLRVHKAPPEVSLPLMS - FRSDAWFCWFLEWLPGAALHPFPCQWLEGAGELVL 119
Db 61 VGRVLLLRVHKAPP--VLPLGLPLADAWFCWFQLTTPRGHLLFPFPCQWLEGAGTLVL 118
QY 120 REGAAKVSQDHHPTLDQORQKESRQVYVSWKTYIEGWPRCLDHTVTKDLDLNIKYSA 179
Db 119 QEGTAKVSWADHHPVLVQOQRELOARQEMQWKAYNPGWPHCLDEKTVEDLELNIKYST 178
QY 180 MNAKLFFKAHSAYTELKVGLLDRGLWRSIREMRRLNFRKTPAAEYVFAHWQEDAFF 239
Db 179 AKNANFYLQAGSAFAEMKIKGLLDKGLWRSINEMKRIENFRRTPAAEHAFEHQEDAFF 238
QY 240 ASOFLNGINPLVLRCHSLPNNPVTDEMVAFLVPGTSLQAELEKGSFLVDHGILSGV 299
Db 239 ASOFLNGLNPLVLRCHYLPKNFPVTDMVAVSLGPGTSLQAELEKGSFLVDHGILSGI 298
QY 300 HTNILNGKPFQSAAPMTLLHOSGSGPLPIAQLKQTEGPNPIFLPSSDDTMDWLLAKT 359
Db 299 QTNVINGKPFQSAAPMTLLYQSPGCGPLPLAQLSQTGPNSPFLPTDDKMDWLLAKT 358
QY 360 WYRNSEFYTHEAVTHLLHAHLIPEVPALATLRQLPRCHPLFKLLIPHRYTLHINTLARE 419
Db 359 WYRNAEFSFHEALTHLLHSHLLPEVFTLATLRQLPHCHPLFKLLIPHRYTLHINTLARE 418
QY 420 LLVAPKGLDKSTGLTGCGFSDLIKNMEOLNYSVLCLPEDIRARGVEDIPGYVYRDDGM 479
Db 419 LLIVPGQVDRSTGIGIEGSELIQRNMKQLNYSLLCLPEDIRTRGVEDIPGYVYRDDGM 478
QY 480 QIWGAIKSVSEIVSIYYPSTVSQDDOELQAWREIFSEGFLGRESGMPSLDRTREAL 539
Db 479 QIWGAVERFVSEIIGIYYPDESQDDRELQAWREIFSKGFLNQGESSGIPSSLETREAL 538
QY 540 VOYITWVITCSAKHAASVSSGQFDSQVWMPNLPPTWQLPPPTS KGOARPESTIATLPAYN 599
Db 539 VOYVTWVITCSAKHAASVAGQFDSQVWMPNLPSPMQLPPTS KGLATCEGFIATLPAYN 598
QY 600 SSSYHIIALWLLSAEPGDORPLGHPDHEFTEDAPRSVAARFKLIQISKIGIRNRNGL 659
Db 599 ATCDVILALWLLSKPEQDORPLGTYPDEHFTTEAPRSIATQSRLAQISRGIQERNRGL 658
QY 660 ALPTYTLDPPPLIENSYSI 677
Db 659 VLPTYTLDPPPLIENSYSI 676
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## RESULT 6

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US-09-862-658-2
; Sequence 2, Application US/09862658
; Patent No. US20020137101A1
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel
; TITLE OF INVENTION: 46638. A NOVEL HUMAN
; TITLE OF INVENTION: MEMBER AND USES THEREOF
; FILE REFERENCE: 10448-053001
; CURRENT APPLICATION NUMBER: US/09/862,658
; CURRENT FILING DATE: 2001-05-22
; PRIOR APPLICATION NUMBER: US 60/205,675
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-862-658-2

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Query Match	51.7%	Score 1864;	DB 9;	Length 711;
Best Local Similarity	50.1%;	Pred. No. 5.9e-170;		
Matches 360;	Conservative 112;	Mismatches 198;	Indels 48;	Gaps 3;
QY	1	MAKCRVRSVTGACGAGCTWBDKVSIVSIVGTGCSPLVDHLGKFSAGAEEDREVTLPQD	60	
DB	1	MAVRLCVTTIGPYLRAGTLDNISVTLTGTCGSPKQLDRNDRGFAPGCVQKYKVRCTAE	60	
QY	61	VGTVLMRLRVHKAPPEVSLPLMSFRSDAWFCRWFLEWLPGAALHFPCCYQWLEGAGELVLR	120	
DB	61	LGELLRLLRVHKE-----RYAFFRKDSWCYSRICVTEPDGVSVSHFPCCYQWIEGYCTVELR	114	
QY	121	EGAAKVSQDHHPTLQDQOROKELSRQKMTSWKTYIEGWPRCLDHETVKDLDL-----	173	
DB	115	PGTARTICQDSLPLLLDHRTELRARQECYRWKIYAFGFCVMDVNSFQMESDKKFPALT	174	
QY	174	-----NIKYSAMQNAKLFFKAHSAYTELKVK	199	
DB	175	KTTTCVDQGGSSGNRYLPGPMMKIDIPSLMYMEPNVRYSATKTISSLNFNAIPASLGMKLR	234	
QY	200	GLLDRTGLMRSLRERMLFNRKTPPAABYVFAHQWEDAFASQPLNGINPVLIRRCHSLP	259	
DB	235	GLLDKSGSKLLDDMQNIFWCHKTFTTYTEHWCEDHFFGYQYLNGVNPVWLHCISLSP	294	
QY	260	NNFPVTDEMVAVLPGPQTSLOAELEKGSFLVDHGLSGVHTNILNKGQPFSAAPMTLLH	319	
DB	295	SKLPVTNDMVAPLLGQDTCLQTELENGNIFLADYWIILAEAPTHCLNGRQYVAAPLCLLW	354	
QY	320	QSSGSGPLLPALQLKQKTPGDPNIPFLPSDDTWDLAKLTWVNSEFVIEAVTHLLHAH	379	
DB	355	LSP-QGALVPLAIQLSQTPGDPSPIFUPTDSEMDWLAKTWVNSEFVIEAVTHNTHFLCTH	413	
QY	380	LIPEVFALATRLQPRCHPLFKLLIPIHRYTLNLTARELLVAPGLIDKSTGLGTGGF	439	
DB	414	LLCEAFAMATLRQLPLCHPIYKULLPHTRYTLQVNTIARATLLNPEGLVDQVTSIGRQGL	473	
QY	440	SDLIKRNMEQLNSVLCPLPDIIRARGVEDIPGYYYRDRDGMQINGAIKSFVSEIVSIYYP	499	
DB	474	IYLMSTGLAHFTYTNFCLPDSLARGVLAIPNHYRDDGLKIWAIESFVSEIVSIYGYYP	533	
QY	500	DTSVDDQDELQAVRETFSGELGRESSGMPSLDITREALVOYITWVIFTCSSAKHAUVSS	559	
DB	534	DASVQDQSEIQWMTGEIFAQAFGRSSGSPSRLLCTPGEMVKFUTAIIFCSCAQHAHAVNS	593	
QY	560	GQFDSVCWMPNLPTMQLPPTSKGARPSFIATLPVANSSSVHIATLLWLSAEPGDQR	619	
DB	594	GQHDFGAWMENA PSSMRQPPQTKGTTTLTKYLDTLTPEVNISCNWLLFLWVSGEPKQDR	653	
QY	620	PLGHYPDEHTEADAPRRSVAAPFKLLIQISKIGIRERNRGLALPTYLDPLIENSVISI	677	
DB	654	PLCTYPDEHTEAPRRSIAAFOSRLAQISRDIOERNQGLALPTYLDPLIENSVISI	711	

## RESULT 7

```

US-10-175-696-23
; Sequence 23, Application US/10175696
; Publication No. US20030092658A1
; GENERAL INFORMATION:
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Meyers, Rachel
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF
; FILE REFERENCE: 10448-193001
; CURRENT APPLICATION NUMBER: US/10/175,696
; CURRENT FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/067,668
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/266,140
; PRIOR FILING DATE: 2001-02-02
; PRIOR APPLICATION NUMBER: 09/823,901
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: PCT/US01/10720
; PRIOR FILING DATE: 2001-04-02
; PRIOR APPLICATION NUMBER: 60/193,920
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 03/862,658
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: PCT/US01/16380
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/205,675
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/882,837
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: PCT/US01/19319
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/211,727
; PRIOR FILING DATE: 2000-06-15
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-175-696-23

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Query Match	51.7%	Score	1864	DB	14	Length	711
Best Local Similarity	50.1%	Pred.	No. 5.9e-170				
Matches	360	Conservative	112	Mismatches	198	Indels	48
Gaps	3						
Qy	1	MAKCRVRS	TGEACGAGT	WDKVSVIS	VGTHGES	PLVPLD	HLGKFS
Db	1	MAVRYLC	VTGTPYLRAG	TLDNIS	VTGTCG	SPKQRL	DRMG
Qy	61	VGTVMLR	VHKA	PPES	VS	PLMS	FRSD
Db	61	LGELLRL	R	VHKE	-----	RYAF	RKDS
Qy	121	EGAAKVS	WQDHH	FTLQ	OROKEL	ESQK	MYSM
Db	115	PGTARTI	CQD	S	PLLLD	HRTREL	RA
Qy	174	-----	-----	-----	-----	-----	-----
Db	175	KTTT	CVQD	GS	GNRY	LP	GP
Qy	200	GLLDRT	GLMRS	LE	MR	LF	N
Db	235	GLLD	R	KG	S	W	K
Qy	260	NNP	PT	DEM	V	AP	VL
Db	319	-----	-----	-----	-----	-----	-----
Qy	295	SKU	P	V	T	N	D
Db	320	QSSG	S	G	S	G	P

Db 355 LSP-QGALVPLAIQLSQTGPDSPIFLPTDSEMDWLLAKTWVRNSEFLVHENNTFLCTH 413  
Qy 380 LIPEVFALATLQRLPRCHPLFKLLPHIRYTHINTLARELLVAPGKLIDKSTGLGTGCF 439  
Db 414 LUCEAFAMATLQRLPCHPIYKLLPHIRYTHINTLARELLVAPGKLIDKSTGLGTGCF 473  
Qy 440 SDLIKRNMBQLNYSVLCPLPEDIRARGVEDIPGYVYRDDGMQIWAIGAKSFVSEIYIYPS 499  
Db 474 IYLMSTGLAHTYTNFCLPDSLARGVLAIPNYHYRDDGLKIWAIESFVSEIYIYPS 533  
Qy 500 DTSVQDDQELQAWVREIFSEGFLGRESSGMPSLDTPALVNSSSYHIIALWLLSAEPGDOR 619  
Db 534 DASVQDDSELQAWTGEIFAQAFLGRESSGMPSLDTPALVNSSSYHIIALWLLSAEPGDOR 653  
Qy 620 PLGHYPDEHFTEDAPRRSVAAFQRLIOISKGIRERNRGLALPYTYLDPPLIENSYSI 677  
Db 654 PLGTYPDEHFTEDAPRRSVAAFQRLIOISKGIRERNRGLALPYTYLDPPLIENSYSI 711  
RESULT 8  
US-10-422-264-2  
; Sequence 2, Application US/10422264  
; Publication No. US20030172391A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. US20030172391A1 Lipoxigenase Proteins and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705.0009-00000  
; CURRENT APPLICATION NUMBER: US/10/422,264  
; CURRENT FILING DATE: 2003-04-23  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-422-264-2  
Query Match 51.7%; Score 1864; DB 14; Length 711;  
Best Local Similarity 50.1%; Pred. No. 5.9e-170;  
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;  
Qy 1 MAKCRVRVSTGEACGAGTWDKVSIVTGTGSSPLVPLDLHLGKFSAGAEEDPEVTLPOD 60  
Db 1 MAVYLCVTTGPLYRAGTLDNISVTLVGTGSSPKORLDNRGDRFAPGSQYKIVKRCYAE 60  
Qy 61 VGTVMMLRVHKAPEVSLPLMSFRSDAFCRWFELWLPALHFFCYQWLLEGAGELVLR 120  
Db 61 LGELLALLRVHKS-----RYAFKDSWCSRICVTEPDGSSVSHFFCYQWISGYCTVELR 114  
Qy 121 EGAAKVSWQDHHTLQDQKQELSKQYKWKTYTEGHPRLCDHETVVDL----- 173  
Db 115 PGTARTICQDSLPLLDLHRTRELRAQECYRWKIYAPGPPCMVDVNSFQEMESKKFALT 174  
Qy 174 -----NPKYSAMKNAKLFKHAHSAYTELKVK 199  
Db 175 KTTTCVQDQSSGNRLYPGPKMKIDIPSLMYPENVRYSATKTTISLLFNALPASLGMKUR 234  
Qy 200 GLIDRTGLNRSIREMRLEFRKTPAAEYVFAHQWQEDAFASQFLNGINPVLIRCHSLP 259  
Db 235 GLIDRKGSKWKLDDMQNIFWCHKTFTTKYVTEHWCEDHFFGYQYLVGNVNPVLMHCISLP 294  
Qy 260 NNPFTVDEMVAVPLVPGTSLQALEKGSFLVDHGLSGVHNNILNGKQFQSAAPMTLLH 319

Db 295 SKLPVTNDMVAPLLGQDTCLQTELERGNI FLADYWI LAEAPTHCLNGRQQYVAAPLCLLM 354  
Qy 320 QSSGSGPLLPALAIQLKQTPGPDNPIFLPSDDTWLAKTWVRNSEFYIHEAVTHLLHAH 379  
Db 355 LSP-QGALVPLAIQLSQTGPDSPIFLPTDSEMDWLLAKTWVRNSEFLVHENNTFLCTH 413  
Qy 380 LIPEVFALATLQRLPRCHPLFKLLPHIRYTHINTLARELLVAPGKLIDKSTGLGTGCF 439  
Db 414 LUCEAFAMATLQRLPCHPIYKLLPHIRYTHINTLARELLVAPGKLIDKSTGLGTGCF 473  
Qy 440 SDLIKRNMBQLNYSVLCPLPEDIRARGVEDIPGYVYRDDGMQIWAIGAKSFVSEIYIYPS 499  
Db 474 IYLMSTGLAHTYTNFCLPDSLARGVLAIPNYHYRDDGLKIWAIESFVSEIYIYPS 533  
Qy 500 DTSVQDDQELQAWVREIFSEGFLGRESSGMPSLDTPALVNSSSYHIIALWLLSAEPGDOR 619  
Db 534 DASVQDDSELQAWTGEIFAQAFLGRESSGMPSLDTPALVNSSSYHIIALWLLSAEPGDOR 653  
Qy 620 PLGHYPDEHFTEDAPRRSVAAFQRLIOISKGIRERNRGLALPYTYLDPPLIENSYSI 677  
Db 654 PLGTYPDEHFTEDAPRRSVAAFQRLIOISKGIRERNRGLALPYTYLDPPLIENSYSI 711  
RESULT 9  
US-10-776-871-23  
; Sequence 23, Application US/10776871  
; Publication No. US20040132087A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria Alexandra  
; APPLICANT: Meyers, Rachel  
; APPLICANT: Rudolph-Owen, Laura A.  
; TITLE OF INVENTION: NOVEL HUMAN ENZYME FAMILY MEMBERS AND USES THEREOF  
; FILE REFERENCE: 10448-193001  
; CURRENT APPLICATION NUMBER: US/10/776,871  
; CURRENT FILING DATE: 2004-02-11  
; PRIOR APPLICATION NUMBER: US/10/175,696  
; PRIOR FILING DATE: 2002-06-20  
; PRIOR APPLICATION NUMBER: 10/067,668  
; PRIOR FILING DATE: 2002-02-04  
; PRIOR APPLICATION NUMBER: 60/266,140  
; PRIOR FILING DATE: 2001-02-02  
; PRIOR APPLICATION NUMBER: 09/823,901  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: PCT/US01/10720  
; PRIOR FILING DATE: 2001-04-02  
; PRIOR APPLICATION NUMBER: 60/193,920  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/862,658  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: PCT/US01/16380  
; PRIOR FILING DATE: 2001-05-21  
; PRIOR APPLICATION NUMBER: 60/205,675  
; PRIOR FILING DATE: 2000-05-19  
; PRIOR APPLICATION NUMBER: 09/882,837  
; PRIOR FILING DATE: 2001-06-15  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 31  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 23  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-776-871-23  
Query Match 51.7%; Score 1864; DB 16; Length 711;  
Best Local Similarity 50.1%; Pred. No. 5.9e-170;  
Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;  
Qy 1 MAKCRVRVSTGEACGAGTWDKVSIVTGTGSSPLVPLDLHLGKFSAGAEEDPEVTLPOD 60



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Db 1 MAVYRLCVTTGPGYLRAGTLDNISVTLVGTGCESPKQRLDRMGDRFAPGSVQKYKVRTAE 60
Qy 61 VGTVMRLVRHKAPEVSLPLMSFRSDAWFCRWFELEMLPGAALHFPCCYQWLEGAGELVLR 120
Db 61 LGELLRLVRHKE-----RYAFFRKDSWYCSRICVTEPDGSGVSHFPCYQWIEGYCTVELR 114
Qy 121 EGAAKVSWQDHHTPLQDORQKELESQKMYSWKTYIEGWPCRLDHETVKDLDL----- 173
Db 115 PGTARTICQDSLPLLDHRTRELARQECYRWKIYAPGFCMVDVNSFQEMESDKKFAIT 174
Qy 174 -----NIKYSAMNNAKLFPKHAISATTELKVK 199
Db 175 KTTTCVQDQSSGNRYLPGFPMKIDIPSLMYMPEVRYSATKTISSLFNAIPASLGKMLR 234
Qy 200 GLLDRKGLWRLSREMRLEFRKTPAAEYVFAHQEDAFASQFLNGINPVLIRRHCHSLP 259
Db 235 GLLDRKGSWKLLDDMONIFWCHKTFTTKYVTEHCEDHFFGYQYLVNGVNPVLMHCISL 294
Qy 260 NNFPVTDWMAVPLGPGTSLQAELEKSLFLVDHGILSGVHTNINLNGKPOPSAAPMTLLH 319
Db 295 SKLPVTNDWMAVPLGQDTCLQTELERGNIFLADYWIILAEAPTHCLNGRQQYVAAPLCILW 354
Qy 320 QSSGSGPLLPATIAIQKOTPGDNPFLPDDTDWLLAKTWVRNSEFYIEAVTHLLHAH 379
Db 355 LSP-QGALVPLAIQLSQTPGDSPIFLPTDSEWDLAKTWVRNSEFLVHENTHFLCTH 413
Qy 380 LIPEVFALATLRLQPRCHPLFKLLIPIRYTLHINTLARELLVAPGKLIDKSTGLGTGGF 439
Db 414 LCEAFAMATLRLQPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVDQVTSIGRQGL 473
Qy 440 SDLIKRNMEQNLNYSVLCPLPDIRARGVEDIPGYRRDGMQIWAISFVSEIYIYVPS 499
Db 474 IYLMSTGLAHFTYTNFCLPSLRARGVLAIPNHYRDDGLKIWAIAIESFVSEIYIYVPS 533
Qy 500 DTSVQDDQELQAWREIFSEGLRESSGMPSLLDTREALVQYITWIFTCSAKHAASV 559
Db 534 DASVQDSELQAWTGEIFAQAFGLRESSGFPRLCTPGEMVKFLTAIFNCSAQHAASV 593
Qy 560 QGFDSQVMMNPLPPTMQLPPTPSKGOARPEFIATLPVNSSVYHIIALWLLSAEPGDOR 619
Db 594 QGHDFGAMFNAPSMRQPPQTGTTTLKTYLTLPEVNI SCNNLLFLWLVSEPKDOR 653
Qy 620 PLGHYPDEHTEAPRSVAAPQRLKIQISGIRERNRGLALPYTYLDPPLIENSVS 677
Db 654 PLGTYPDEHTEAPRSVAAPQRLKIQISRDIOERNQGLALPYTYLDPPLIENSVS 711
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## RESULT 10

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US-10-422-264-24
; Sequence 24, Application US/10422264
; Publication No. US20030172391A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander, Jr.
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Nehls, Michael
; APPLICANT: Friedrich, Glenn
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20030172391A1el Lipoxigenase Proteins and Polynucleotides
; TITLE OF INVENTION: Encoding the Same
; FILE REFERENCE: 7705.0009-00000
; CURRENT APPLICATION NUMBER: US/10/422,264
; CURRENT FILING DATE: 2003-04-23
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 867
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-422-264-24
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Query Match 51.7%; Score 1864; DB 14; Length 867;  
Best Local Similarity 50.1%; Pred. No. 8.1e-170;

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Matches 360; Conservative 112; Mismatches 198; Indels 48; Gaps 3;
Qy 1 MAKCRVTVSTGEACGAGTWDKVSIVVGTGHSPLVLDHLGKEFSAGAEEDFEVTLPOD 60
Db 157 MAVYRLCVTTGPGYLRAGTLDNISVTLVGTGCESPKQRLDRMGDRFAPGSVQKYKVRTAE 216
Qy 61 VGTVMRLVRHKAPEVSLPLMSFRSDAWFCRWFELEMLPGAALHFPCCYQWLEGAGELVLR 120
Db 217 LGELLRLVRHKE-----RYAFFRKDSWYCSRICVTEPDGSGVSHFPCYQWIEGYCTVELR 270
Qy 121 EGAAKVSWQDHHTPLQDORQKELESQKMYSWKTYIEGWPCRLDHETVKDLDL----- 173
Db 271 PGTARTICQDSLPLLDHRTRELARQECYRWKIYAPGFCMVDVNSFQEMESDKKFAIT 330
Qy 174 -----NIKYSAMNNAKLFPKHAISATTELKVK 199
Db 331 KTTTCVQDQSSGNRYLPGFPMKIDIPSLMYMPEVRYSATKTISSLFNAIPASLGKMLR 390
Qy 200 GLLDRKGLWRLSREMRLEFRKTPAAEYVFAHQEDAFASQFLNGINPVLIRRHCHSLP 259
Db 391 GLLDRKGSWKLLDDMONIFWCHKTFTTKYVTEHCEDHFFGYQYLVNGVNPVLMHCISL 450
Qy 260 NNFPVTDWMAVPLGPGTSLQAELEKSLFLVDHGILSGVHTNINLNGKPOPSAAPMTLLH 319
Db 451 SKLPVTNDWMAVPLGQDTCLQTELERGNIFLADYWIILAEAPTHCLNGRQQYVAAPLCILW 510
Qy 320 QSSGSGPLLPATIAIQKOTPGDNPFLPDDTDWLLAKTWVRNSEFYIEAVTHLLHAH 379
Db 511 LSP-QGALVPLAIQLSQTPGDSPIFLPTDSEWDLAKTWVRNSEFLVHENTHFLCTH 569
Qy 380 LIPEVFALATLRLQPRCHPLFKLLIPIRYTLHINTLARELLVAPGKLIDKSTGLGTGGF 439
Db 570 LCEAFAMATLRLQPLCHPIYKLLPHTRYTLQVNTIARATLLNPEGLVDQVTSIGRQGL 629
Qy 440 SDLIKRNMEQNLNYSVLCPLPDIRARGVEDIPGYRRDGMQIWAISFVSEIYIYVPS 499
Db 630 IYLMSTGLAHFTYTNFCLPSLRARGVLAIPNHYRDDGLKIWAIAIESFVSEIYIYVPS 689
Qy 500 DTSVQDDQELQAWREIFSEGLRESSGMPSLLDTREALVQYITWIFTCSAKHAASV 559
Db 690 DASVQDSELQAWTGEIFAQAFGLRESSGFPRLCTPGEMVKFLTAIFNCSAQHAASV 749
Qy 560 QGFDSQVMMNPLPPTMQLPPTPSKGOARPEFIATLPVNSSVYHIIALWLLSAEPGDOR 619
Db 750 QGHDFGAMFNAPSMRQPPQTGTTTLKTYLTLPEVNI SCNNLLFLWLVSEPKDOR 809
Qy 620 PLGHYPDEHTEAPRSVAAPQRLKIQISGIRERNRGLALPYTYLDPPLIENSVS 677
Db 810 PLGTYPDEHTEAPRSVAAPQRLKIQISRDIOERNQGLALPYTYLDPPLIENSVS 867
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## RESULT 11

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US-10-275-998-3
; Sequence 3, Application US/10275998
; Publication No. US20040023354A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAS, Debopriya
; APPLICANT: REDDY, Roopa
; APPLICANT: YAO, Monique G.
; APPLICANT: NGUYEN, Darniel B.
; APPLICANT: LU, Yan
; APPLICANT: TRIBOULEY, Catherine M.
; APPLICANT: YUS, Henry
; APPLICANT: KHAN, Farrah A.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: AU-YOUNG, Janice
; APPLICANT: LAL, Preeti
; APPLICANT: KEARNEY, Liam
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: DING, Li
; APPLICANT: THORNTON, Michael
; TITLE OF INVENTION: LIPID METABOLISM ENZYMES
```

; FILE REFERENCE: PI-0095 USN  
; CURRENT APPLICATION NUMBER: US/10/275,998  
; CURRENT FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: US 01/15210  
; PRIOR FILING DATE: 2001-05-11  
; PRIOR APPLICATION NUMBER: US 60/203,511  
; PRIOR FILING DATE: 2000-05-11  
; PRIOR APPLICATION NUMBER: US 60/207,903  
; PRIOR FILING DATE: 2000-05-25  
; PRIOR APPLICATION NUMBER: US 60/210,150  
; PRIOR FILING DATE: 2000-06-07  
; PRIOR APPLICATION NUMBER: US 60/213,392  
; PRIOR FILING DATE: 2000-06-23  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PERL Program  
; SEQ ID NO 3  
; LENGTH: 711  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. US20040023354A1 7473234CD1  
US-10-275-998-3

Query Match 51.6%; Score 1858; DB 15; Length 711;  
Best Local Similarity 50.0%; Pred. No. 2.2e-169;  
Matches 359; Conservative 112; Mismatches 199; Indels 48; Gaps 3;

QY 1 MAKCRVYVSTGEACAGTWDKVSIVTGHGSPVLPVLDHLGKFSAGAEEDFEVTLPOD 60  
DB 1 MAVYLCVVTGPVLRAGTLDNISVLTGCGSPKQRLDRMGDRDPAGSVQKYKVRCTAE 60  
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAWFCRWFELEWLPFGAALHPPCYQWLLEGAGELVLR 120  
DB 61 LGELLLLRVHKE-----RYAFPRKDSWYCSRICVTEPDGSGVSHPPCYQWIEGYCTVELR 114  
QY 121 EGAAKVSWQDHHTPTLQDORQKELSRQKMYSWKTYIEGWPRCLDHTETVKDLDL----- 173  
DB 115 PGTARTICQDSLPLLDHRTRELRARQECYRWKIYAPGFPVCMVDVNSFQEMESDKKFAIT 174  
QY 174 -----NIKYSAMKNALFFKAHSAYTELKVK 199  
DB 175 KTTTCVQDGSNGRYLPFGPMKIDIPSLMYEPNVRYSATKTIISLLFNAIPASLGMLR 234  
QY 200 GLLDRTGLWRSIREMRLENFRKTPAAEYVFAHWQEDAFASQFLNGINPVLIRCHSLP 259  
DB 235 GLLDKSGWKLLDQNIWFCHKTFTTKVYTHWCEDHFFGVQYLVGNVPMVLMHCISLP 294  
QY 260 NNFPVTDEMVAVLPGTSLQAELEKGSFLVDHGILSGVHTNINLNGKQFSAAPMTLLH 319  
DB 295 SKLPVTNDMVAPLLGQDTCQTELERGNIFLADYWLAEAPTHCLNGRQYVAAAPLCILW 354  
QY 320 QSSGSGFLPIALQKOTPGDNPIFLPSDDTDWLLAKTWRNSEFYIHEAVTHLLHAH 379  
DB 355 LSP-QQALVPLAQLSQTGPGSPIFLPTDSEWDMLLAKTWRNSEFLVHNNTHFLCTH 413  
QY 380 LIPEVFALATLQRLPCHPLFKLLIPHYRTHINTLARELLVAPGKLDKSTGLGTGTF 439  
DB 414 LICEAFAMAILQLPCHPIYKLLPHRYTQVNTIARATLNLPEGLVDQVTSIGRQL 473  
QY 440 SLLIKENMBQLNYSVLCLEPDIRARGVEDIPGYYYRDGQWIGAIKFSVSIYIYPS 499  
DB 474 IYLMSTGLAHFTYTNFCLPDSLARGVLAIPNHYRDDGLKIWAALIESFVSIYGYPS 533  
QY 500 DTSVQDDQELQAWRIESEGFLGRSSGMPSLDTRALVQYITWVITCSAKHAANVS 559  
DB 534 DASVQDDSELAWTGIFQAFLGRSSGFPRLCTPGEMVFLTAIIIFNCQAHAANVS 593  
QY 560 GQPDSCVWPNLPPTMQLPPPTSQKQARPEFIATLPAVNSSSYHIIALWLLSAEPGDQR 619  
DB 594 GQMTLGAMFNAPSSWRQPPQTGTTTLKTYLDLPEVNI SCNNLLLLFWLSQBPQDQR 653  
QY 620 PLGHYPDEHFTEDAPRRSVAAPFQRLQIQISKIRERNRGLALPYTYLDPPLIENSVS 677

DB 654 PLGTYPDEHFTEDAPRRSIAAPQSRQAQISRDIQERNOGLALPYTYLDPPLIENSVS 711  
RESULT 12  
US-09-853-053-2  
; Sequence 2, Application US/09853053  
; Patent No. US20020037554A1  
; GENERAL INFORMATION:  
; APPLICANT: Braash, Alan  
; APPLICANT: Boeglin, William  
; APPLICANT: Kim, Richard  
; TITLE OF INVENTION: ISOLATED AND PURIFIED 12R-LIPOXYGENASE PROTEIN AND NUCLEIC ACIDS  
; FILE REFERENCE: Attorney Docket No. US20020037554A1 1242/7/2  
; CURRENT APPLICATION NUMBER: US/09/853,053  
; CURRENT FILING DATE: 2001-05-11  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 2  
; LENGTH: 701  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-053-2

Query Match 49.8%; Score 1795; DB 9; Length 701;  
Best Local Similarity 47.9%; Pred. No. 2.6e-163;  
Matches 339; Conservative 121; Mismatches 210; Indels 38; Gaps 3;

QY 1 MAKCRVYVSTGEACAGTWDKVSIVTGHGSPVLPVLDHLGKFSAGAEEDFEVTLPOD 60  
DB 1 MATYKRVATGTDLLSGTRDSISLTIIVGTQGESHKQLLNHFGRDPATGAVGYTVQCPOD 60  
QY 61 VGTVLMRLVHKAPPEVSLPLMSFRSDAWFCRWFELEWLPFGAALHPPCYQWLLEGAGELVLR 120  
DB 61 LGELIIIRLHKE-----RYAFFPKDPWYCNVVOICAPNGRIYHPAPQWMDGYETLALR 114  
QY 121 EGAAKVSWQDHHTPTLQDORQKELSRQKMYSWKT----- 154  
DB 115 EATGKTTADDLSLPVLLHREKBEIRAKQDFYHWRVFLPGLPSYVHIPSPYRPPVRRHRPNR 174  
QY 155 -----YIRGWRCLDHEVTVDLDLNIKYSAMKNALFFKAHSAYTELKVGLLDRTGLWR 209  
DB 175 PEWNGYIPGFPILINFKATKFLNLMRYSLFKTASFFVRLGPMALAFKVRGLLDCKHSWK 234  
QY 210 SILREMRLENFRKTPAAEYVFAHWQEDAFASQFLNGINPVLIRCHSLPNNFPVTDEM 269  
DB 235 RLKDIRKIFPGKSVSVYVAEHAEDTFFGVQYLVGNVPGILIRCTRIPDKFPVTDMMV 294  
QY 270 APVLPGTSLQAELEKGSFLVDHGILSGVHTNINLNGKQFSAAPMTLLHQSSGSGPLLP 329  
DB 295 APFLGEGTCLQAELEKGNILADYRIMEGIPTVELSGRKHHCAPLCILH-FGPGKOMP 353  
QY 330 TAIQLKOTPGDNPIFLPSDDTDWLLAKTWRNSEFYIHEAVTHLLHAHLIPEVPALAT 389  
DB 354 TAIQLSQTGPGDPIFLPSDSEWDMLLAKTWRVYAEFYSHAIAHLLETHLLTAFAFCLAL 413  
QY 390 LRQLPCHPLFKLLIPHYRTHINTLARELLVAPGKLDKSTGLGTGFSGLIKRNMEO 449  
DB 414 LENLPMCHPLYKLLIPHYRYTQVINSIGRAVLLNEGGLSAGMSLVGEFAGVMVRLSE 473  
QY 450 LNYSVLCLEPDIRARGVEDIPGYYYRDGQWIGAIKFSVSIYIYPSDTSVQDDQBL 509  
DB 474 LTYDSLPLPNDPVERGVQDLPGYYYRDDS LVAWNALEKYVTETIIYYYPDSAAVEGDPBL 533  
QY 510 QAWVREIIESEGFLGRSSGMPSLDTRALVQYITWVITCSAKHAANVSQGFDSQVMP 569  
DB 534 QSWQVEIFKCELLGRSSGFPRLCTVPFELIRYTVITCSAKHAANVTQMEFTAMP 593  
QY 570 NLPPTMQLPPPTSQKQARPEFIATLPAVNSSSYHIIALWLLSAEPGDQRPLGHYPDEH 629  
DB 594 NFPASMRNPPTQKGLTLETFTMDLPDVKTYCTILLVLTLSRFPDDEPRLGHYPDIHF 653  
QY 630 TEDAPRRSVAAPFQRLQIQISKIRERNRGLALPYTYLDPPLIENSVS 677



US-10-422-264-10  
; Sequence 10, Application US/10422264  
; Publication No. US20030172391A1  
; GENERAL INFORMATION:  
; APPLICANT: Turner, C. Alexander, Jr.  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Nehls, Michael  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. US20030172391A1el Lipoxigenase Proteins and Polynucleotides  
; TITLE OF INVENTION: Encoding the Same  
; FILE REFERENCE: 7705.0009-00000  
; CURRENT APPLICATION NUMBER: US/10/422,264  
; CURRENT FILING DATE: 2003-04-23  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 10  
; LENGTH: 615  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-422-264-10

Query Match 40.6%; Score 1464; DB 14; Length 615;  
Best Local Similarity 47.5%; Pred.No.1.8e-131;  
Matches 286; Conservative 95; Mismatches 173; Indels 48; Gaps 3;

QY	1	MAKCRVRVSTGEACGAGTWDKVSIVGTHGESPLVPLDLHLGKFSAGAEEDFEVTLPOD	60
Db	1	MAVYRLCVTTGPYLRAGTLNDSIVLVGTCGESPKQRLDRMGDRDPAGSVQYKVRCTAE	60
QY	61	VGTVLMLRVHKAPPEVSLPLMSFRSDANFCRWFELEWLFGAALHFFCYQWLEGAGELVLR	120
Db	61	LGELJLLLRVHKE-----RYAFPRKDSWYCSRICVTEPDGVSVSHFPCYQWIEGYCTVELR	114
QY	121	EGAAKVSWQDHPTLQDQKQKLESGRQKMYSWKTYIEGHPRLCDHETVKDLDL-----	173
Db	115	PGTARTICQDSLPLLDLHRTRELRARQECYRWKIYAPGPPCMVDVNSFQEMESDKKALT	174
QY	174	-----NIKYSAMKNAKLFFKAHSAYTELVK 199	
Db	175	KTTTCVDQDSSGNRYLPFGPMKIDIPSLMYMEPNVRSATKTISSLFNAIPASLGOMKLR	234
QY	200	GLLDRITGLWRSLSREMRLLFNFRKTPAAEYVFAHWQEDAFASQFLNGINPVLIRRCHSLP	259
Db	235	GLLDRKGSWKLLDDMQNIWCHKTFTKYVTEHWCEDEHFFGYQLNGVNPVMLHICISLP	294
QY	260	NNPPTVDENWAPVLGPGTSLQAELEKGSFLVDHGIILSGVHTNILINGKQFSAAPMTLLH	319
Db	295	SKLPVTNDWVAPLLGQDTCLOTLELERNIFLADYWLAEAPTHCLNGRQQYVVAAPLCLLW	354
QY	320	QSSGSGPLPIAQLKQTPGPNPIELPSDDTDWMLLAKTWVRNSEFYIHEAVTHLLHAH	379
Db	355	LSP-QQALVPLAIQUSQTGPGDSPIFPLPTDSEWMLLAKTWVRNSEFLVHENTHFLCTH	413
QY	380	LIPEVPALATRLQPLRCHPLFKLLIPHYRYTLHINTLARELLVAPKLDKSTGLTGTF	439
Db	414	LLCEAFAMATLQLPLCHPIYKLLPHTYTLQVNTIARATLLNPEGLVDQVTSIGROQL	473
QY	440	SLIKRMNQNLNYSVLCLPEDIRARGVEDIPGYVYRDDQGIWGAIKSPVSEIVSIYYP	499
Db	474	IYLMSTGLAHFTYTNFCLPDSLARGVLAIPNHYVRDDGLKIWAATIESFVSEIVGYYP	533
QY	500	DTSVQDDQELQAWREIFSEGLFRESSGMPSLDTRALVQYITWVIFTCSAKHAAYSS	559
Db	534	DASVQDDSELQAWTGEIFAQFLGRESSGPPSRCLCTPGEMVRFELTAIIFNCSAQHAAYNS	593
QY	560	GQ 561	
Db	594	GQ 595	

Search completed: July 18, 2005, 22:06:55  
Job time : 107.244 secs